

CC cell. The B chain binds to cell receptors and facilitates the
CC transfer of the substrate to the A chain. The A chain is responsible
CC for cell agglutination (lectin activity). It binds to beta-D-
CC galactopyranoside moieties.
CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC SUBUNIT: Disulfide-linked dimer of A and B chains.
CC DOMAIN: The B chain is composed of two domains, each domain
CC consists of 3 homologous subdomains (alpha, beta, gamma).
CC FUNCTION: The MAJOR A CHAIN IS GLYCOSYLATED IN POSITION 45 AND THE
CC MAJOR B CHAIN IS GLYCOSYLATED IN POSITION 45. BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYRS 2 RIP SUBUNIT.
CC SIMILARITY: Contains 2 rich B-type lectin domains.
CC CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF. 1, REF. 2 AND REF. 3).
CC DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 31 of February 2003;
CC WWW=ftp://www.expasy.org/spotlight/articles/spl1031.html".
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CC
CC EMBL, X01179; CAA6639.1; -
CC EMBL, X01179; CAA6639.1; -
CC EMBL, X01388; CAA6630.1; -
CC EMBL, A12892; CAA1058.1; -
CC PIR, A24041; R1CSD.
CC
CC PDB; 2RA1; 31-JAN-94.
CC PDB; 1APG; 31-JAN-94.
CC PDB; 1MP; 31-OCT-93.
CC PDB; 1176; 14-JAN-98.
CC PDB; 11PT; 14-JAN-98.
CC PDB; 11EQ; 14-JAN-98.
CC PDB; 11ES; 31-OCT-93.
CC PDB; 10BT; 16-JUN-97.
CC PDB; 1BR5; 02-SEP-98.
CC PDB; 1BR6; 02-SEP-98.
CC PDB; 1113; 16-JAN-02.
CC PDB; 1114; 16-JAN-02.
CC PDB; 1119; 16-JAN-02.
CC GlycoSiteDB; P02879; -
CC InterPro; IPR00772; Ricin_3_lectin.
CC InterPro; IPR00774; Ricin_3_lectin.
CC Pfam; PF00161; R1P; 1-lectin; 6.
CC PRINTS; PR00396; SHIDAICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS00275; SHIG_RICIN; 1.
CC Plant defense; Hydrolase; Protein synthesis inhibitor; toxin; Repeat;
CC Glycoprotein; Lectin; Signal; 3D-structure.
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Best Local Similarity 92.2%; Pred. No. 8,1e-108;
Matches 235; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
QY 1 YERLRVTHQTGGVEYFRFTLLRDYVSSGFSNEIPLLQSTIPVSDAQRFVLVELTN 60
DB 1 YERLRVTHQTGGVEYFRFTLLRDYVSSGFSNEIPLLQSTIPVSDAQRFVLVELTN 60
QY 61 QQDSXTAIDVTNAYVAYQAGQSYFLADAPRGASTHLFTGTRXSSLPFGXSYDLE 120
DB 61 QQDSVTAAIDVTNAYVAYQAGQSYFLADAPRGASTHLFTGTR-SELPFGXSYDLE 119
QY 121 FYAGHDDIPLGKXQVYALRPGSTFYQARSILLIOMSEARFNELRWYRQX 180
DB 120 FYAGHDDIPLGKXQVYALRPGSTFYQARSILLIOMSEARFNELRWYRQY 179
QY 181 INSGXSFPLDYHMLETSWQSQSTOVQSTGDFVFNPRXLAIXGNFVLTANRXVIA 240
DB 180 INSGXSFPLDYHMLETSWQSQSTOVQSTGDFVFNPRXLAIXGNFVLTANRXVIA 239
QY 241 LAIMLVGGERPSS 255
DB 240 LAIMLVGGERPSS 254

RESULT 5

ABRC ABRP STANDARD; ERT; 562 AA.
AC P28550;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abirin-c precursor [Contains: Abirin-c A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abirin-c B chain)]
DE Abirus Precursor [Contains: Abirus A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abirus B chain (rRNA N-glycosidase)]
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID:3816;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=91266957; PubMed=2050149;
RA Wood K.A., Lord J.M., Nawzynczak E.J., Piatak M.;
RT "Preproabrin: genomic cloning, characterization and the expression of
the A chain in *Abirus*." *Plant Cell* 10:131-140 (1998).
RI Eur. J. Biochem. 198:722-732 (1991).
CC -I- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE
B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -I- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -I- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -I- INACTIVATING PROTEIN FAMILY TYPE 2 Rip SUPERFAMILY.
CC -I- SIMILARITY: Contains 2 ricin B-type lectin domains.
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entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X55667; CAA39202.1; -
DR HSS: S16024; S16024.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.

Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00459; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGARICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 34
FT CHAIN 35 285
FT ACT_SITE 285 285
FT CHAIN 286 562
FT CHAIN 563 562
FT DOMAIN 307 434
FT DOMAIN 437 561
FT REPEAT 317 359
FT REPEAT 360 400
FT REPEAT 403 435
FT REPEAT 448 483
FT REPEAT 487 526
FT REPEAT 529 562
FT ACT_SITE 198 198
FT DISULFID 281 303
FT DISULFID 320 348
FT DISULFID 451 464
FT DISULFID 490 507
FT MOD_RES 35 35
FT CARBOHYD 234 234
FT CARBOHYD 395 395
FT CARBOHYD 435 435
SQ SEQUENCE 562 AA; 62817 MW; 1FD0ABC7D7BA6278 CRC64;
Query Match 43.8%; Score 113.9; Db 1; Length 562;
Basic Local Similarity 46.1%; Pred. No. 1.1e-190; Indels 11; Gaps 9;
Matches 242; Conservative 82; Mismatches 82; 91
QY 9 THOTGKXFRFTLLRDYVSSGFSNEIPLLQSTIPVSDAQRFVLVELTNQXSDXTA 68
DB 43 TEGATSSQKQFIALRQL-TGLIHDPVLPDPT-TVERNRVITVELSNRESIEV 100
QY 69 AIDVTNAYVAYQAGQSYFLADAPRGASTHLFTGTRXSSLPFGXSYDLEIRYAGH-RD 127
DB 101 GIDVTNAYVAYQAGQSYFLADAPRGASTHLFTGTR-SELPFGXSYDLEIRYAGH-RD 127
QY 128 QIPGLIXQVYALRPGSTFYQARSILLIOMSEARFNELRWYRQXINSGXSF 187
DB 160 EISGLQALTHAIFLRSGASNEEKARTLIVIIOMASEARFYINRQVGSIRGTAF 219
QY 188 LPXVYHLETSWQSQSTOVQSTGDFVFNPRXLAIXGNFVLTANRXVIAIIMLF 246
DB 220 QPDPAMLSLNNNDNLSCGQSQVDTPFNNVILLINRQVGVVDSLSHPTVAVIALMF 279
QY 247 YCGERPSSSVYVPLVIRPVADVDVCSAS-EPTVIRVGRXKXGVYRDDDFDGNQIQ 305
DB 280 YCVP-FNANGS---FLIRSVESKICSRVEYFVIRQSGRQCVVDYDYGNGRII 335
QY 306 LWFPSKNNNDNLQATIKRXTIRSGSLTVGTAGVYVWFPCNTAVAEATVQWKN 365
DB 336 AMKCKORLEBNQJTLKSKRTIRSGKLTTEGVAPQNYVMYDCTSAVAEATVWEIMN 395
QY 366 GTIINPRNLVLAASSGIKGTTITVQTLDTYTGQGMAGNDTAPREVTIYGFRLCWEN 425
DB 396 GTIINPKSALVLAESSSSNGGTTITVQNEVLMRQWRTGNTSPFVTSISGYSLLCMAQ 455
QY 426 XGVSVVETPCXSSQXQXVAYLVDGDSIRPQDQCLTGDVSDVTVINIVSCSXEXXQ 485
DB 456 GSNVWLADCNKKQ-QVALYTDGSIIRSVQNTNCLTSKDHQKGSPIVLMACSNQASQ 514
QY 486 RWVFTNEALIMLXXXXVQANPKLRITITPATGKNGQWL 530
DB 515 KNUFDGDSIYNLHDDWMDVKSQDPSLKEILLPHYHGFQIWL 559

RESULT 6
 ID ABIN-ABRP STANDARD; PRT; 527 AA.
 AC Q06077; P61374; (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abin-b precursor [Contains: Abin-b A chain (rRNA N-glycosidase)
 (BC 3.2.2.22); Abin-b B chain].
 OS Abus precatorius (Indian licorice) (Crab's eye).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosid 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 NCBI_TaxID=3616;
 XP MEDLINE=93132799; PubMed=8421313;
 RP HUNG C.-H., LEE M.-C., LEE T.-C., LIN J.-Y.;
 RA "Primary structure of three distinct isoabrin determined by cDNA
 RT sequencing. Conservation and significance.";
 RL J. Mol. Biol. 229:263-267(1993).
 RN [2]
 RC SEQUENCE OF 260-527.
 RD TISSUE=seed;
 RA MEDLINE=93169023; PubMed=7763422;
 RP KIMURA M., SUMIZAWA T., FUNATSU G.;
 RA "The complete amino acid sequences of the B-chains of abrin-a and
 RT abrin-b, two distinct isoforms of the proteinase inhibitor, abrin."
 RL Biochem. Biophys. Res. Commun. 171:166-169(1990).
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific asparagine on the 28S rRNA. A AND B CHAINS
 CC -!- SUBUNIT: DISULFIDE-BINDING DIMER OF TWO DOMAINS. EACH DOMAIN
 CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; M98345; AAA32625.1; --
 DR PIR; S32430; S32430.
 DR HSSP; P11140; 1ABR.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00196; SHIGARICIN.
 DR SMART; SM00456; RICIN; 2.
 DR PROSITE; PS00271; SHIGARICIN.
 DR PROSITE; PS00271; SHIGARICIN.
 DR Plant defense; Hydrolases; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
 FT CHAIN 1 250 ABRIN-B A CHAIN.
 FT PEPTIDE 251 260 LINKER PEPTIDE.
 FT CHAIN 261 527 ABRIN-B B CHAIN.
 FT DOMAIN 272 339 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 402 526 RICIN B-TYPE LECTIN 2.
 FT REPEAT 282 324 1-ALPHA.

FT REPEAT 325 365 1-BETA.
 FT REPEAT 368 400 1-CANMA.
 FT REPEAT 413 448 2-ALPHA.
 FT REPEAT 452 491 2-BETA.
 FT REPEAT 494 527 2-GANMA.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT DISULFID 448 448 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 449 449 BY SIMILARITY.
 FT DISULFID 450 450 BY SIMILARITY.
 FT DISULFID 451 451 BY SIMILARITY.
 FT DISULFID 452 452 BY SIMILARITY.
 FT MOD_RES 455 472 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CONFLICT 282 282 N -> D (IN REF. 2).
 FT CONFLICT 291 291 D -> N (IN REF. 2).
 FT CONFLICT 298 298 AE -> EQ (IN REF. 2).
 FT CONFLICT 378 378 L -> N (IN REF. 2).
 FT CONFLICT 426 426 Y -> M (IN REF. 2).
 FT CONFLICT 428 428 Y -> D (IN REF. 2).
 FT CONFLICT 431 431 N -> S (IN REF. 2).
 FT CONFLICT 484 484 R -> K (IN REF. 2).
 FT CONFLICT 491 491 N -> S (IN REF. 2).
 FT CONFLICT 493 493 H -> Y (IN REF. 2).
 FT CONFLICT 502 502 K -> G (IN REF. 2).
 FT CONFLICT 509 509 E -> Q (IN REF. 2).
 FT CONFLICT 513 513 H -> W (IN REF. 2).
 FT CONFLICT 516 516 H -> T (IN REF. 2).
 SQ SEQUENCE 527 AA; 59114 MW; 3253AE450CB9494A CRC64;
 Query Match 42.5%; Score 1113; DB 1; Length 527;
 Best Local Similarity 45.5%; Pred No. 3, 3e-102; Indels 12; Gaps 10;
 Matches 239; Conservative 83; Mismatches 191;
 QY 9 TQGTGXYFFRITLIRDYVSGSPFSEIPLLRQSTIPVSDAQRFLVRLNQGMDXTA 68
 DB 9 TEGATSGYKQFEALRQRL-TGGLIHGIPVLPDPT-TLOERNYISVLSNDSIESA 66
 QY 69 AIDVNNXYVAYQAGQSYFLRDAAPRAETHLPTGTRXSSLPFGSYVDLRYAGH-RD 127
 DB 67 GIDVSNVYVAYAGNRSYFLRDAAPRAETHLPTGTRXSSLPFGSYVDLRYAGH-RD 125
 QY 128 QIPGLXQLQISYALRYXPGSGTQASRILITQWISSEAFNFILMXKQSGXSP 187
 DB 126 QIPGLQALRHAIISFLQS-GTDDQELARTLIVIIQWSEAAARYFISYVGVSRINTAF 184
 QY 188 LPDYMLELSTSGGQSQSTQVQSTGTFVNFNFXLAXGNFVTLXNV-RXVITSLALMLF 246
 DB 185 QPDAMISLENNMDNLGSGQSQVQDPTFNATVLRVNNQFVIVDSITHQSVALLALMF 244
 QY 247 VCGERSSSDVVRVPIRVIRVIADDTVCSAS-BPTVRIVGRXGMXVDVDDDFHGNQIQ 305
 DB 245 VCNPF-PNMQS---PILRSIVKSKISGRYEPFVRIGRMGMCDVDYDGHNGNII 300
 QY 306 LPPSKNNDPNQWLTIKEDYTERNSGLITTYGTAGYVMIFQCVATREMTWIKWN 365
 DB 301 AMKKORLEENQLWTKSDNTRNSGKCLITTEGYPAGNYVMIVDCTSAVAEATYWEINDN 360
 QY 366 GTINPRSNVLAASSSGIKGTLVQTLVDTLQGWLAGNDTAPREVTIYGFRLCMESN 425
 DB 361 GTINPKSALVLAASSSGMGTLVQTEYMLMQGNETGNNTSPFVTSISGSDLCMQAQ 420
 QY 426 XGSVWETCSXSNQXWALVGGSRPKQNDQCLTXGRDSVTVTNIVSCSXXSXQ 485
 DB 421 GSNVLAYCDNNKQO-QWALVDTGTSRVSNTKNCUTSNDKGGSPVLMACSNQMASQ 479
 QY 486 RVVTFEXALINLXXXXXVQAQANPKLRILIIYPATGKNQMWL 530
 DB 480 RVLFRDNGSIYNLHDDMVNVERSDPSLKEILLHPYHGKNGQWL 524

RESULT 7
AGGLUTININ
AC AGGLUTININ STANDARD; PRT; 564 AA.
DT 01-JAN-1988 (Rel. 06, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidia I; Malpighiales; Euphorbiaceae; Ricinus.
BX Ref_taxisID=3986;
PF SEQUENCE FROM N.A.
RA MEDLINE=86059449; PubMed=2999130;
RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
RT "The primary sequence of Ricinus communis agglutinin. Comparison with
RL ricin.";
RL J. Biol. Chem. 260:15682-15686(1985).
RP SEQUENCE OF 303-564.
RC TISSUE=Seed;
RA Araki T., Yoshioka Y., Funatsu G.;
RT "The complete amino acid sequence of the B-chain of the Ricinus
communis agglutinin isolated from large grain castor bean seeds.";
RL Biochim. Biophys. Acta 872:277-285(1986).
RN [3]
RP SEQUENCE OF 303-337.
RX MEDLINE=80178723; PubMed=6768555;
RA Lin T.-S., Li S.-L.;
RT "Purification and physicochemical properties of ricins and
RL agglutinins from Ricinus communis";
CC Eur. J. Biochem. 105:453-459(1980).
CC -I- CATALYTIC ACTIVITY: Endonuclease.
CC -I- SPECIFICITY: IN THE N-TERMINAL SECTION. BELONGS TO THE RIBOSOME-
CC -I- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -I- SIMILARITY: Contains 2 ricin B-type lectin domains.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
DR ENBL; M12089; AAB33869.1; --
DR ENBL; S40368; AAB22584.1; --
DR PIR; A24261; RLCBAG.
DR HSSP; P02879; IIR6.
DR GlycoSuiteDB; P06750; --
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; P00396; SHIGARICIN.
DR PROSITE; PS00231; RIBIN_B_LECTIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 290 AGGLUTININ A CHAIN.
FT PROPEP 291 302 LINKER PEPTIDE.
FT CHAIN 303 564 AGGLUTININ B CHAIN.
FT DOMAIN 309 436 AGGLUTININ B CHAIN.
FT DOMAIN 439 563 RICIN B-TYPE LECTIN 1.
FT REPEAT 319 361 RICIN B-TYPE LECTIN 2.
FT REPEAT 362 402 1-BETA.
FT REPEAT 403 437 1-GAMMA.

PT REPEAT 450 485 2-ALPHA.
PT REPEAT 489 528 2-BETA.
PT REPEAT 531 558 2-GAMMA.
FT ACT_SITE 200 200 BY SIMILARITY.
FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
FT DISULFID 322 341 BY SIMILARITY.
FT DISULFID 365 382 BY SIMILARITY.
FT DISULFID 453 466 BY SIMILARITY.
FT DISULFID 492 509 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLNAC). (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLNAC).
FT CARBOHYD 397 397 N-LINKED (GLNAC).
FT CARBOHYD 437 437 N-LINKED (GLNAC).
FT CONFLICT 331 331 F -> T (IN REF. 2).
FT CONFLICT 362 362 N -> D (IN REF. 2).
FT CONFLICT 374 374 R -> G (IN REF. 2).
FT CONFLICT 404 404 R -> T (IN REF. 2).
FT CONFLICT 552 552 F -> V (IN REF. 2).
SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;
Query Match 42.4%; Score 1109.5; DB 1; Length 564;
Best Local Similarity 45.2%; Pred. No. 7.9e-14; Indels 19; Gaps 10;
Matches 242; Conservative 79; Mismatches 195;
QY 9 THQTGKYEPRFTLLRYYSSGS-PSNEIPLL-RQSTIPVSDAQRFVLVELTNOQXDSX 66
DB 37 TADATVSTNFRVRSHTTGDVNRHEIPVLPNRVGLPIS--CRFVLVLSNHAELSV 94
QY 67 TAAIDVTNXYVAYQGDQSYFLR-DAPRGAE--THFTGTTTRASSLPFKSGXYDLERYA 123
DB 95 TLALDVTNAYVYCGRAGNSAYFFHPNQEDAEALTHLFTDQVQSTFAPGNDYRLBQLG 154
QY 124 GRHDIPLGIQLIQSVLAL---RFGSGSTXQARISILILQVISEARSPNPLKRXQX 180
DB 155 GURENILETGTLEDALNLYVYVSTQGTQPTLANSFVCLQWISSEARSPQIEGEMTR 214
QY 181 INSGKSLPDXYMLELTSWGQSTQVQHSVDGVNFXELALXKGNFVTLXNVRXVIAV 240
DB 215 IRYNRSEADPSVITLLENSMGLSTALQSNQGFASFLQORNGSKFNVDVSLPI 274
QY 241 LAIMEFYVCCRPSSSVYRMPVIRPVAD---DVTCASASEPFIIVKXGKXVYVDRDD 297
DB 275 IALVYRCAPPSSQ----FSLILFVFPVFNADV-CHDFEPIVAVNGNLGVCVYVSEE 329
QY 298 FHDGQIOLMKSNDNDQNTLTKESYITNSGCLTGTGTVAGVYVWIFDCNTAVREA 357
DB 330 FDEENPLQWPKCNTDNNQLWLTLSKSTITNSGKLTLSKSSPPQQWVYVNCSTATVGA 389
QY 358 TIHQIWNQNTIINERNVLAASSGKGTTLVTQTLDTLGGQWLAGNCTAPREVITVGF 417
DB 390 TRNQIWNQNTIINPRGLVLAATNSGCTKLTQVITVANSQWLPNTNTPQFPYTVGL 449
QY 418 RDLCEENKSGSVWYETCKSXQXVXWALYVIGSGIRPKQNDQCLTKGKDSVSTVINIVS 477
DB 450 YGMCLOANGKRWLEDCSTSEKAEQ-QWALYAGSGIRPKQNDQCLTKGKDSVSTVINIVS 508
QY 478 CSXKX 532
DB 509 CGPSSQGRWFNDKDTILNLYNGLVLDVRRSDPSLKLQILVHFPFGHNLQIWLJPL 563
RESULT 8
NIGR SAMMI
ID NIGR SAMMI STANDARD; PRT; 563 AA.
AC P31183; P31183; P31542; Created
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nigra b precursor (Agglutinin VI) (SNAP) [Contains: Nigra b A chain
DE (rRNA N-glycosidase) (EC 3.2.2.22); Nigra b B chain].
OS Samucus nigr (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OK NCBI_taxid=4202;
 RX SEQUENCE FROM N.A.
 RC TIGR0015449; PubMed=8647092;
 RA MEDLINE=96215449; PubMed=8647092;
 RT "Characterization and molecular cloning of *Sambucus nigra* agglutinin V
 from the bark of elderberry (*Sambucus nigra*).";
 RL Eur. J. Biochem. 237:505-513(1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TIGR0015449; PubMed=8647092;
 RA MEDLINE=96215449; PubMed=8647092;
 RT "Isolation and partial characterization of *Sambucus nigra* agglutinin V
 novel type 2 ribosome-inactivating protein from the bark of *Sambucus
 nigra* L.";
 RL Plant Mol. Biol. 22:1181-1186(1993).
 CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
 PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
 SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
 ENOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 or send an email to license@ebi.ac.uk)
 CC EMBL; U01299; AAB39475.1; .
 DR FIR; S37382; S37382.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR SMART; S000386; SHIGARICIN.
 DR SMART; S000386; SHIGARICIN.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 297 NIGRIN B A CHAIN.
 FT CHAIN 298 563 NIGRIN B B CHAIN.
 FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 434 559 RICIN B-TYPE LECTIN 2.
 FT REPEAT 316 356 1-ALPHA.
 FT REPEAT 357 397 1-BETA.
 FT REPEAT 400 482 2-GAMMA.
 FT REPEAT 483 524 2-DELTA.
 FT REPEAT 527 554 2-GAMMA.
 FT ACT SITE 188 188 BY SIMILARITY.
 FT DISULFID 274 302 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 319 338 BY SIMILARITY.
 FT DISULFID 360 377 BY SIMILARITY.
 FT DISULFID 448 463 BY SIMILARITY.
 FT DISULFID 489 506 BY SIMILARITY.

FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFICT 39 39 X -> V (IN REF. 2).
 SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;
 Query Watch 31.4%; Score 820.5; DB:1; Length 563;
 Best Local Similarity 37.0%; Best NC: 2; e-
 Matches 197; Conservative 88; Mismatches 211; Indels 37; Gaps 16;
 QY 17 YFRTITLLDYSGSGFS-NEIFLLRQSTIPVSDAQRFLVELTNGQSDXDAADVTNX 75
 DB 43 YRDFSLNLRKTATGTYEVNGLFVLRES-EVQVKSFRFLVPLNNGNTVTLAVDVTNL 101
 QY 76 YVVAQAGQSYPIADAPRGASTHFTGTTEXSSLPFGXSYDXLERYAG-HRQDIPLGIX 134
 DB 102 YVFAFGNRRNPFYFKDAFTEVQKSMFVG-TQNTLSFTGNYDNLTAATRRRESIELGFS 160
 QY 135 QLQSVXALRFXGSTRQXARHILLIOMIGSEARFNPLKXQINSXGSPKDYXML 194
 DB 161 PLDGAITSI-VHDSY--ARSLAVIQWSEARFVIEQVRESIQOASTFPMALMG 216
 QY 195 ELETSGQOSTQVQHSIDGV-----FNPKRLAIXGNFVTLANVRXVIASLAI 243
 DB 217 SNNKSSMSLEIQAGNNVSPFGTVQLNLYDHTHLV---DNFELYK-----ITGIAI 269
 QY 244 MLFVQGERPSSSDVRYWPLVIR--PVIADDTVCASEPTVR-IVGRXGXVDVDDDFH 299
 DB 270 LIFRCSS-PSHDNARMLPDLAGEKNYNDGECTIARTSFNTNIVRGDLGVNRGYDT 328
 QY 300 DNGOIQLESKSNPNQMLTKIKDYTIKRSNGSLTGYTYGYVYVYVYVYVYVYVYVYV 359
 DB 329 DCTQLQNEFCQTOR-NQWTFDSDOTIRSNKCKNTANGNNGSVIVFNCSTAEANIK 386
 QY 360 MWIXWNTIIPNSMLVLAASSGKTITVTQTLDTYLGQGLAGNDTAPREVTYVGRD 419
 DB 387 MEVTDGSIINPSSGLVWTPAPASHTILLENTYASQGTNNVNVKPIVASIVGYKE 446
 QY 420 LQMESN--XGSVYVETCYSSQXQXWALNGDSIRFQKQDQLTXGDSVSVTINVS 477
 DB 447 MCLQSGENGVNMEDEATSLQOQ-OMALYQDRTIVNSTGLCVITNGSKDLIILX 505
 QY 478 CSKXSKXGVYVFNKALINLKKKXKXQXQXQXQXQXQXQXQXQXQXQXQXQXQXQX 530
 DB 506 CQGLP-SQWFFNSDGLVNPKSHVDVRAVSRLIILPPTATGNPQGV 557

RESULT 9
 RIP2_BRYDI
 ID RIP2_BRYDI STANDARD; PRT: 282 AA.
 AC P98184; Q98800;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 18-Feb-2003 (Rel. 41, Last annotation update)
 DE Glycosylase 3.2.2.22 [EC:3.2.2.22]
 OS Bryonia dioica (Red Bryonia)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
 OK NCBI_taxid=3652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Siegel C.B., Gawlak S.L., Marquardt H.;
 RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant
 Bryonia dioica.";
 RL Patent number US5597569, 28-JAN-1997.
 RC SEQUENCE OF 22-42.
 RC TISSUE=ROOT;
 RX MEDLINE=95151812; PubMed=7849072;

RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 RA Marquardt H.;
 RA "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocytotoxins"; J. Biol. Chem. 268:423-429(1994).
 CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; 134238; ; NOT ANNOTATED CDS.
 DR HSSP; P09989; 1MRJ;
 DR InterPro; IPR001574; RIP;
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Multigene family; Glycoprotein; Signal;
 KW Ribosome-inactivating protein; Ribosome-inactivating toxin;
 FT SIGNAL 1 21
 FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
 FT ACT SITE 183 183 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 282 AA; 30754 MW; C52B2F6A873769C CRC64;
 SQ
 Query Match 12.3%; Score 322.5; DB 1; Length 282;
 Best Local Similarity 36.4%; Fragment 2; se-24;
 Matches 86; Conservative 37; Mismatches 100; Indels 17; Gaps 9;
 QY 13 TGKEYFRITLLRDYVSSG-PSNEIPLLRQSTIPVSDAQFVLVNLNGDSTAAID 71
 DB 32 TGATYKTFIRNLATLTVGTPEVYDIPVLRNMAAGLA--RFQVLTVNNGESVTVLD 88
 QY 72 VTNVYVAYQGDQSYFIADAPGAEATHLFTGTXSLSLPFGSYXDLRYAGH--PDQI 129
 DB 89 VVNVYVAYRAGNTAYFIADASTANNVFNAGINRVLPGYNGDLEAGRISREMI 147
 QY 130 PLGKQLIQSVKAL--KPGSGTQXASILLIQVISEARFNFLRWKXKNSXSF 187
 DB 148 ELGFSEISALGNWFRNPGTSV---PRAFVILQTVSEARFPYIEQRVSE--NVGTF 202
 QY 188 LPDXMLETSNGQSTQVQ--HSTDGVFNFXELALXGNFVTLXVRX--VIALSLAM 244
 DB 203 KEDPAFLSLQANGSLSEQIQIATQTRGGEFARFVELATVSTNPTFTVNVSPVYKGIALL 262
 QY 245 LF 246
 DB 263 LY 264
 RESULT 10
 RIPT TRICK
 AC P09989 STANDARD; PRT; 289 AA.
 DT 01-NOV-1989 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein alpha-trichosanthin precursor
 OS (-RNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
 DE Trichosanthes kirilowii (Mongolian snake-guard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes;

OX NCBI_TaxID=3677;
 RN (1) _TaxID=3677;
 RP SEQUENCE FROM N.A.
 RC STRAIN-Maximowicz;
 RX MEDLINE=91153657; PubMed=1999291;
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RT "Cloning of trichosanthin cDNA and its expression in Escherichia
 RT coli."; J. Biol. Chem. 265:8670-8674(1990).
 RL Gene 97:267-272(1991).
 RN [2]
 RP SEQUENCE FROM N.A. TISSUE=Leaf;
 RC STRAIN-Maximowicz;
 RX MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;
 RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RT type I ribosome-inactivating protein."; J. Biol. Chem. 265:8670-8674(1990).
 RL [3]
 RP SEQUENCE OF 24-270.
 RC STRAIN-Maximowicz; TISSUE=Tuberos root;
 RX MEDLINE=90256789; PubMed=2341399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RA Wu P., Huang K., Piatak M.;
 RT "Primary amino acid sequence of alpha-trichosanthin and molecular
 RT cloning of trichosanthin cDNA and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
 RL [4]
 RP SEQUENCE OF 24-270.
 RC TISSUE=Tuberos root;
 RX Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
 RA Tian G.Y., Ni C.Z.;
 RT "Scientific evaluation of Tian Hua Pen (THP): history, chemistry and
 RT application."; J. Nat. Prod. 58:789-798(1996).
 RL [5]
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
 RT "Structure of trichosanthin at 1.88-A resolution."; Proteins 19:4-13(1994).
 RL [6]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=95344583; PubMed=7619000;
 RA Huang Q., Liu S.;
 RT "Studies on crystal structures of active-centre geometry and
 RT mechanism of trichosanthin on two ribosome-inactivating proteins."; Biochem. J. 309:285-298(1995).
 CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
 CC -!- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M34858; AAA34207.1;
 DR EMBL; J05434; AAA34206.1;
 DR PIR; J05666; RUTZT
 DR PDB; 1MRJ; 07-FEB-95.
 DR PDB; 1TCS; 10-JUL-95.
 DR PDB; 1J4G; 28-JAN-03.
 DR PDB; 1NLI; 21-JAN-03.
 DR PDB; QDZ2; 28-JAN-00.
 DR InterPro; IPR001574; RIP.

QY	73	TNXYVAYQADSDSYFLDRA--PQGEATHLFTGTRKSLSPFXGXYKDLERYAGH-RDQIP	130
DB	90	TNVIIMVYQADGTSVTFEASATEAKYVFKDMRKVTLFVSGNYBRQTAQKREMP	149
QY	131	LGIMQLIQSWALRPGSGTRQARSILLQMSAARNFLLWRXQXKNGSKSLPD	190
DB	150	LGAPDASAITLTFYNNAS--ASHAWLLQTSQDAKIKIQOIGKVDK--TFLPS	205
QY	191	XYXLEETSSGQSTQVO--HSTGQFNFXKLAIXGNSFVLNVRX--VIASLAIML	245
DB	206	LAI-SLENSGALSQIGQIASTNGQSFSPVLINAQNRQVITNDVAGVTSNIALLL	264
RESULT 11			
ID	RIPS	TRIKI	STANDARD; PRT; 289 AA.
DT	Q1	MAR-1992 (Rel. 21, Created)	
DT	15	DEC-1998 (Rel. 37, Last sequence update)	
DT	28	FEB-2003 (Rel. 41, Last annotation update)	
DE	Ribosome-inactivating protein karasurin precursor (RNA		
DE	N-glycosidase) (EC 3.2.2.22).		
DS	Trichosanthes kirilowii (Mongolian snake-gourd).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	Caryophyllales; Cuniculitaceae; Cucurbitaceae; Trichosanthes.		
OC	NGL_184243671;		
EN	[1]		
PC	SEQUENCE FROM N.A.		
PC	TISSUE=Root tuber;		
PC	MEDLINE=9212998; PubMed=9212998;		
RA	Mizukami H., Iida K., Kondo T., Ogihara Y.;		
RT	"Cloning and bacterial expression of a gene encoding ribosome-		
RT	inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes		
RT	kirilowii var. japonica,";		
RT	J Biol. Pharm. Bull. 20:711-713 (1997).		
RL	[20]. Pharm. Bull. 20:711-713 (1997).		
RL	Chem. Pharm. Bull. 39:1244-1249 (1991).		
CC	-1- SEQUENCE OF 24-270.		
CC	MEDLINE=92005921; PubMed=1914000;		
CC	Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;		
CC	"The complete amino acid sequence of an abortifacient protein,		
CC	karasurin."		
CC	-1- SPECIFIC ADENOSINE ON THE 28S RNA		
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	TYPE 1 RIP SUBFAMILY.		
CC	-----		
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CC	-----		
CC	EMBL; AB000666; BAA21786.1; -.		
CC	DR PIR; JCS606; JCS606.		
DR	PIR	JU0393; JU0393.	
DR	HSSP; P09889; IMRG.		
DR	InterPro; IPR001574; RIP.		
DR	Pfam; PF00161; RIP.1.		
DR	PRINTS; P000396; SHIGACIN.		
DR	PROSITE; PS00275; SHIGACIN.1.		
DR	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;		
KW	Signal. 1		
FT	CHAIN	21	POTENTIAL.
FT	CHAIN	22	KARASURIN-C.
FT	CHAIN	24	KARASURIN-A.
FT	PROPEP	271	REMOVED IN MATURE FORM.

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rpt

Page 1

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18; Search time 41.0829 seconds

Title: US-09-601-667c-1; (419000 alignments)

Sequence: 1 YERLRLRYHTGTGEXYFR.....RRIITYPATGKQNWMPVX 533

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_muc:*

8: sp_oryzae:*

9: sp_plant:*

10: sp_ricinus:*

11: sp_ricinus:*

12: sp_ricinus:*

13: sp_vertebrate:*

14: sp_vertebrate:*

15: sp_vertebrate:*

16: sp_bacteria:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2478	521	10	Q8XN6	Q8XN6 vitiscum albu
2	2224	515	10	Q8XN6	Q8XN6 vitiscum albu
3	1246	580	10	Q8XN6	Q8XN6 vitiscum albu
4	1243	47.5	580	Q8XN6	Q8XN6 vitiscum albu
5	1230	47.0	541	Q8XN6	Q8XN6 vitiscum albu
6	1197.5	45.8	549	Q8XN6	Q8XN6 vitiscum albu
7	1196.5	45.7	581	Q8XN6	Q8XN6 vitiscum albu
8	1137.5	43.5	528	Q8XN6	Q8XN6 vitiscum albu
9	1113.5	42.6	249	Q8XN6	Q8XN6 vitiscum albu
10	1094.5	41.8	254	Q8XN6	Q8XN6 vitiscum albu
11	1067.5	41.2	249	Q8XN6	Q8XN6 vitiscum albu
12	1054.5	40.3	249	Q8XN6	Q8XN6 vitiscum albu
13	1029.5	39.4	249	Q8XN6	Q8XN6 vitiscum albu
14	977.5	37.4	251	Q8XN6	Q8XN6 vitiscum albu
15	968.5	37.0	592	Q8XN6	Q8XN6 vitiscum albu
16	968.5	37.0	592	Q8XN6	Q8XN6 vitiscum albu

17	961.5	35.8	572	10	Q8XN6	Q8XN6 vitiscum albu
18	877.5	33.2	570	10	Q8XN6	Q8XN6 vitiscum albu
19	876.5	33.5	564	10	Q8XN6	Q8XN6 vitiscum albu
20	876.5	33.5	564	10	Q8XN6	Q8XN6 vitiscum albu
21	874	33.4	564	10	Q8XN6	Q8XN6 vitiscum albu
22	852.5	32.6	563	10	Q8XN6	Q8XN6 vitiscum albu
23	849.5	32.5	570	10	Q8XN6	Q8XN6 vitiscum albu
24	828.5	31.7	565	10	Q8XN6	Q8XN6 vitiscum albu
25	825.5	31.6	604	10	Q8XN6	Q8XN6 vitiscum albu
26	822.5	31.4	563	10	Q8XN6	Q8XN6 vitiscum albu
27	820.5	31.4	563	10	Q8XN6	Q8XN6 vitiscum albu
28	807	30.6	566	10	Q8XN6	Q8XN6 vitiscum albu
29	764.5	28.2	603	10	Q8XN6	Q8XN6 vitiscum albu
30	755	27.7	569	10	Q8XN6	Q8XN6 vitiscum albu
31	725	26.1	316	10	Q8XN6	Q8XN6 vitiscum albu
32	526.5	20.1	316	10	Q8XN6	Q8XN6 vitiscum albu
33	525.5	20.1	316	10	Q8XN6	Q8XN6 vitiscum albu
34	525.5	20.1	316	10	Q8XN6	Q8XN6 vitiscum albu
35	504.5	19.3	320	10	Q8XN6	Q8XN6 vitiscum albu
36	494.5	18.9	320	10	Q8XN6	Q8XN6 vitiscum albu
37	494.5	18.9	320	10	Q8XN6	Q8XN6 vitiscum albu
38	460.5	17.2	252	10	Q8XN6	Q8XN6 vitiscum albu
39	454.5	17.4	251	10	Q8XN6	Q8XN6 vitiscum albu
40	453.5	17.3	251	10	Q8XN6	Q8XN6 vitiscum albu
41	447.5	17.1	251	10	Q8XN6	Q8XN6 vitiscum albu
42	443.5	17.0	252	10	Q8XN6	Q8XN6 vitiscum albu
43	309.5	11.8	289	10	Q8XN6	Q8XN6 vitiscum albu
44	306	11.7	299	10	Q8XN6	Q8XN6 vitiscum albu
45	303.5	11.6	247	10	Q8XN6	Q8XN6 vitiscum albu

ALIGNMENTS

RESULT 1

Q8XN6 PRELIMINARY; PRT; 531 AA.

AC Q8XN6; (EMBL) 21, Created

DT 01-MAR-2003 (EMBL) 21, Last sequence update

DT 01-MAR-2003 (EMBL) 21, Last sequence update

DE Lectin chain A isoform 1 (EC 3.2.2.2) (RNA N-glycosidase)

OS (Fragment)

CC Vitiscum album (European mistletoe)

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;

CC Santalales; Viscaceae; Viscum.

OX NCBI_TaxID=3972;

RS SOURCE FROM N.A.

RC TISSUE=leaf

RA Paramasivam M., Misra V., Srinivasan A., Singh T.P.;

RT "Viscum album (Indian) mRNA for Mistletoe lectin A isoform 1 and

RL chain B";

RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC -1- STIMULATORY; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC EMBL; A001140; A001140.1; -

CC EMBL; A001140; A001140.1; -

CC EMBL; A001140; A001140.1; -

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Page 2

	Matches	483; Conservative	5; Mismatches	42; Indels	2; Gaps	2
Qy	1	YERLKLAVHTQTXEYRFPYTLADVDYSGSGSFENEIPLAGSITPVSDAGFVLELTN				60
Db	1	YERLKLAVHTQTXEYRFPYTLADVDYSGSGSFENEIPLAGSITPVSDAGFVLELTN				60
Qy	61	QGRSDXNHPDITWYXALVYVAGADDSYFLADPQGLPFLPTGTAKSLIPFGSTYDL				120
Db	61	QGRSDXNHPDITWYXALVYVAGADDSYFLADPQGLPFLPTGTAKSLIPFGSTYDL				120
Qy	121	RYVGRHQIPELGIYXOIGVYALAPFGSGRQKASRILILQVISEAPRFLIMAKKX				180
Db	120	RYVGRHQIPELGIYXOIGVYALAPFGSGRQKASRILILQVISEAPRFLIMAKKX				180
Qy	161	INSKGLTEPLXMLETFSWQSGSTQVQSHSTGVFNENRRLAIXGAFVTLNREVIAS				240
Db	160	INSKGLTEPLXMLETFSWQSGSTQVQSHSTGVFNENRRLAIXGAFVTLNREVIAS				240
Qy	241	LALMLPFCSEPRSSDSYVMDITPVLADDTQSAASEPTIRVGRGXVDVADPPD				300
Db	240	LALMLPFCSEPRSSDSYVMDITPVLADDTQSAASEPTIRVGRGXVDVADPPD				300
Qy	301	GNQIOLPFSKSNPNQVLMITKEDTIRNSGSLCTVYTGAVYMLPFGTAFAEATLV				360
Db	300	GNQIOLPFSKSNPNQVLMITKEDTIRNSGSLCTVYTGAVYMLPFGTAFAEATLV				360
Qy	361	QIMXGTLINPNSULVLAASSGKKTITLVQDITLTQGMALNDTAPEVITVGFEDL				420
Db	360	QIMXGTLINPNSULVLAASSGKKTITLVQDITLTQGMALNDTAPEVITVGFEDL				420
Qy	421	CHBSKXGSGVWELTGSQXQXQXVYVQSGIIPRQNDQCLXKGRDVSIVNIVTSGX				480
Db	420	CHBSKXGSGVWELTGSQXQXQXVYVQSGIIPRQNDQCLXKGRDVSIVNIVTSGX				480
Qy	461	XSXXQRTVTEKXALINTKXXXXXVQVADNPRLRIITIVPAGTQXNDMLPY 532				500
Db	479	GBSGQKWTINMGALINLNGALAMGVGSGNPELKKIITIVPAGTQXNDMLPY 530				500
RESULT 2						
ID	Q9M243	PREDIMINARY:	prt,	565	AA.	
AC	Q9M243					
DT	01-MAR-2002	(ZEMBLArel, 20, Created)				
DR	01-MAR-2002	(ZEMBLArel, 22, Last sequence update)				
DE	VCA p19c2002 (ZEMBLArel, 22, Last annotation update)					
OS	Viscum album subsp. coloratum					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
CC	Gentiales; Viscaceae; Viscum.					
NCBI	taxid=159976;					
LN	1	SEQUENCE FROM N.A.				
RZ	1	RefSeq N.A.				
RT	1	"Cloning of Viscum album subsp. coloratum (Korean material)".				
RT	1	Biochem. Biophys. Res. Commun. 010-012002				
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-D-GALACTOSIDIC BOND AT ONE					
CC	-1- SPECIFIC ADENOSINE ON THE 28S RRNA.					
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.					
CC	EMBL; AF636961; AAL0417.1. "					
DR	InterPro; IPR000772; Rctn_B_Lectin.					
DR	InterPro; IPR001574; RLP.					
DR	RefSeq; PF00042; Rctn_B_Lectin; 6.					
DR	RefSeq; PF00042; Rctn_B_Lectin; 6.					
DR	PRINTS; PR00346; SHIGABACTIN.					
DR	SMART; SMO0486; RCTN; 2.					
DR	PROSITE; PS50231; RCTN_B_LectIN; 2.					
KW	Hydrolase; Signal; Toxin.					
FT	1	SIGNAL				
FT	23	POTENTIAL				
FT	309	VCA ALPHA CHAIN.				
FT	309	VCA BETA CHAIN.				
SEQUENCE	565	AA; 62401 MW; 991E3994D0A05F11 CRC64;				

Query Match	58.0%; Score 2224.5; DB 10; Length 565;
Best Local Similarity	81.8%; Pred. No. 146-218;
Matches	49; Conservative 18; Mismatches 69; Indels 11; Gaps 4
Qy	1 YERLANTVHTQCTEXYREFFILADTVSSGSPENETPLRGSTIPVSDAORFVLELTN 60
Dh	34 YERLANTVHTQCTEXYREFFILADTVSSGSPENETPLRGSTIPVSDAORFVLELTN 93
Qy	61 QGSDXPLADVTWYVVAQADDSFPRLDPAGKEVTHFTGTRKSLSPKSGXPLE 120
Dh	94 QGSDTIPALDVTWYVVAQADDSYFLRDPAGEEHLFTGTR -SLPTSGSYTLE 152
Qy	121 FVARGRDPICGLICXOLGSLVAKLPGSGTRKXSLILILQISEANENPILMXEX 180
Dh	153 FVARGRDPICGLICXOLGSLVAKLPGSGTRKXSLILILQISEANENPILMXEX 212
Qy	181 INGSXSLDPYMLAEFTSGQOSTGYASTDGYFNKXSLAIXGAPFLMXRXVLS 240
Dh	213 INGSXSLDPYMLAEFTSGQOSTGYASTDGYFNKXSLAIXGAPFLMXRXVLS 272
Qy	241 LAIMFVCGSRSSSDVYEWPLTRPVIL----ADVTCASEPTVAIGSGMWVDV 295
Dh	273 LAIMFVCGSRSSSDVYEWPLTRPVILISNCSGLTQVAGYVADPCLWTR 332
Qy	296 DPHQHQKQLWLBKSNDDPRLTIRPXTISNCSGLTQVAGYVADPCLWTR 355
Dh	389 BALWQVWKGILINRSNLVLAAGSSGTLTQVAGYVADPCLWTRPREVIT 448
Qy	356 BATIOVWNGGILINRSNLVLAAGSGITGLTQVADTVAGGMALNQTAPREVIT 415
Qy	416 GPDLCEKNGNSGIVTCSSXNNXKXALYCDGSIRPKNQDCLTYGSDYSTVIN 475
Dh	449 GFENLCMEANAGASVETCCSGXENQKALYAGNSIRPKNQDCLTYGSDYSTVIN 507
Qy	476 VSGSXKXGQWTFMEKALILKXXXXVDVAQANKEKILITYPAGKPGNQMLCV 532
Dh	508 VSGSXKXGQWTFMEKALILKXXXXVDVAQANPSILRILITYPAGKPGNQMLCV 564
RESULT 3	
Q94BM4	PRELIMINARY; PRT; 580 AA.
Q94BM4	
1D	Q94BM4
2D	Q94BM4
3D	Q94BM4
4D	Q94BM4
5D	Q94BM4
6D	Q94BM4
7D	Q94BM4
8D	Q94BM4
9D	Q94BM4
10D	Q94BM4
11D	Q94BM4
12D	Q94BM4
13D	Q94BM4
14D	Q94BM4
15D	Q94BM4
16D	Q94BM4
17D	Q94BM4
18D	Q94BM4
19D	Q94BM4
20D	Q94BM4
21D	Q94BM4
22D	Q94BM4
23D	Q94BM4
24D	Q94BM4
25D	Q94BM4
26D	Q94BM4
27D	Q94BM4
28D	Q94BM4
29D	Q94BM4
30D	Q94BM4
31D	Q94BM4
32D	Q94BM4
33D	Q94BM4
34D	Q94BM4
35D	Q94BM4
36D	Q94BM4
37D	Q94BM4
38D	Q94BM4
39D	Q94BM4
40D	Q94BM4
41D	Q94BM4
42D	Q94BM4
43D	Q94BM4
44D	Q94BM4
45D	Q94BM4
46D	Q94BM4
47D	Q94BM4
48D	Q94BM4
49D	Q94BM4
50D	Q94BM4
51D	Q94BM4
52D	Q94BM4
53D	Q94BM4
54D	Q94BM4
55D	Q94BM4
56D	Q94BM4
57D	Q94BM4
58D	Q94BM4
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61D	Q94BM4
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64D	Q94BM4
65D	Q94BM4
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67D	Q94BM4
68D	Q94BM4
69D	Q94BM4
70D	Q94BM4
71D	Q94BM4
72D	Q94BM4
73D	Q94BM4
74D	Q94BM4
75D	Q94BM4
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79D	Q94BM4
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91D	Q94BM4
92D	Q94BM4
93D	Q94BM4
94D	Q94BM4
95D	Q94BM4
96D	Q94BM4
97D	Q94BM4
98D	Q94BM4
99D	Q94BM4
100D	Q94BM4

[illegible]

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KW Hydrolyase, Signal, Toxin.
FT SIGNAL 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CHAIN 33 580 CINNOMONIN II.
SQ SEQUENCE 580 AA; 6425 MW; 37242896CCECP6 CRC64;

Query Match
Best Local Similarity 50.4%; Pred. No. 1-96-118;
Matches 274; Conservative 69; Mismatches 177; Indels 24; Gaps 13;

9 THQTKGKFRFTLLRDYSSGSGSNEIPILRQ-STIPVSAPORFVLELTKQXSGX
40 TKAKTSYQPIELRAQALASGEHPGIPWREBASTVP--DSKRFILVLSMADSPV
68 A-AIDVNNXYVAAQAGQSYFIR-DAPRGAEHLFTQTKXSLPEXSYDLERVAGH
98 ALAVDYNNAVVAIRGSGSFLIEDPDAIENLDPTEKY-TEPESGYDLERVAGE
126 -RDQFGIXQILQSYALAKXRG-OSTRQARSLILQYISAPRNPILAKXQKINS
157 LRRELLQMDPLEMAISLMTSMQALASLSLIVLQVMAKVRFRILEKVESLIR
184 GXSPFLPXVLELETSWGQSGTOVQSHSTD-GVFNPKXSLAXXGNPFLXVY-
217 AEWFRDPFALSLFNKWSLSNAYQSQNGYFSSPELKSINPEVYVGSVDRIISGL
242 AMLFVPC--GERPSSDVRWVPLVIRVLIAD-----DYTCASAPFTVIVKXNM
277 AMLFPCSSSDISDOFIDHLMIRPLADVADADADNDPDLQDFEPTVIRISRGK
290 XYVRRDDPHDNGIQLPMSKSNMPNQLATIRKDDIRANSGLCTYGTGYYVMIFD
337 CVDVQKQKNNGNPIQLWPCCKNSDVQQLATIRDDQIRNSGKCLITNGYSADPVYIYD
350 CNTAVREKTIWQIKNGTIIIPRSNLYLAASGIKETLLVQTLDTYLGQWLAGNDIAP
397 CKTPVTAISWQFANGTIIIPQSLALVLSRESGSPETLLVQANIVASQWLAGNTEP
410 REVTVIGRDLQESNKSQSWETCKSSQKQXKXALIGDSIRPKQNDQCLT-XGRDS
457 FVTSIVGRDLQMDQMDMMWVVEGSSKED-KMLIPDSIRKHQDRKSLSTDHNS
469 VSTVINIVSCSXKXQRMVTEKALINLXXXXXQVQAQNPFLRIIYPATGKPNQK
516 QGSIILISCSFGSBOGRWVNDGTIILNKXGLVMDVQSGNSPISHOIIMPATGKPNQ
529 WLPV 532
576 WLP 579

RESULT 4
ID Q94BM3 PRELIMINARY; PRT; 580 AA.
AC Q94BM3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnomonin III precursor
DS 3.2.2.22 (EC 3.2.2.22) (RNA N-glycosylase).
OS Cinnomonin (Cinnomoninaceae).
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Eukaryota; Viridiplantae; Streptophyta; Laurales; Cinnamomum.
OX NCBI_TaxId=13429;
RN (1)
RP SEQUENCE FROM N. A.
RT Yang Q., Gong Z. Z., Liu W. Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnomonin proteins and study of their expression
RT (2002)
RT Submitted (JUN-2001) to the EMBL/GenBank/DBS databases
CC -!- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
  SPECIFIC ADENOSINE ON THE 28S RRNA.

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CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL:AY039603; AK82460.1; Rictin_B_lectin.
DR InterPro: IPR000772; Rictin_B_lectin.
DR InspecPro: IPR001574; RIP.
DR Pfam: PF00552; Rictin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: P00396; SHIGACIN.
DR SMART: SM0058; RICTIN; 2.
DR PROSITE: PS00231; RICTIN_B_LECTIN; 2.
FT SIGNAL 33 580 CINNOMONIN II.
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
SQ SEQUENCE 580 AA; 64421 MW; 940D10P0L7B558 CRC64;

Query Match
Best Local Similarity 50.4%; Pred. No. 3-86-118;
Matches 274; Conservative 71; Mismatches 175; Indels 24; Gaps 13;

9 THQTKGKFRFTLLRDYSSGSGSNEIPILRQ-STIPVSAPORFVLELTKQXSGX
40 TKAKTSYQPIELRAQALASGEHPGIPWREBASTVP--DSKRFILVLSMADSPV
68 A-AIDVNNXYVAAQAGQSYFIR-DAPRGAEHLFTQTKXSLPEXSYDLERVAGH
98 ALAVDYNNAVVAIRGSGSFLIEDPDAIENLDPTEKY-TEPESGYDLERVAGE
126 -RDQFGIXQILQSYALAKXRG-OSTRQARSLILQYISAPRNPILAKXQKINS
157 LRRELLQMDPLEMAISLMTSMQALASLSLIVLQVMAKVRFRILEKVESLIR
184 GXSPFLPXVLELETSWGQSGTOVQSHSTD-GVFNPKXSLAXXGNPFLXVY-
217 AEWFRDPFALSLFNKWSLSNAYQSQNGYFSSPELKSINPEVYVGSVDRIISGL
242 AMLFVPC--GERPSSDVRWVPLVIRVLIAD-----DYTCASAPFTVIVKXNM
277 AMLFPCSSSDISDOFIDHLMIRPLADVADADADNDPDLQDFEPTVIRISRGK
290 XYVRRDDPHDNGIQLPMSKSNMPNQLATIRKDDIRANSGLCTYGTGYYVMIFD
337 CVDVQKQKNNGNPIQLWPCCKNSDVQQLATIRDDQIRNSGKCLITNGYSADPVYIYD
350 CNTAVREKTIWQIKNGTIIIPRSNLYLAASGIKETLLVQTLDTYLGQWLAGNDIAP
397 CKTPVTAISWQFANGTIIIPQSLALVLSRESGSPETLLVQANIVASQWLAGNTEP
410 REVTVIGRDLQESNKSQSWETCKSSQKQXKXALIGDSIRPKQNDQCLT-XGRDS
457 FVTSIVGRDLQMDQMDMMWVVEGSSKED-KMLIPDSIRKHQDRKSLSTDHNS
469 VSTVINIVSCSXKXQRMVTEKALINLXXXXXQVQAQNPFLRIIYPATGKPNQK
516 QGSIILISCSFGSBOGRWVNDGTIILNKXGLVMDVQSGNSPISHOIIMPATGKPNQ
529 WLPV 532
576 WLP 579

RESULT 5
ID Q41174 PRELIMINARY; PRT; 541 AA.
AC Q41174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rictin A chain (EC 3.2.2.22) (RNA N-glycosylase)
DS (fragment).
OS Rictinus communis (Cactaceae).
OC Eukaryota; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot; Rosales;
  eustosids I; Malpighiales; Euphorbiaceae; Rictinus.

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QX NCBI_TaxID=3986;
RN [1]
RZ SEQUENCE FROM N.A.
RA MEDLINE=2238977; PubMed=163311;
RX Roberts L.M., Tregear U.N.;
RT "Molecular cloning of ricin."
RL Targeted Diagn. Ther. 7:81-97(1992).
CC -I- CATALYTIC ACTIVITY: ENDOXYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE OF THE TWO SERINE RESIDUES OF THE N-GLYCOSYLATION SITE OF A PROTEIN.
CC -II- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HEP5 IP00879; IRB2582.1; -.
DR HESP IP00879; IRB2582.1; -.
DR InterPro: IPRO00772; Ricin_B_lectin.
DR InterPro: IPRO01574; RID.
DR InterPro: IPRO01400; Somatochrysin.
DR Pfam: PF00652; Ricin_E_lectin; 6.
DR Pfam: PF00161; RID; 1.
DR PRINTS: PR00396; SHRIAGRICN.
DR SMART: SMD5651; Ricin_A_lectin; 2.
DR SMART: SMD5651; Ricin_B_lectin; 2.
DR PROSITE: PS00275; SHICA_RICIN; 1.
DR PROSITE: PS00338; SOMATOCHRYN_2; 1.
KW Hydrolase; Toxin.
KW NON TER
QT SEQUENCE 541 aa; 60281 MW; 2875ECDFEPIF2B9D5 CRC64;

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Query Match	48.0%;	Score 1230;	DB 10;	Length 541;
Best Local Similarity	48.0%;	Pred. No. 7,36-117;		
Matches	262;	Conservative 176;	Mismatches 176;	Indels 20; Gaps 11.
QY	9	THQTKAEPRFTLLDLYVSGS--FSNEIPLL-RGSTIPVSDADRFVETLNNQKXKX	66	
Db	13	TMAGTVOSTNTEINRSLKLTQADVHDEPLTSDVGLPEK--QKILVELSHAEKLV	70	
QY	67	TALNLTNNXYVAVVAVNGQSGSFLPR-DAPGAE--THEPTMRKSLPEKSGXVLDREYV	123	
Db	71	TALDYTNVAVVGRKMSAFAFPHDQDPAELHETLQVQRKTEPAAGNYHREOLA	130	
QY	124	GH-RDQIPFGIXQLISYVA--LXPGSGTSKXASSTILLIMISARPRFPLMRQ	179	
Db	131	GNLKNELTNGPNEHSAISALYRISTGQLPLASFCLIDIMISARPRFVISEKNT	190	
QY	180	XINSGSEPLPEXMMETLSTMGQGVQVGHGQVQPNVRLXIKQNTYNNRYLA	239	
Db	191	RHYRFSAPDPVSITLTNLSMERLTALQSNQCAPSPQLQGRNSKFSYDVGSILP	250	
QY	240	SLAIMEVGGPSSSDVRYVPIVRRPLAD--DYTSASBPYKLYVRKXKAVYEDD	295	
Db	251	ILMLNQLRCAPEPSSQ---FSLIRTPVYVNNRAD-CQDEFEKNSMLQVWDVG	305	
QY	297	PHDNDQQLGMSKSNQPNQMLTIRKDTIRNSKGLTYGRTGYVYVPEQNTAR	356	
Db	306	RPNENALQMGKCSATPANDLTETKEDMTISNGKCLTYGSGYVYVYDQNTAFD	365	
QY	357	ATTWQIVKNGSTINPNSULVVAASGIGKFTLLTYQTLDTYLGQENLAKNDVRETYV	416	
Db	366	ATKWDIVKNGSTINPNSULVVAASGIGKFTLLTYQTLDTYLGQENLAKNDVRETYV	425	
QY	417	PHLIMSNXGYSWATCKSGKQXKMLXNDGSREKQNDCTKXGNSVSTNYV	476	
Db	426	LYGLCLQANSQGVIEDSGSEKAP-QMLVADGISIRFQQRNDCTISNSIRETYVIL	484	
QY	477	SGGXSKXGQWVFVTEKXALINLKKXXXXVDVAAPKRLRIIFVATKPKQWQV	532	
Db	485	SGPSSBSQKQWVFVTEKXALINLKKXXXXVDVAAPKRLRIIFVATKPKQWQV	540	
RESULT 6				
QSFV22		PRELIMINARY;	PRT;	549 AA.
ID	QSFV22;			
DT	01-MAR-2001	(YEMBL:rel. 16, Created)		
OT	01-MAR-2001	(YEMBL:rel. 16, Last sequence update)		

DT 01-OCT-02 (TREMELLE, 22. Last annotation update)
 DE TYPE II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (ZERNER)
 OS N-glycosidase (fragment)
 OC Enzyme (protein)
 OC Enzyme (protein) (tree)
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Laurales; Lauraceae; Cinnamomum
 NC NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu Y., Wang B.-D.;
 RA Molecular cloning of cinnamomin A-, B-chain and the expression,
 RA characterization and localization of the BMD/GeneBank/DBD database
 RI Submitted (Sep-2000)
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT
 CC -1- SPECIFIC ADRENOSIN TO THE 268 RSNA.
 DR -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
 DR EMBL: AF295848; AAFA8978.2; -.
 DR HSPB: P02879; ZMAI.
 DR InterPro: IPR007772; Rctin_E_Lectin.
 DR InterPro: IPR005544; RLP.
 DR DR DDB: J010001; Rctin_E_Lectin; 5.
 DR Pfam: PF00161; RLP.
 DR PRINTS: PR00366; SHIGARICIN.
 DR SMART: SM00458; RCTIN; 2.
 DR PROSITE: PS02031; RCTIN_B_LECTIN; 2.

FT	NON TER	SEQUENCE	549 AA;	60648 MW;	02607E607CA44B0 CRC64;	
1	1					
Query Match			45.8%;	Score 1197.5;	DB:10;	Length 549;
Best Local Similarity			48.8%;	Pred: N1.66-113;		
Matches 266;	Conservative	71;	Mismatches 183;	Indels	25;	Gaps 133
Ds	9	THQTCKEYEPRLTLEAYVSGSGSNELRLRQ	STIPSDAGQPVYELTNGQVDS-X	66		
Ds	6	TKXAKTSTYQPIELALRQAQSGDEEPGFVWRSESTVP	-DSKRFITLESMLNADPVP	65		
Ds	67	TAIVLVNXYVVAQKQGGQSYFR	DAPRGAETHLTGTTRKXSLFPXGQSYXDLERYAG-	124		
Ds	66	TLAVVNVNVAARVSGSFPREDPDPALREMLPQTRY	TFPSSGSTDLEAVGE	123		
Ds	125	HRDQYICXQLTQSLYALRKPQ	GSTRKQASLILNIMSLAPRRIELMRKQXNS	184		
Ds	125	REBILDLMDPLNLAHLSINLQGRALRSILVIOVNA	VAVERRIERIRGSSIR	184		
Ds	184	GXSPFEPXWVLETSWGQGTQVGHST	-GVFNPNXSLALXGKGFLLTXNVR	XYIASL	241	
Ds	185	AEHFEPDPMAISLENSKASLSNAVQSGQGVFSFVSLSS	ISNRPVYSGSDRYISGL	244		
Ds	242	ALNTPG-C	-GGSPSDVRYEPLRYRPLAD-	-----DYTSASAPNTNEXKGM	289	
Ds	245	ALNLTCSRPAASQGTIDPHMLNRL	RLVLVDAVLAIOALNDOTCAPERYLRSGRL	304		
Ds	299	XVVEDDDPDHNDIOLQAPESGNDPQWLMTIRKDT	ILRSNGCLTYGTYGVYVMI	FD	349	
Ds	305	CVYDADKKNYNNIDQLMPCKQSDVQWLMTLRFDAL	IRSNQCLTYGTSAGYVMI	FD	364	
Ds	350	CATNFAEATINQVWNGTINPNSHLVLAASG	IKQITVLTDTLQCGMLADNLP	409		
Ds	365	CRFPTVATKQKQVNTINRSQVLSHSSNPTFLV	QVGNILNPNQSD-K	424		
Ds	410	RETVTVYFRLQMSXGQVWETLSXSOXNQXWL	VGDSIRFEPQND--QCLTYGRD	467		
Ds	425	FVTSIVSEFNDLQVAGNPMWVEECSVARE	-EMALVPDSIRFHPDPPGPAFLIDNR	483		
Ds	466	SVBTVINAVSGXKXQWMTFNEXAL	ILNLKXXXXXVQVQANPLKRLIIPYTSQNO	527		
Ds	484	PGQSLILHSSCPSSGKRNVRFRDGV	VLNADQLMDNGSFLDQIILVPIRTPRHH	533		
Ds	528	NNLPV	532			
Ds	544	EWLP	548			

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```
RESULT 7
ID Q94BMS PRELIMINARY; PRT; 561 AA.
AC Q94BMS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 129 3 2 123 (RNA N-glycosylase) (Fragment)
DE 129 3 2 123 (RNA N-glycosylase) (Fragment)
DE Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Lin W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns" (JUN-2001) to the EMBL/GenBank/DBJ databases
RT -1: CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1: SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY039801; AAK2458.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR PRINTS; PR00161; RIF_1.
DR SMART; SM00386; SHIGACIN.
DR PROSITE; PS00213; RICHIN_2_LECTIN; 2.
KW Hydrolyase; Signal; Toxin.
FT SIGNAL 33 561
FT CHAIN 1 32
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN 1.
SQ SEQUENCE 561 AA; 64215 MW; 6E85F8BFA3D196 CRC64;
Query Match 45.7%; Score 1196.5; DB 10; Length 561;
Best Local Similarity 48.8%; Pred. No. 2,2e-113; Index 25; Gaps 13;
Matches 266; Conservative 70; Mismatches 184;
9 THQTKXKYEFTLLADYVSSGSSNEFLILQ-STPYSDAPQVYVELTQKXNS-X-66
40 TKRATKSTYQFIALPQALASGEHPGVFRERSTVP--DEKPFIVELSMVAIDSPV 97
DB 67 TAAIDVTKVYVAGADQSYFLR-DAPRGATLFTGTTRXSLFPKSGXYDLREYAG- 124
DB 38 TLAVDVNAVYVAFKGSQSFLENDPDALEMLPDTKRY-TPESSASYDLREYAGR 156
DB 125 HRQCPPLAQILOSVALKRPQ-GSTRKQASILLIOMISFAAPNPILMKXQXNS 183
DB 157 RFEELIOMPLFNAJISAKTSMKQKRAJASIVYVOMVAVRFRIRYKROSLR 216
DB 184 GKSFLPDYVLELETSWQSGSTOVQSTQ-GVFNNKPRALXXGNPFLTXNR-VYIASI 241
DB 217 AEMFRPDAVLSLENKMSALNNVQASQGVFSSFEVLSISNPPVYVGSVSRVIGL 276
DB 242 AVMFVYC--GEPPSSDYRWPLVLRPAD-----DYCSASEFTVIRVEXM 289
DB 277 ALMFLICSTIRASQOPIDMLMIRPLIDVAVATKANDDQVQDPKIRASRGL 336
DB 290 XVDVDDPHDNOICLWPSKSNBPQMLTXKDXITRANSGCLTYGTAGVYVYLF 349
DB 337 CVDRKQKNNAPQLWPCQKSDVWGLTFRBDALISNGCLITNGSADVYVYID 396
DB 350 CNTAVRATWQYKNGTINPSLVLAASSGKICITLVYQTLVYLQGNLANDPAR 409
DB 397 CRPLVDAISWQPMANGETIRPOSALVLSASGSPFTLVQAKTVASRQMLASGNTPE 456
DB 410 RVTYVGPRLGSSNGSWWATCKSKQKXKXMAKGGOSIRKQNGO--GLTXKRD 467
DB 457 EVTSIVGNDLTCQANGDAMWVEFESSKAR--FMALVYDQSIIRHDDPQAPAPFLNNH 515
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Query Match 46.8%; Score 1137.5; DB 10; Length 528;
Best Local Similarity 46.1%; Pred. No. 2,1e-107; Index 11; Gaps 9;
Matches 242; Conservative 63; Mismatches 189;
9 THQTKXKYEFTLLADYVSSGSSNEFLILQ-STPYSDAPQVYVELTQKXNS-X-66
40 TKRATKSTYQFIALPQALASGEHPGVFRERSTVP--DEKPFIVELSMVAIDSPV 97
DB 67 TAAIDVTKVYVAGADQSYFLR-DAPRGATLFTGTTRXSLFPKSGXYDLREYAG- 124
DB 38 TLAVDVNAVYVAFKGSQSFLENDPDALEMLPDTKRY-TPESSASYDLREYAGR 156
DB 125 HRQCPPLAQILOSVALKRPQ-GSTRKQASILLIOMISFAAPNPILMKXQXNS 183
DB 157 RFEELIOMPLFNAJISAKTSMKQKRAJASIVYVOMVAVRFRIRYKROSLR 216
DB 184 GKSFLPDYVLELETSWQSGSTOVQSTQ-GVFNNKPRALXXGNPFLTXNR-VYIASI 241
DB 217 AEMFRPDAVLSLENKMSALNNVQASQGVFSSFEVLSISNPPVYVGSVSRVIGL 276
DB 242 AVMFVYC--GEPPSSDYRWPLVLRPAD-----DYCSASEFTVIRVEXM 289
DB 277 ALMFLICSTIRASQOPIDMLMIRPLIDVAVATKANDDQVQDPKIRASRGL 336
DB 290 XVDVDDPHDNOICLWPSKSNBPQMLTXKDXITRANSGCLTYGTAGVYVYLF 349
DB 337 CVDRKQKNNAPQLWPCQKSDVWGLTFRBDALISNGCLITNGSADVYVYID 396
DB 350 CNTAVRATWQYKNGTINPSLVLAASSGKICITLVYQTLVYLQGNLANDPAR 409
DB 397 CRPLVDAISWQPMANGETIRPOSALVLSASGSPFTLVQAKTVASRQMLASGNTPE 456
DB 410 RVTYVGPRLGSSNGSWWATCKSKQKXKXMAKGGOSIRKQNGO--GLTXKRD 467
DB 457 EVTSIVGNDLTCQANGDAMWVEFESSKAR--FMALVYDQSIIRHDDPQAPAPFLNNH 515
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Db	302	AMKCKRLENNQAMLTSLTSLTSSNGKSLCTGEGAGHNPVAVIDGSSVAALATVETLNN	361
Qy	366	GIINIRSNINVTAASSGIGITLTIVQGLDTLQAGQVLAQNDPAPREVTYFQDLCMEEN	425
Db	362	GIINIRSNFALVAPASSNGGTLITVQNEILNRGGRGNNSSPVTSSISQYDCMQAQ	421
Qy	426	KASIVATVETCSKQKQKMLACGSSIRPKQNDQGLTCAQSVSYVNIIVGSCSKSKAQ	485
Dy	422	GSNVTATLQNNKKKKQALYDITSLHAYQVDTSLKMKKQSPSLVLELSSNGMAQ	480
Qy	486	RVVETFEALINIKKKKKKIDVQAQNRKLEKIIIVPAVTRKNNQMTI	530
Db	481	RAFLKDKDSTLYSLYDQWVDKSPSLKQIIILVPTKTRKNNQMTI	525

RESULT 9	
Q8RXH7	
ID Q8RXH7	PRELIMINARY;
AC Q8RXH7.	PRT; 249 AA

D1	01-GUN-2002	(TREMHEIrel_21, Created)
DT	01-GUN-2002	(TREMHEIrel_21, Last sequence update)
DE	Leclith 2003	(TREMHEIrel_21, Last annotation update)
DE	Leclith 2003	A isoform 2 (EC 5.7.5.1.22) (RNA N-glycosylase)
OS	Viscum album (European mistletoe).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots;	
OC	Santalales; Viscaceae; Viscum.	
RN	[1]	_rRNA9372,
RP	SEQUENCE FROM N.A.	
RC	Tissue=leaf;	
RA	Parasatayam M., Srinivasan A., Singh T.P.;	
CC	Viscum Album (Indian Mistletoe) Lectin Chain A, Isoform 2,"	
CC	- CATALYTIC ACTIVITY: ENDOPHYLLOUS OF THE N-DICARBOXYLIC BOND AT ONE	
CC	SPECIFIC AMINOACIDS ON THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	EMBL; AY081163; AA84705.1;	
DR	InterPro; IPRO01574; RIF.	
DR	RefSeq; NP_060114.1;	
KM	Hydrolase; ToxinA1F; 1.	
PT	NON TER	1
PT	NON TER	1
QC	MON TER	249
QC	SEQUENCE	249 AA; 27944 MW; 89FAEF8309A6B35 CRC64;

Query Match	42.64;	Score 1113.5;	DB 10;	Length 249
Best Local Similarity	89.28;	Pred. No. 2.1e-105;		
Matches 223; Conservative	3;	Mismatches 23;	Indels	1;

Best local similarity 85.23; Freq. NO. 2.1e-105;
Matches 223; Conservative 3; Mismatches 23; Indels 1; Gaps 1

QY YERLRAPMTGTCGKEVPEPPTLADSVSSGSPENRDLROSTIYVSHAPRYLZLN 60
Db YERLRAPMTGTCGKEVPEPPTLADSVSSGSPENRDLROSTIYVSHAPRYLZLN 60
QY 1 YERLRAPMTGTCGKEVPEPPTLADSVSSGSPENRDLROSTIYVSHAPRYLZLN 60
QY 61 QGKXSTALDIDVNNKYVAQAQDGSEFLDAPAGSETHLFTGTRKXSLFFKSGSYDLE 120
Db 61 EKGXSTALDIDVNNKYVAQAQDGSEFLDAPAGSEHNFETSTRSELFFKSGSYDLE 119
QY 121 RKAGKRDQPLGIGLIGLOSVYALRKPGRSTKXQNSLIILDMISEBAPNPLIRKXQ 180
Db 120 RKAGKRDQPLGIGLIGLOSVYALRKPGRSTKXQNSLIILDMISEBAPNPLIRKXQ 179
QY 181 INSGSEPLPKPMWELTSSWQSGSLRQVSGSPKQNSLITLQWSEBAPNPLIRKXQ 240
Db 180 INSGSEPLPKPMWELTSSWQSGSLRQVSGSPKQNSLITLQWSEBAPNPLIRKXQ 239
QY 241 LAIRLFFVQGE 250
Db 240 LAIRLFFVQGE 249

Q81K06	PRELIMINARY	ERT	254 AA.
1D	Q81K06		
2D	Q81K06		
3D	Q81K06		
4D	01-OCT-2002 (Tremblay, 22, Created)		
5D	01-OCT-2002 (Tremblay, 22, Last sequence update)		
6D	01-MAR-2003 (Tremblay, 23, Last annotation update)		
7D	Lectin chain A isoform 1 (EC 3.2.2.22) (tRNA N-glycosidase)		
8D	(Fragment)		
9D	01-MAR-2003 (Tremblay, 23, Last sequence update)		
10D	Bursaphysa viridiplanetae, Streptophyta; Embryophyta; Tracheophyta;		
11D	Samaracaceae, Magnoliophyta, eudicotyledons, core eudicots;		
12D	Santalales; Viscaceae; Viscum.		
13D	NCBI TaxID=159976;		
14D	11		

RA Pak C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
BT mistletoe (*Viscum album coloratum*)".

RN	MoJ.	Ca12	12:215-220(2001).
KL	[2]		
RA	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RE	SEQUENCE FROM N.A.		
RD	SEQUENCE FROM N.A.		
RC	Submitted (MAY-2002)		to the EMBL/Genbank/DBJ databases.
CC	-1-CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE		SPECIFIC ADENOSINE ON THE 28S RRNA.
CC	-1-SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	LOCUS: C65030.1 (1990-01-12)		
DR	EMBL	AF015749	1..175
DR	Genbank	AF015749	1..175
DR	Fram: P00161	R1P	1..175
DR	PRINIS	P000366	SHGACATCN.
KR	HYDROLASE; TOXIN.		
FT	NON-TER	253	1
FT	NON-TER	253	1
FT	NON-TER	253	1
SEQUENCE	251 AA;	26446 MW;	6DB5C3B18F4AF5E0 CRC64;
Query Match			
Best Local Similarity	41.8%;	Score 1694.5;	DB 10; Length 254;
Matches 219	Conservative	8; Mismatches 27;	Indels 1; Gaps
Oy	1	YKRLALVYHQTGCKYKPEPILTLADYVSSSGFENRIFLPGSTIPVSGAPRFLVLELN	
Db	1	YKRLALVYHQTGCKYKPEPILTLADYVSSSGFENRIFLPGSTIPVSGAPRFLVLELN	

Db 61 QGGDSTALADIVNLVVAVQGDQSYFLRDAPDGAERHLFTGTR-SSLPTG

00 61 QGGSILAIADVINLIVAA:QASQSI FLKRPDGAERHPL IGI IK-SSLPF IOSI IUDS II?

Dc	120	RFGHRCQCPGAREHLISYSAALRPGSMTDQAOSFILLQMISEAAFNPLUMFAQCX	179
Oy	161	INSGASZFLPDXYMELTEFSNGOOSTOVOSTDGVFPNNFXSLAIXXNPFYTXANRYVIAVS	240
Dd	180	ISSGSSTLDDYIIOLEFSNGOOSTOVOSTDGVFPNNPILATISTGVFTLSNRDVIAVS	239
Oy	241	LAIIM.FVCCERSSS	255
Dd	240	LAIIM.FVCCERSSS	254
RESULT	11		
CNAME9	ID	Q9MK69	PRT: 547 AA.
	AC	Q9MK69;	
DT	01-OCT-2000	(Trembl)rel. 15,	Created
DT	01-MAR-2000	(Trembl)rel. 15,	Last sequence update)
DT	01-MAR-2003	(Trembl)rel. 23,	Last annotation update)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicotyledons; Rosidae;
 OC Eurosid 1; Fabiales; Fabaceae; Papilionoideae; Mimosae; Mimosae;
 OX NCBI_TaxID:3816;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE:3010702; PubMed:10636890;
 RA Liu C.T., Tsai C.C., Lin S.C., Hsu C.I., Hwang M.T.,
 RA Lin J.T.; Structure and function analysis of the abrus precatorius
 RA lectin, a protein with a unique structure and function.
 RT J. Biol. Chem. 275:1897-1901(2000)
 CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AF190173; AF28309.1; -
 DR HSSP: F1140; IABR.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RLP.
 DR Pfam: PF00132; Ricin_L_lectin; 6.
 DR PRINTS: PR00136; SHGCRICIN.
 DR SMART: SM00458; RICIN_2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KM Hydrolase; Toxin.
 SQ SEQUENCE 547 AA; 61248 MW; 355A325C354A1BD CRC64;
 Query Match 41.3%; Score 1079.5; DB 10; Length 547;
 Best Local Similarity 43.8%; Pred. No. 1.9e-101; Indels 31; Gaps 10;
 Matches 234; Conservative 190; Mismatches 139;
 Db 9 THOCTGKXEPFETTLIRPVSSGSPFNEIPILROSTIPVSDKOPVLYELNQGXDXTA 68
 28 TSATPSPASNOFDALRERLGLIYG-IPVADSE-TVAKNOYVTELSYDVAICD 85
 QY
 69 AIDVNNVYVYQKDSQYPLKDAFPGATLTLTGTRKSSLPFGSYXDLEKRYAH-ED 127
 86 GIDLNNVYVYVYQKDSQYPLKDAFPGATLTLTGTRKSSLPFGSYXDLEKRYAH-ED 144
 QY 128 QIPGKICQISYVYALRYGSGTQKRSRSTIIIONSEAPRRLIMKRXKQINSKSF 187
 145 RISTGELALRGKIFKESGASDDEINLTILVILQVAAAEFRVYSLVLTISNMAF 204
 QY 188 LPDYKMLETSWQOOSTOVQSHDGVFVPMKXLAIXKGFVTLXVNR----- 236
 205 QDPSPMLSTNTEPEPLSAVQVODTF--FQV-----VTLINRQEVVSSISHP 254
 Db 237 VIASLALMELTFCGSESSDVRWVLYRPIVADVTGAS-EPPIRYKSKGVADVD 295
 255 SVSASALMELTFCGSESSDVRWVLYRPIVADVTGAS-EPPIRYKSKGVADVD 310
 QY 296 DDPHDMQOQLMPSKANDPNQMLTKIKXTISNGSLTYGYTAGYVWIFDCAVY 355
 311 NAYNNGNPIILMKCOLEFQMLTILKSDTKIKSKLTYGYTAGYVWIFDCAVY 370
 QY 356 EATINQWNGIINRNSNVLNLSGIRKTLTVQGLDLYLGGQMLAGMTAPREVTY 415
 371 EATINQWNGIINRNSNVLNLSGIRKTLTVQGLDLYLGGQMLAGMTAPREVTY 430
 Db 416 GPRDLCSKNGSYWETCCSSQKXKXVYADGSLRPNQKQCLTGDSVSTYIN 475
 431 GFPKLCWENHSGSWMLDVCTIYERQ-QAVYDPSGIPVQVTKNCLTCEEHQCALIYW 489
 QY 476 VSCSXKXQWVYFTEKALINLKKKXXDYVDAKFKRRIIIVPATGPKQW 529
 490 MGSNANASQWPKSGDTIYLYVDNMDVDSKQIILWPFYGNANQW 543
 Db

AC O8LK02
 DT 01-OCT-2002 (TrEMBLrel. 22. Created)
 DT 01-OCT-2002 (TrEMBLrel. 22. Last annotation update)
 DT 01-MAR-2003 (TrEMBLrel. 23. Last annotation update)
 DB Lectin chain B isoform 2 (fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicotyledons;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID:15976;
 RN 1
 RP SEQUENCE FROM N.A.
 RX MEDLINE:2166752; PubMed:11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RL Mol. Cells 12:215-220(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 DB EMBL: AF503918; AF504696.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF00652; Ricin_B_lectin; 5.
 DR SMART: SM00458; RICIN_2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KM NON_TYR
 FT NON_TYR
 SQ SEQUENCE 263 AA; 29150 MW; B68BCB7C9ACBDF CRC64;
 Query Match 49.5%; Score 1060.5; DB 10; Length 263;
 Best Local Similarity 76.0%; Pred. No. 5.9e-109;
 Matches 200; Conservative 19; Mismatches 43; Indels 1; Gaps 1;
 Db 270 DDTVTSSEPTVYVGRKXGVYDADDPDHGQQLMFKSNNDPNQMLTKRDXTRS 329
 1 DDTVTSSEPTVYVGRKXGVYDADDPDHGQQLMFKSNNDPNQMLTKRDXTRS 347
 QY 330 NSGCLITGYTAGYVWIFDCAVYADGSLRPNQKQCLTGDSVSTYIN 389
 61 NSGCLITGYTAGYVWIFDCAVYADGSLRPNQKQCLTGDSVSTYIN 407
 QY 390 VQDLYLGGQMLAGMTAPREVTYRPIVADVTGAS-EPPIRYKSKGVADVD 449
 121 VQDLYLGGQMLAGMTAPREVTYRPIVADVTGAS-EPPIRYKSKGVADVD 467
 QY 450 GSIRKNDQCLTGDSVSTYINVSQSSXKXQWVYFTEKALINLKKKXXDYVDA 509
 180 GSIRKNDQCLTGDSVSTYINVSQSSXKXQWVYFTEKALINLKKKXXDYVDA 527
 QY 510 NPELRRIIIVPATGPKQW 532
 240 NPELRRIIIVPATGPKQW 550
 Db
 RESULT 13
 O8LK02
 DT 01-OCT-2002 (TrEMBLrel. 22. Created)
 DT 01-OCT-2002 (TrEMBLrel. 22. Last annotation update)
 DT 01-MAR-2003 (TrEMBLrel. 23. Last annotation update)
 DB Lectin chain A isoform 2 (BC 3.2.2.22) (RNA N-glycosidase) (fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicotyledons;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID:15976;
 RN 1
 RP SEQUENCE FROM N.A.

RA MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
R "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum)."
RL Mol. Cells 12:215-220(2001).
RN [2].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
C -1- SITES. SITES: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508919; PubMed=11710524; 1.
DR InterPro: IPR001574; 31F.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 249 1
SQ SEQUENCE 249 AA; 27821 MW; 3C5870F8338BDAB5 CRC64;
Query Match 40.3%; Score 1054.5; DB 10; Length 249;
Best Local Similarity 84.3%; Pred. No. 2,3e-99;
Matches 209; Conservative 13; Mismatches 25; Indels 1; Gaps 1;
QY 1 YERLRATVHTGKXEPRETLADYSSGSESENPILROSTTPYSGAQRPTLHEIN 60
DB 1 YERLRATVHTGKXEPRETLADYSSGSESENPILROSTTPYSGAQRPTLHEIN 60
QY 61 QKXDSXTAIDVNNXYVAVQAGDQSYFLDAPRGAEFTLFTGTRXSLSLPGKSTXDL 120
DB 61 QKXDSXTAIDVNNXYVAVQAGDQSYFLDAPRGAEFTLFTGTRXSLSLPGKSTXDL 120
QY 181 INSGXSELPDXYMRLFTSGGQSTQVQSGSTPGYRNEXLAXXGRTTAMTXVTS 240
DB 181 INSGXSELPDXYMRLFTSGGQSTQVQSGSTPGYRNEXLAXXGRTTAMTXVTS 240
QY 180 ISGSGSLPDYVILQLETSGGQSTQVQSGSTPGYRNEXLAXXGRTTAMTXVTS 239
DB 180 ISGSGSLPDYVILQLETSGGQSTQVQSGSTPGYRNEXLAXXGRTTAMTXVTS 239
QY 241 LAIMLFCV 248
DB 241 LAIMLFCV 248
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DB 240 LAIMLFCV 247
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AC Q8LXQ1
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Lactin chain B isoform 3 (fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=15976;
RN [1].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
C -1- SITES. SITES: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508919; PubMed=11710524; 1.
DR InterPro: IPR001574; R1P; 1.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 251 1
SQ SEQUENCE 251 AA; 28090 MW; A1177489012E989 CRC64;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF508919; PubMed=11710524; 1.
DR InterPro: IPR000772; Ricin B lectin.
DR Pfam: PF00652; Ricin B lectin; 6.
DR SMART: SM00458; Ricin; 2.
DR PROSITE: PS00231; Ricin B lectin; 2.
FT NON TER 1
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SQ SEQUENCE 263 AA; 29071 MW; 3F9C4DA860F061D CRC64;
Query Match 39.4%; Score 1029.5; DB 10; Length 263;
Best Local Similarity 74.5%; Pred. No. 8.8e-97;
Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;
QY 270 DVTCSASEPTVIVGKXGMVDRDQDFHDSGQIQMFSSKNNDFNOLMTIREKXTIR 329
DB 1 DGTCTSEPTVIVGKXGMVDRDQDFHDSGQIQMFSSKNNDFNOLMTIREKXTIR 329
QY 330 NSGCTPTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
DB 61 NSGCTPTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 390 VQTDYTLGQMLAGNDFAPREPTVIGFRLCHESNKGSWWERTCKSSQANQXALYGD 449
DB 121 VQTDYTLGQMLAGNDFAPREPTVIGFRLCHESNKGSWWERTCKSSQANQXALYGD 449
QY 450 GSIRPQKQDCLTGKDSVSTYINIVSCXKXKXKXKXKXKXKXKXKXKXKXKXKX 509
DB 180 GSIRPQKQDCLTGKDSVSTYINIVSCXKXKXKXKXKXKXKXKXKXKXKXKXKX 239
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DB 240 YPKRRIITVPAKCPKQKMPV 262
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AC Q8LXQ4
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Lactin chain A isoform 3 (Ec 3.2.2.22) (RKN N-51Ccosidae)
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=15976;
RN [1].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
C -1- SITES. SITES: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508919; PubMed=11710524; 1.
DR InterPro: IPR001574; R1P; 1.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 251 1
SQ SEQUENCE 251 AA; 28090 MW; A1177489012E989 CRC64;

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Best Local Similarity 80.9%; Pred. No. 1.7e-91;
Matches 203; Conservative 7; Mismatches 36; Indels 5; Gaps 3;

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DB 60 QGKWDSTIHALDVTMLVYAYQAGDSYELADPAGAEHLPFGTTRSSAPKSYX 118
QY 118 DIERVAGHRDQIFLAIQLIGVXALFXPGSSTRXQASLILILQWISFAAFNPILMEX 177
DB 119 DIERVAGHRDQIFLAIQLIGVXALFXPGSSTRXQASLILILQWISFAAFNPILMEX 178
QY 178 RQXNGKASFLPDYVTLBELTSMGQSTQVGHSTGVFNNPKRLAIXXGNFTLXNTRXV 237
DB 179 RQXNGKASFLPDYVTLBELTSMGQSTQVGHSTGVFNNPKRLAIXXGNFTLXNTRXV 238
QY 238 IASLIMLPYC 248
DB 239 IASLIMLPYC 249
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Search completed: December 11, 2003, 14:00:58
Job time : 44.0829 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 52.666 seconds

Title: US-09-601-667c-1
(without alignments)

Sequence: 2616
1 YERILKLVTHQTGKEYRRF.....RRILIVPATGPNQNMVYX 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting filter 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2535	96.9	533	20	AAV25970
2	2535	96.9	533	20	AAV25973
3	2535	96.9	533	20	AAV25976
4	2519	96.3	531	20	AAV25979
5	2519	96.3	532	20	AAV25982
6	2505	95.8	564	18	AAV10021
7	2505	95.8	564	20	AAV90127
8	2157.5	83.6	551	23	AAV9450
9	1291	49.4	264	20	AAV25987

10	1291	49.4	264	20	AAV25988	Mistletoe lectin B
11	1291	49.4	265	20	AAV25990	Mistletoe lectin B
12	1291	49.4	265	20	AAV25993	Mistletoe lectin B
13	1290	49.3	264	20	AAV25986	Mistletoe lectin B
14	1290	49.3	264	20	AAV25990	Mistletoe lectin B
15	1290	49.3	265	20	AAV25996	Mistletoe lectin B
16	1289	49.3	265	20	AAV25992	Mistletoe lectin B
17	1289	49.3	264	20	AAV25989	Mistletoe lectin B
18	1286	49.2	265	20	AAV25995	Mistletoe lectin B
19	1286	49.2	264	20	AAV25978	Mistletoe lectin B
20	1286	49.2	264	20	AAV25972	Mistletoe lectin B
21	1286	49.2	263	20	AAV25985	Mistletoe lectin B
22	1277.5	48.8	264	20	AAV25991	Mistletoe lectin B
23	1277.5	48.8	263	19	AAV25992	Mistletoe lectin B
24	1267.5	48.5	263	19	AAV25991	Mistletoe lectin B
25	1267.5	48.5	264	18	AAV25992	Mistletoe lectin B
26	1267.5	48.5	264	18	AAV25993	Mistletoe lectin B
27	1267.5	48.5	267	19	AAV25990	Mistletoe lectin B
28	1261	47.1	574	10	AAV25993	Mistletoe lectin B
29	1231	47.1	576	18	AAV25987	Mistletoe lectin B
30	1231	47.1	576	21	AAV25992	Mistletoe lectin B
31	1231	47.1	576	21	AAV25991	Mistletoe lectin B
32	1231	47.1	576	22	AAV25990	Mistletoe lectin B
33	1230	47.0	565	6	AAV25986	Mistletoe lectin B
34	1230	47.0	565	22	AAV25980	Mistletoe lectin B
35	1224	46.8	574	8	AAV25985	Mistletoe lectin B
36	1224	46.7	565	7	AAV25984	Mistletoe lectin B
37	1222	46.7	565	22	AAV25980	Mistletoe lectin B
38	1216	46.4	565	22	AAV25984	Mistletoe lectin B
39	1215	46.4	566	19	AAV25985	Mistletoe lectin B
40	1193.5	45.6	267	19	AAV25986	Mistletoe lectin B
41	1192	45.2	562	10	AAV25979	Mistletoe lectin B
42	1173	44.8	255	20	AAV25974	Mistletoe lectin A
43	1173	44.8	255	20	AAV25974	Mistletoe lectin A
44	1171.5	44.8	256	20	AAV25981	Mistletoe lectin A
45	1171.5	44.8	256	20	AAV25987	Mistletoe lectin A

ALIGNMENTS

AAV25970	standard; protein; 533 aa.
AAV25970	(first entry)
18-OCF-1999	
Mistletoe lectin protein consensus sequence 1.	
Mistletoe lectin; antitumor; immunostimulant; A-chain; MDA; immunity; lymphokine 28S subunit; non-cytotoxic; T-cell activation; immune response; cancer; cytotoxicity; antigen; leioform.	
Viscum album.	
Key	Location/Qualifiers
Misc-difference 15	/label= Asp, Glu
Misc-difference 63	/label= Gly, Gln
Misc-difference 66	/label= Ile, Val
Misc-difference 75	/label= Leu, Ala
Misc-difference 117	/label= Asp, Arg or none
Misc-difference 117	/label= Asn, Thr
Misc-difference 117	/label= Pro, Thr

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FT	Misc-difference	114	/label= Asp, Glu
FT	Misc-difference	141	/label= Ser, Thr
FT	Misc-difference	145	/label= Phe, Tyr
FT	Misc-difference	177	/label= Thr, Ala
FT	Misc-difference	180	/label= Ala, Tyr
FT	Misc-difference	185	/label= Tyr, Asp
FT	Misc-difference	191	/label= Ala, Glu
FT	Misc-difference	224	/label= Val, Met
FT	Misc-difference	224	/label= Ile, Phe
FT	Misc-difference	225	/label= Pro, Ser
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FT	Misc-difference	325	/label= Cys, Arg
FT	Misc-difference	364	/label= Gly, Asn
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FT	Misc-difference	439	/label= Val, Asp
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FT	Misc-difference	484	/label= Ser, Gly
FT	Misc-difference	493	/label= Gly, Ser
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FT	Misc-difference	501	/label= Asn, Ser, Thr, Lys
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XX	PD		
XX	12-ATG-1999,		

PF	03-FEB-1998;	98DE-1004210.
PR	03-FEB-1998;	98DE-1004210.
PA	(BIO-) BLOSAN ARANEMITTEI, GMEH.	
PI	Morris P, Stiefel T, Voelter W, Welters P;	
PR	WP: 1999-44535/78.	
XX	Preparation of mistletoe lectins in heterologous systems.	
XX	Particularly for use as anticancer agents and immunostimulants	
PS	Claim 1: Page 25-26; 78p; German.	
XX		
CC	This invention describes a novel mistletoe lectin (I) and its fragments	
CC	which have antitumor and immunostimulatory activity. The A-chain (MA)	
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of	
CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and	
CC	macrophage killing macrophages, so-called cell-growth particularly	
CC	fragments are used for immunomodulation and for the treatment of	
CC	cancers and if they lack cytotoxicity, they stimulate immunity. (I) and its	
CC	immune response, particularly to a co-administered antigen, enhance of the	
CC	(tumour-associated, bacterial or viral). The method allows production of	
CC	mistletoe lectin, and its individual chains, in many different isoforms	
CC	and on a large scale, at any time of the year. Recombinant products are	
CC	free from toxins present in natural mistletoe extracts. This sequence	
CC	represents a consensus sequence of the mistletoe lectin described in the	
CC	specification.	
XX		
XX	Sequence 533 Ab;	
Query Match	96.9%; Score 2355; DB 20; Length 533;	
Best Local Similarity	100.0%; Pred. 1.7e-270;	
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DB	1 YERLRLVTHQTGKXFRFILLRDVSSGSFSENLPLRSGTIPVSDARFVLETLN 60	
QY	61 QGDSYNAIDMTNYYVAQAGQSGYLRAPRGFPHFGTTXSGSPKSGYXTE 120	
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DB	61 QGDSYNAIDMTNYYVAQAGQSGYLRAPRGFPHFGTTXSGSPKSGYXTE 120	
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DB	481 KXQXQWVYTBKALINIKKXXXXDVAGANPKLRRIIYFATGKGNQNMPLFV 532	
DB	481 KXQXQWVYTBKALINIKKXXXXDVAGANPKLRRIIYFATGKGNQNMPLFV 532	

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Page 3

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RESULT 2
AAV25973 standard; protein; 533 AA.
XX
AAV25973;
AC
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin protein consensus sequence 2.
XX
XX Mistletoe lectin; antitumor; immunostimulant; B-chain; NTA; immunity;
XX ribosome 268 subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform.
XX
OS Viscum album.
XX
PH Key Location/Qualifiers
PT Misc-difference 15 /label= Asp, Glu
PT Misc-difference 16 /label= Gly, Glu
PT Misc-difference 66 /label= Ile, Val
PT Misc-difference 75 /label= Leu, Ala
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PT DE19804210-AL.
PT 12-APR-1999.
PT 03-FEB-1998; 98DE-1004210.
PT 03-FEB-1998; 98DB-1004210.
PT (BIOS-1) BIOSYN ARZEMITTEL GMBH.
PT Morris P, Stiefel T, Voelker W, Welters P;
PT WPI; 1999-45335/38.
PT Preparation of mistletoe lectins in heterologous systems,
PT particularly for use as anticancer agents and immunostimulants
PT Claim 4; Page 28-29; 79pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (NLA)
XX of the mistletoe lectin binds to, and inhibits, the growth of cells
XX of the immune system (e.g., T-lymphocytes, B-cells and subsets of
XX lymphokine-producing macrophages) so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin described in the
XX specification.
XX
XX Sequence 533 AA:
XX
XX Query Match 96.9%; Score 2535; DB 20; Length 533;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-270;
XX Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YERLAKYHQTGKXKXFRPITLADYVSSGSPRNETLPLROSTPVSDAKRFTVETLN 60
XX DB 1 YERLAKYHQTGKXKXFRPITLADYVSSGSPRNETLPLROSTPVSDAKRFTVETLN 60
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Db 181 INSGSRPDYXMEFTSGQOOSTQVSTDTGPHNEXLAIKXGPTLXNEXVLA 240
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Db 241 LAIMLFCGERSSSDYRYPVPIPIADVTCASPEPTVRIVGRXGXVVDDEPHD 300
Qy 301 GNOIQIWPSSKNDPQQLMTIKDXTTRNSGCLTTCYVTAQVYVMEPCQTAVERATW 360
Db 301 GNOIQIWPSSKNDPQQLMTIKDXTTRNSGCLTTCYVTAQVYVMEPCQTAVERATW 360
Qy 361 QIWXGTTIMPNSVVIASSGIKGTITMOTIDYTGCGIAGVWLEPCNIAVERATW 420
Db 361 QIWXGTTIMPNSVVIASSGIKGTITMOTIDYTGCGIAGVWLEPCNIAVERATW 420
Qy 421 CMESXGSWVETCSXQXQXWALYGDGSIKPKQNDQCLTXGRDSVTVINIVSGSX 480
Db 421 CMESXGSWVETCSXQXQXWALYGDGSIKPKQNDQCLTXGRDSVTVINIVSGSX 480
Qy 481 XSKXQWVPTNEXAIILKXXXXXVQANPFIIRILLIYPATCKNQWMLPV 532
Db 481 XSKXQWVPTNEXAIILKXXXXXVQANPFIIRILLIYPATCKNQWMLPV 532

RESULT 3
AAZ5976
ID AAZ5976 standard; protein; 533 AA.
XX AC AAZ5976;
XX DT 18-OCT-1999 (first entry)
XX DX
XX DX Mistletoe lectin protein consensus sequence 3.
XX KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
XX KW lysozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
XX KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX KW cancer; cytotoxicity; antigen; isoform.
XX OS
XX OS Viscum album.
XX Key Location/Qualifiers
XX MISC-difference 15 /label= Asp, Glu
XX MISC-difference 62 /label= Gly, Glu
XX MISC-difference 66 /label= Ile, Val
XX MISC-difference 75 /label= Leu, Ala
XX MISC-difference 107 /label= Asp, none
XX MISC-difference 113 /label= Asn, Thr
XX MISC-difference 117 /label= Pro, Thr
XX MISC-difference 134 /label= Asp, Glu
XX MISC-difference 141 /label= Ser, Thr
XX MISC-difference 145 /label= Phe, Tyr
XX MISC-difference 152 /label= Thr, Ala
XX MISC-difference 177
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FT /label= Ala, Tyr
FT MISC-difference 180
FT /label= Tyr, Asp
FT MISC-difference 185
FT /label= Ala, Glu
FT MISC-difference 191
FT /label= Val, Met
FT MISC-difference 219
FT /label= Ile, Phe
FT MISC-difference 224
FT /label= Pro, Ser
FT MISC-difference 225
FT /label= Thr, Thr
FT MISC-difference 232
FT /label= Thr, Ser
FT MISC-difference 236
FT /label= Asp, Ser
FT MISC-difference 287
FT /label= Asn, Ser
FT MISC-difference 290
FT /label= Cys, Arg
FT MISC-difference 325
FT /label= Gly, Asn
FT MISC-difference 364
FT /label= Gly, Asp
FT MISC-difference 426
FT /label= Gly, Glu
FT MISC-difference 435
FT /label= Val, Asp
FT MISC-difference 439
FT /label= Gln, Lys
FT MISC-difference 442
FT /label= Gly, none
FT MISC-difference 443
FT /label= Arg, Lys
FT MISC-difference 464
FT /label= Cys, Ser, Val
FT MISC-difference 480
FT /label= Ala, Gly
FT MISC-difference 481
FT /label= Gly, Ala
FT MISC-difference 483
FT /label= Ser, Gly
FT MISC-difference 484
FT /label= Gly, Ser
FT MISC-difference 493
FT /label= Gly, Tyr
FT MISC-difference 500
FT /label= Asn, Ser, Thr, Lys
FT MISC-difference 501
FT /label= Ser, Gly
FT MISC-difference 502
FT /label= Leu, Pro
FT MISC-difference 503
FT /label= Ala, Met
FT MISC-difference 504
FT /label= Met, Val
FT MISC-difference 533
FT /label= Pro, Phe
XX DB19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P,
XX WPI; 1999-44535/38.
```

XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 40; Page 37-38; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC the ribosome. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX
 XX Sequence 533 AA;
 SQ

Query Match 96.3%; Score 2519; DB 20; Length 533;
 Best Local Similarity 100.0%; Pred. No. 1.7e-270;
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRVTHQGTGAEFFETLLRDYVSSGSFSEINPILMQSTIPVSDAKRFVLTN 60
 DB 1 YERLRVTHQGTGAEFFETLLRDYVSSGSFSEINPILMQSTIPVSDAKRFVLTN 60
 QY 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 DB 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 QY 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 DB 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 QY 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 180
 DB 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 180
 QY 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 180
 DB 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 180
 QY 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 240
 DB 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 240
 QY 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 240
 DB 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 240
 QY 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 300
 DB 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 300
 QY 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 300
 DB 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 300
 QY 301 GNOIQLMPSKSNDDPNQWLTIRKDXITISNSGCLTGYTGAGVYVLPDGNVRENTV 360
 DB 301 GNOIQLMPSKSNDDPNQWLTIRKDXITISNSGCLTGYTGAGVYVLPDGNVRENTV 360
 QY 361 QHWNGITINPNSNVLAAASGIGKTLTQVLIDYLGQMLKANTPAPEVITVGRRL 420
 DB 361 QHWNGITINPNSNVLAAASGIGKTLTQVLIDYLGQMLKANTPAPEVITVGRRL 420
 QY 421 CWESNKGYSWWTCKSSQXKXKXWALYGDGSIKRPXKQNOQCLTXGDSVATVIVSCX 480
 DB 421 CWESNKGYSWWTCKSSQXKXKXWALYGDGSIKRPXKQNOQCLTXGDSVATVIVSCX 480
 QY 481 KXKXQWTFNEMALILMOKKXKXDDQAKNFKRRIIPVATKRPQMLPV 532
 DB 481 KXKXQWTFNEMALILMOKKXKXDDQAKNFKRRIIPVATKRPQMLPV 532

RESULT 4
 AA25979 standard; Protein: 531 AA.
 XX AA25979;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin I protein fragment.
 DE

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 XX
 XX Vascun album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOOS-) BIOSYN ARZNEIMITTEL GMBH.
 PI Morris P, Stiefel T, Voelter W, Welters P;
 DR WPT, 1999-44535/38.
 DR N-50DB; AA05103.
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 7; Fig 1b; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC the ribosome. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 XX
 XX Sequence 531 AA;
 SQ

Query Match 96.3%; Score 2519; DB 20; Length 531;
 Best Local Similarity 92.5%; Pred. No. 1e-268;
 Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;

QY 1 YERLRVTHQGTGAEFFETLLRDYVSSGSFSEINPILMQSTIPVSDAKRFVLTN 60
 DB 1 YERLRVTHQGTGAEFFETLLRDYVSSGSFSEINPILMQSTIPVSDAKRFVLTN 60
 QY 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 DB 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 120
 QY 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 119
 DB 61 GGDHSGTAIDVNNYVAVYQAGDSYFLADPRGATHTLTGTRKXSPKXSYXDE 119
 QY 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 180
 DB 121 RYAGHDQIPFGXOLIGSVAKRFGSSTRQASILLLOMISBAARNPILWXRQX 179
 QY 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 240
 DB 181 INSGSRPDXWMLTETMQSGSTQVGHSTQVNNPRLAKKGFLLNRYVLS 239
 QY 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 300
 DB 241 LAIMLPVCGRPSSSDYRWVPIRVFADVTCSASEPTVRAIVGSKMAYVDODDFD 299
 QY 301 GNOIQLMPSKSNDDPNQWLTIRKDXITISNSGCLTGYTGAGVYVLPDGNVRENTV 360
 DB 301 GNOIQLMPSKSNDDPNQWLTIRKDXITISNSGCLTGYTGAGVYVLPDGNVRENTV 359
 QY 361 QHWNGITINPNSNVLAAASGIGKTLTQVLIDYLGQMLKANTPAPEVITVGRRL 420
 DB 361 QHWNGITINPNSNVLAAASGIGKTLTQVLIDYLGQMLKANTPAPEVITVGRRL 420

Db 360 QIWKNGTIIINPRSNLVAASGSKGTITLVOTLDYTLGGGLAGNDIPREVTIYGFRL 419
 Qy 421 CMESNGSWVETCSQXQXKXWALYDGSIRKQNDQCLTXGRDSVTVINVC SX 480
 Db 420 CMESNGSWVETCSQXQXKXWALYDGSIRKQNDQCLTXGRDSVTVINVC SX 478
 Qy 481 XSKXGRWFTNEKALIKXXXXXDPQAPKRLRRIIIPATGRKQMLPV 532
 Db 479 GSSGQRWFTNEKALIKKXGLANDVQANPKRLRRIIIPATGRKQMLPV 530

RESULT 5
 AAY25982
 ID AAY25982 standard; Protein; 532 AA.
 AC AAY25982;
 DT 18-OCT-1999 (first entry)
 XX Mistletoe lectin I (variant) protein fragment.
 XX
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 OS Vascum album.
 XX
 XX DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA
 PI Morris P, Stiefel T, Voelker W, Welters F;
 XX MPI, 1999-445335/38.
 XX DR N-PSDB; AKZ09106.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 4B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MAA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC immunopotentiating macrophages and T-lymphocytes. (I) and its
 CC fragments are used to stimulate growth (the stimulant)
 CC (cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 XX
 XX Sequence 532 AA;
 SQ

Query Match 96.3%; Score 2519; DB 20; Length 532;
 Best Local Similarity 97.5%; Pred. No. 16-266;
 Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;

Qy 1 YERLRLVTHQGTGHEPRFTILADYVSSGSENFILRQSTIPVSDQRFVLELTM 60
 Db 1 YERLRLVTHQGTGHEPRFTILADYVSSGSENFILRQSTIPVSDQRFVLELTM 60

Qy 61 QGKSDXTALIDVTKXVAVYQAGDSYFLRDPAGATLFTGTTRKXSLPFGKSYDLR 120
 Db 61 QGSDSITLALIDVTKXVAVYQAGDSYFLRDPAGATLFTGTTRKXSLPFGKSYDLR 119
 Qy 121 RYAHGRDQFLGIXQGLQSTYALXFGQSTTXQNSLIIIIQWISFAARPIIMEXCX 180
 Db 120 RYAHGRDQFLGIXQGLQSTYALXFGQSTTXQNSLIIIIQWISFAARPIIMEXCX 179
 Qy 181 INSGXFLPDYXMLETSMGQOSTQVQSHSDVFPNRIILAPPNPFVTLNNDVIAS 240
 Db 180 INSGXFLPDYXMLETSMGQOSTQVQSHSDVFPNRIILAPPNPFVTLNNDVIAS 239
 Qy 241 LAIMLFCGERPSSSDVYVPIVPIVADVTCASAEPTVIRGXKXVDVDDDFHD 300
 Db 240 LAIMLFCGERPSSSDVYVPIVPIVADVTCASAEPTVIRGXKXVDVDDDFHD 299
 Qy 301 GNGIOLMPSKSNDDPQWLTIRKQITIRNSGCLTTCGTACQVMTFQCTNPREATM 360
 Db 300 GNGIOLMPSKSNDDPQWLTIRKQITIRNSGCLTTCGTACQVMTFQCTNPREATM 359
 Qy 361 QIWKNGTIIINPRSNLVAASGSKGTITLVOTLDYTLGGGLAGNDIPREVTIYGFRL 420
 Db 360 QIWKNGTIIINPRSNLVAASGSKGTITLVOTLDYTLGGGLAGNDIPREVTIYGFRL 419
 Qy 421 CMESNGSWVETCSQXQXKXWALYDGSIRKQNDQCLTXGRDSVTVINVC SX 480
 Db 420 CMESNGSWVETCSQXQXKXWALYDGSIRKQNDQCLTXGRDSVTVINVC SX 478
 Qy 481 XSKXGRWFTNEKALIKXXXXXDPQAPKRLRRIIIPATGRKQMLPV 532
 Db 479 GSSGQRWFTNEKALIKKXGLANDVQANPKRLRRIIIPATGRKQMLPV 530

RESULT 6
 AAM10021
 ID AAM10021 standard; Protein; 564 AA.
 AC AAM10021;
 DT 18-DEC-1997 (first entry)
 XX Prepro mistletoe lectin.
 XX
 XX Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.
 XX
 XX Vascum album.
 XX
 XX EP751221-A1.
 XX
 XX 02-JAN-1997.
 XX
 XX 26-JUN-1995; 95EP-0109949.
 XX
 XX 26-JUN-1995; 95EP-0109949.
 XX
 XX (MADU) MADUS KOEHN AG.
 PA
 PI Baur A, Eck U, Lantzen H, Zinke H;
 XX MPI, 1997-054678/06.
 XX DR N-PSDB; AAT70473.
 XX
 XX Nucleic acid encoding pre-pro form of mistletoe lectin - for
 PT therapeutic or diagnostic use
 XX
 XX Claim 12; Fig 4C; 30pp; German.
 XX
 XX Mistletoe lectin is a cytotoxic agent that has been used for tumour
 CC therapy. It can be used in immunotoxic and medicaments. Nucleic
 CC acid fragments can be used in diagnostic methods. Mistletoe lectin (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).
 XX
 XX Sequence 564 AA;
 SQ

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Page 7

Query Match 95.83; Score 2505; DB 18; Length 564;
Best Local Similarity 91.98; Pred. No. 3.9e-267;
Matches 489; Conservative 2; Mismatches 39; Indels 2; Gaps 2;

QY 1 YERLRKVTHTQGTGKVEFRFTLLRLDYVSSGSFSNE:PLRQSTIPVSDAQRFVVELTN 60
DB 34 YERLRKVTHTQGTGKVEFRFTLLRLDYVSSGSFSNE:PLRQSTIPVSDAQRFVVELTN 93
QY 61 GQDSTKALIDVTKYVVAQSGYFLADAPRCAFTLFTGTTRASSLPKSGSYDLE 120
DB 94 GQDSTKALIDVTKYVVAQSGYFLADAPRCAFTLFTGTTRASSLPKSGSYDLE 152
QY 121 RYAGHDDQIPLAGXOLQSVYALKXGSTRQASSTILLQMSAARFNPILMRXQ 180
DB 153 RYAGHDDQIPLAGXOLQSVYALKXGSTRQASSTILLQMSAARFNPILMRXQ 212
QY 181 INSGKSPFDXWMELETSWQSGSTVQSHSTGVNNEPKALIXKNEFTLXKXVYIAS 240
DB 213 INSGKSPFDXWMELETSWQSGSTVQSHSTGVNNEPKALIXKNEFTLXKXVYIAS 272
QY 241 LAIWLFCGERPSSSDYRWPLVIRPIADDTYCSASEPTVRIYKXQVDRDDDFD 300
DB 273 LAIWLFCGERPSSSDYRWPLVIRPIADDTYCSASEPTVRIYKXQVDRDDDFD 332
QY 301 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAERATW 360
DB 333 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAERATW 392
QY 361 QIWKNGTINRKNVLAASGKIGTTLTQGLDITLGGMLAGNDLAPERTYIGRDL 420
DB 393 QIWKNGTINRKNVLAASGKIGTTLTQGLDITLGGMLAGNDLAPERTYIGRDL 452
QY 421 CHESNGSVWETFCSSQXKXKXALYDGSIFPKQKQDCLTXGSDSVATVNIYSCX 480
DB 453 CHESNGSVWETFCSSQXKXKXALYDGSIFPKQKQDCLTXGSDSVATVNIYSCX 511
QY 481 XSKXQWVFTEKXALINLAKXXXXDVAAQAPKRLRIITTPATGPNQWMLPV 532
DB 512 GSGQKRWFTNEGRLMLAKGCLANDVAAQAPKRLRIITTPATGPNQWMLPV 563

RESULT 7
AAM90127
ID AAM90127 standard; Protein; 564 AA.
XX
AC AAM90127;
XX
DT 20-MAR-2003 (updated)
XX
DT 30-APR-1999 (first entry)
XX
DB Mistletoe lectin prepro-protein.
XX
KW ML; mistletoe lectin; ML; transgenic plant; glycosylation;
XX
KW dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
XX
OS Viscum album.
XX
XX EP864388-A1.
XX
XX 16-DEC-1998.
XX
XX 26-JUN-1995; 98EP-0105660.
XX
XX 26-JUN-1995; 95EP-0105949.
XX
XX 26-JUN-1995; 98EP-0105660.
XX
XX (MADU) MADAYS KOELN AG.
XX
XX Baur A., Eck J., Lentzen H., Zinke H.
XX
XX KPI, 1999-026582/03.
XX

DR N-PSDB; AAV74182.
XX New transgenic plant expressing mistletoe lectin - useful for
XX producing recombinant lectin in e.g. cancer diagnosis and therapy
XX
XX Claim 1a; Fig 4c; 10pp; German.
XX
PS This invention describes a novel transgenic plant transformed with a
CC vector capable of encoding a mistletoe (Viscum album) lectin
CC preproprotein or a biologically active fragment. The specification
CC also describes a polypeptide produced by a plant where the polypeptide
CC exhibits at least one enzymatic modification other than the glycosylation
CC modification of the polypeptide dimer. The plants are used for large-scale
CC production of mistletoe lectin for diagnostic or therapeutic purposes
CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
CC used in the method of the invention.
CC
XX (updated on 20-MAR-2003 to correct PF field.)
SQ Sequence 564 AA.
Query Match 95.83; Score 2505; DB 20; Length 564;
Best Local Similarity 91.98; Pred. No. 3.9e-267;
Matches 489; Conservative 2; Mismatches 39; Indels 2; Gaps 2;

QY 1 YERLRKVTHTQGTGKVEFRFTLLRLDYVSSGSFSNE:PLRQSTIPVSDAQRFVVELTN 60
DB 34 YERLRKVTHTQGTGKVEFRFTLLRLDYVSSGSFSNE:PLRQSTIPVSDAQRFVVELTN 93
QY 61 GQDSTKALIDVTKYVVAQSGYFLADAPRCAFTLFTGTTRASSLPKSGSYDLE 120
DB 94 GQDSTKALIDVTKYVVAQSGYFLADAPRCAFTLFTGTTRASSLPKSGSYDLE 152
QY 121 RYAGHDDQIPLAGXOLQSVYALKXGSTRQASSTILLQMSAARFNPILMRXQ 180
DB 153 RYAGHDDQIPLAGXOLQSVYALKXGSTRQASSTILLQMSAARFNPILMRXQ 212
QY 181 INSGKSPFDXWMELETSWQSGSTVQSHSTGVNNEPKALIXKNEFTLXKXVYIAS 240
DB 213 INSGKSPFDXWMELETSWQSGSTVQSHSTGVNNEPKALIXKNEFTLXKXVYIAS 272
QY 241 LAIWLFCGERPSSSDYRWPLVIRPIADDTYCSASEPTVRIYKXQVDRDDDFD 300
DB 273 LAIWLFCGERPSSSDYRWPLVIRPIADDTYCSASEPTVRIYKXQVDRDDDFD 332
QY 301 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAERATW 360
DB 333 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAERATW 392
QY 361 QIWKNGTINRKNVLAASGKIGTTLTQGLDITLGGMLAGNDLAPERTYIGRDL 420
DB 393 QIWKNGTINRKNVLAASGKIGTTLTQGLDITLGGMLAGNDLAPERTYIGRDL 452
QY 421 CHESNGSVWETFCSSQXKXKXALYDGSIFPKQKQDCLTXGSDSVATVNIYSCX 480
DB 453 CHESNGSVWETFCSSQXKXKXALYDGSIFPKQKQDCLTXGSDSVATVNIYSCX 511
QY 481 XSKXQWVFTEKXALINLAKXXXXDVAAQAPKRLRIITTPATGPNQWMLPV 532
DB 512 GSGQKRWFTNEGRLMLAKGCLANDVAAQAPKRLRIITTPATGPNQWMLPV 563

RESULT 8
AB879450
ID AB879450 standard; Protein; 551 AA.
XX
XX AB879450;
XX
XX 08-JUL-2002 (first entry)
XX
XX Galactose-recognition mistletoe lectin.
XX

KM Mistletoe/ galactose-recognising mistletoe lectin, MLI11.
 XX Viscum album.
 OS
 XX Key Location/Qualifiers
 FH MISC-difference 223 /note= "Encoded by ARG"
 FT MISC-difference 251 /note= "Encoded by TTT"
 FT MISC-difference 344 /note= "Encoded by TCG"
 FT MISC-difference 380 /note= "Encoded by GCC"
 FT MISC-difference 448 /note= "Encoded by GTG"
 FT DE1004027-A1.
 XX
 PN 14-MAR-2002.
 XX
 PD 06-SEP-2000; 2000DB-1044027.
 XX
 XX 06-SEP-2000; 2000DB-1044027.
 XX
 PR (VISC-) VISCUM AG.
 XX
 PA (VISC-) VISCUM AG.
 XX
 PI Kieff S;
 XX
 PI NPI; 2002-316737/36.
 DR
 DR N-PSDB; ABL56947.
 XX
 PT New nucleic acid encoding preprotein of mistletoe lectin, useful as
 XX diagnostic and therapeutic agents, also encodes polypeptide -
 XX
 XX Claim 1; Fig 1; 6pp; German.
 XX
 CC The invention relates to a nucleic acid molecule (AB56947) that encodes
 CC a preprotein (AB579450) which, after maturation, has the biological
 CC activity of the galactose-recognising mistletoe lectin (MLI11). The MLI11
 CC encoding nucleic acid molecule, primers specific to it or complements of
 CC it, and encoded (oligomeric) polypeptides are useful as diagnostic and
 CC therapeutic agents.
 XX
 XX Sequence 551 AA.
 SQ
 Query Match 83.6%; Score 2187.5; DB 23; Length 551;
 Best Local Similarity 83.8%; Pred. No. 4.1e-232;
 Matches 429; Conservative 14; Mismatches 62; Indels 7; Gaps 3;
 QY 1 YERLRRLVHTQTKXKPRFTLLRDVSSSSSNEPLRLAQSTTPVSDAGRPVLVELIN 60
 DB 34 YERLRRLVHTQTKXKPRFTLLRDVSSSSSNEPLRLAQSTTPVSDAGRPVLVELIN 93
 QY 61 GQXSTALITMYNYVYAAQAGQSTFPRARQAZTHLFTCTKXSLPFGGYDLE 120
 DB 94 GQDSTLAIIDVTNLVYAAQAGQSTFPRARQAZTHLFTCTKXSLPFGGYDLE 152
 QY 121 RYAGHRDQIPGIXOLISYXALXPGQSTXQASLIIILIONISEKARFPIIMRKXK 180
 DB 153 RYAGHRDQIPGIEBILISVSLRPGQSTLQARSLIIILIONISEKARFPIIMRKXK 212
 QY 181 INSGKSLPDXMYLALSTNGQOSTQYQSTQGVFNXEXLAIXXNPYLXWVXVTLAS 240
 DB 213 INSGKSLPDXMYLALSTNGQOSTQYQSTQGVFNXEXLAIXXNPYLXWVXVTLAS 272
 QY 241 LAIMLVYCGSRPSSSDVRYWPLVYRPYI-----ADYTCGASRPTVRYIGXKQNVVDH 295
 DB 273 LAIMLVYCGSRPSSSDVRYWPLVYRPYI-----ADYTCGASRPTVRYIGXKQNVVDH 332
 QY 296 DDFHGNQIOLMPSKSNNDPNOLWTIRKXITISNOSCLTYGTAGVYVIMFDQNTVA 355
 DB 333 GKFHGNQIOLMPSKSNNDPNOLWTIRKXITISNOSCLTYGTAGVYVIMFDQNTVA 392

QY 356 BATIOIYKNGTIIINRNSNVLAAASGIIQKTTTLVQVLYLGGQMIAGNDPAREVTY 415
 DB 393 BATIOIYKNGTIIINRNSNVLAAASGIIQKTTTLVQVLYLGGQMIAGNDPAREVTY 452
 QY 416 GFRDLCMESNGSVWETCSXQXQXVXALYDGSIRPQNDQCLTYGRPSVSTVNI 475
 DB 453 GFRDLCMESNGSVWETCSXQXQXVXALYDGSIRPQNDQCLTYGRPSVSTVNI 511
 QY 476 VSCSYKXKQVFTREXATILNKKXKXDXVA 507
 DB 512 VSCSYKXKQVFTREXATILNKKXKXDXVA 543
 RESULT 9
 ID AAY25987 standard; Protein: 264 AA.
 AC AAY25987;
 AC 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B2 protein fragment.
 XX
 KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLI; immunity;
 KM ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B2.
 XX
 OS Viscum album.
 XX
 XX DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Welbers P,
 XX WPI; 1999-445335/38.
 XX
 XX N-PSDB; AAZ09111.
 DR
 DR Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9; Fig 99; 79pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (Aa)
 CC of the mistletoe lectin binds to, and activates T-cell and B-cell
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B2 protein.
 XX
 XX Sequence 264 AA.
 SQ
 Query Match 49.4%; Score 1291; DB 20; Length 264;
 Best Local Similarity 92.4%; Pred. No. 1.3e-133;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 270 DQVYCSABEPYRIYGRKXQVYVDQDFDQNGIOLMPSKSNNDPNOLWTIRKXITIS 329
 DB 1 DQVYCSABEPYRIYGRKXQVYVDQDFDQNGIOLMPSKSNNDPNOLWTIRKXITIS 60

QY 330 MNSCLITGYGTAGYVWIFDCNPAVREXITWQIMNGTIIIPRSMLVLAASSGIGKGTIT 389
 DB 61 MNSCLITGYGTAGYVWIFDCNPAVREXITWQIMNGTIIIPRSMLVLAASSGIGKGTIT 120
 QY 390 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESXKGSVWVETCKSSQXKXWALYGD 449
 DB 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESXKGSVWVETCKSSQXKXWALYGD 180
 QY 450 GSIRPKQKODQCLTGWGDSVSTVINIVSCSXKXKQWVFTNEXAIIINLAKXXXXVVAQA 509
 DB 181 GSIRPKQKODQCLTGWGDSVSTVINIVSCSXKXKQWVFTNEXAIIINLAKXXXXVVAQA 240
 QY 510 NPKLRITITPATKPKQKMLPV 532
 DB 241 NPKLRITITPATKPKQKMLPV 263

RESULT 10

AAZ5988
 ID AAZ5988 standard; Protein: 264 AA.

AAZ5988;
 18-OCT-1999 (first entry)

DE Mastlece lectin B3 protein fragment.
 KW Mastlece; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B3.

OS Vascum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P. Stiefel T. Voelter W. Welters P;
 PI WPI: 1999-44535/36.
 DR N-PSDB; AA09112.

PT Preparation of mastlece lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Claim 9; Fig 10B; 78pp; German.
 XX This invention describes a novel mastlece lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mastlece lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mastlece lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mastlece extracts. This sequence
 CC represents a fragment of a mastlece lectin B3 protein.

Sequence 264 AA;
 Query Match 49.4%; Score 1291; DB 20; Length 264;
 Best Local Similarity 92.4%; Pred. No. 1,3e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 270 DQWTCASAEPTVRIYGRXKQWVYRDQDPDQDQOLMPSKNNPDQWLTIXDXTIS 329
 DB 1 DQWTCASAEPTVRIYGRXKQWVYRDQDPDQDQOLMPSKNNPDQWLTIXDXTIS 60
 QY 330 MNSCLITGYGTAGYVWIFDCNPAVREXITWQIMNGTIIIPRSMLVLAASSGIGKGTIT 389
 DB 61 MNSCLITGYGTAGYVWIFDCNPAVREXITWQIMNGTIIIPRSMLVLAASSGIGKGTIT 120
 QY 390 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESXKGSVWVETCKSSQXKXWALYGD 449
 DB 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESXKGSVWVETCKSSQXKXWALYGD 180
 QY 450 GSIRPKQKODQCLTGWGDSVSTVINIVSCSXKXKQWVFTNEXAIIINLAKXXXXVVAQA 509
 DB 181 GSIRPKQKODQCLTGWGDSVSTVINIVSCSXKXKQWVFTNEXAIIINLAKXXXXVVAQA 240
 QY 510 NPKLRITITPATKPKQKMLPV 532
 DB 241 NPKLRITITPATKPKQKMLPV 263

RESULT 11

AAZ5994
 ID AAZ5994 standard; Protein: 265 AA.

AAZ5994;
 18-OCT-1999 (first entry)

DE Mastlece lectin B3 variant protein fragment.
 KW Mastlece; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B3.

OS Vascum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P. Stiefel T. Voelter W. Welters P;
 PI WPI: 1999-44535/36.
 DR N-PSDB; AA09118.

PT Preparation of mastlece lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Disclosure; Fig 16B; 78pp; German.
 XX This invention describes a novel mastlece lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mastlece lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mastlece lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mastlece extracts. This sequence
 CC represents a fragment of a variant mastlece lectin B3 protein.

XX Sequence 265 AA;
SQ
Query Match 49.4%; Score 1291; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1.3e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
OY 270 DVTCSASPEPTVAVGKXGKAVVDRDDPHDGNQIQLPKSKNDPNQMLTKIKEDYTRS 329
DB 1 DVTCSASPEPTVAVGKXGKAVVDRDDPHDGNQIQLPKSKNDPNQMLTKIKEDYTRS 60
OY 330 NSGCLITVGTAGVYVMEFCNTAVREXITWQWKNQITINPSNVLVAASGKKTTLT 389
DB 61 NSGCLITVGTAGVYVMEFCNTAVREXITWQWKNQITINPSNVLVAASGKKTTLT 120
OY 390 VQTLDTYLLGQMLAGNDAPREVTIYGFRLCNSKSGSWVETCSQXQXKALYGD 449
DB 121 VQTLDTYLLGQMLAGNDAPREVTIYGFRLCNSKSGSWVETCSQXQXKALYGD 180
OY 450 GSIRPKONODCLTVGRDSVSTVINIVSCSXSKXQRFVETNEKXILNLKXXXXVDAQA 509
DB 181 GSIRPKONODCLTVGRDSVSTVINIVSCSXSKXQRFVETNEKXILNLKXXXXVDAQA 240
OY 510 NPKLRILIIYPATGKPNQMLPV 532
DB 241 NPKLRILIIYPATGKPNQMLPV 263

RESULT 12

AAZ5993
ID AAZ5993 standard; Protein; 265 AA.
XX
XX AAZ5993;

18-OCT-1999 (first entry)

Mistletoe lectin B2 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-445335/38.

XX N-PSDB; AA209117.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 15B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and to cause T-cell cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B2 protein.

XX Sequence 265 AA;

SQ
Query Match 49.4%; Score 1291; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1.3e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 270 DVTCSASPEPTVAVGKXGKAVVDRDDPHDGNQIQLPKSKNDPNQMLTKIKEDYTRS 329
DB 1 DVTCSASPEPTVAVGKXGKAVVDRDDPHDGNQIQLPKSKNDPNQMLTKIKEDYTRS 60
OY 330 NSGCLITVGTAGVYVMEFCNTAVREXITWQWKNQITINPSNVLVAASGKKTTLT 389
DB 61 NSGCLITVGTAGVYVMEFCNTAVREXITWQWKNQITINPSNVLVAASGKKTTLT 120
OY 390 VQTLDTYLLGQMLAGNDAPREVTIYGFRLCNSKSGSWVETCSQXQXKALYGD 449
DB 121 VQTLDTYLLGQMLAGNDAPREVTIYGFRLCNSKSGSWVETCSQXQXKALYGD 180
OY 450 GSIRPKONODCLTVGRDSVSTVINIVSCSXSKXQRFVETNEKXILNLKXXXXVDAQA 509
DB 181 GSIRPKONODCLTVGRDSVSTVINIVSCSXSKXQRFVETNEKXILNLKXXXXVDAQA 240
OY 510 NPKLRILIIYPATGKPNQMLPV 532
DB 241 NPKLRILIIYPATGKPNQMLPV 263

RESULT 13

AAZ5986
ID AAZ5986 standard; Protein; 264 AA.
XX
XX AAZ5986;

18-OCT-1999 (first entry)

Mistletoe lectin B1 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-445335/38.

XX N-PSDB; AA209110.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 8B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity; (1) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B1 protein.

SQ Sequence 264 AA;

Query Match

Best Local Similarity 92.4%; Score 1290; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 1.6e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 270 DDTCSASEPTVIRVGRKXKVVVDVDDPHDNOIQLPKSKNDPQMLTKKXDTIR 329
 DB 1 DDTCSASEPTVIRVGRKXKVVVDVDDPHDNOIQLPKSKNDPQMLTKKXDTIR 60
 QY 330 NSCLTYGYTGYVYVIMFDONAVREATTIWIQIXNGTIIIPRSNLVLAASGKKTTL 389
 DB 61 NSCLTYGYTGYVYVIMFDONAVREATTIWIQIXNGTIIIPRSNLVLAASGKKTTL 120
 QY 390 VQTLDTLGGWMLAGNDTPAPEVTIYGRDLQMSXGSSVWETCSQXQXWALYGD 449
 DB 121 VQTLDTLGGWMLAGNDTPAPEVTIYGRDLQMSXGSSVWETCSQXQXWALYGD 180
 QY 450 GSIRPKQNDQCLTSGDSVETIIVISCSGSSGRVWFTNEGAILNKSLMDVVAQA 509
 DB 181 GSIRPKQNDQCLTSGDSVETIIVISCSGSSGRVWFTNEGAILNKSLMDVVAQA 240
 QY 510 NPKLRRIIIVPATKRNQWMLPV 532
 DB 241 NPKLRRIIIVPATKRNQWMLPV 263

RESULT 14

AAV25590

ID AAV25590 standard; Protein; 264 AA.

AC AAV25590;

DT 18-OCT-1999 (first entry)

DB Mistletoe lectin B5 protein fragment.

KW Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;

KW cancer; cytotoxicity; antigen; isoform; lectin B5.

OS Viscum album.

DB19804210-A1.

PD 12-AUG-1999.

PF 03-FEB-1998; 98DE-1004210.

PR 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Walters P;

XX WPI; 1999-445335/38.

XX N-PSDB; AA209114.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

BS Claim 9; Fig 12b; 78pp; German.

CC This invention describes a novel mistletoe lectin (1) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity; (1) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B5 protein.

SQ Sequence 264 AA;

Query Match

Best Local Similarity 92.4%; Score 1290; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 1.6e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 270 DDTCSASEPTVIRVGRKXKVVVDVDDPHDNOIQLPKSKNDPQMLTKKXDTIR 329
 DB 1 DDTCSASEPTVIRVGRKXKVVVDVDDPHDNOIQLPKSKNDPQMLTKKXDTIR 60
 QY 330 NSCLTYGYTGYVYVIMFDONAVREATTIWIQIXNGTIIIPRSNLVLAASGKKTTL 389
 DB 61 NSCLTYGYTGYVYVIMFDONAVREATTIWIQIXNGTIIIPRSNLVLAASGKKTTL 120
 QY 390 VQTLDTLGGWMLAGNDTPAPEVTIYGRDLQMSXGSSVWETCSQXQXWALYGD 449
 DB 121 VQTLDTLGGWMLAGNDTPAPEVTIYGRDLQMSXGSSVWETCSQXQXWALYGD 180
 QY 450 GSIRPKQNDQCLTSGDSVETIIVISCSGSSGRVWFTNEGAILNKSLMDVVAQA 509
 DB 181 GSIRPKQNDQCLTSGDSVETIIVISCSGSSGRVWFTNEGAILNKSLMDVVAQA 240
 QY 510 NPKLRRIIIVPATKRNQWMLPV 532
 DB 241 NPKLRRIIIVPATKRNQWMLPV 263

RESULT 15

AAV25596

ID AAV25596 standard; Protein; 265 AA.

AC AAV25596;

DT 18-OCT-1999 (first entry)

DB Mistletoe lectin B5 variant protein fragment.

KW Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;

KW cancer; cytotoxicity; antigen; isoform; lectin B5.

OS Viscum album.

DB19804210-A1.

PD 12-AUG-1999.

PF 03-FEB-1998; 98DE-1004210.

PR 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Walters P;

XX WPI; 1999-445335/38.

Thu Dec 11 16:09:41 2003

us-09-601-667c-1.rag

DR N-PSDB; AA209120.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 185; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated antigens).
CC Mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
XX
SQ Sequence 265 AA;
Query Match 49.3%; Score 1290; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1.6e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 270 DDTCSASPTATVIRKXKXNDPDDPHDNCIQLPKSNPDPQMTTKKXITRS 329
DB 1 DDTCSASPTATVIRKXKXNDPDDPHDNCIQLPKSNPDPQMTTKKXITRS 60
QY 330 NSCLTYGTAGVYVIMPDNTAVRENTIMQIXGTLINPSNVLAASSGKXTLT 389
DB 61 NSCLTYGTAGVYVIMPDNTAVRENTIMQIXGTLINPSNVLAASSGKXTLT 120
QY 390 VQTLDTLQSGMLAGNDTAPREVTYIGFRDLCMESXGSAWVEFCXSSQXKXWALYGD 449
DB 121 VQTLDTLQSGMLAGNDTAPREVTYIGFRDLCMESXGSAWVEFCXSSQXKXWALYGD 180
QY 450 GSIRPKMNOQCLTKRBSVSTINIVSCSXKXKRWTFNEXAIIKXXXXXQVQA 509
DB 181 GSIRPKMNOQCLTKRBSVSTINIVSCSXKXKRWTFNEXAIIKXXXXXQVQA 240
QY 510 NPKLRRIIIPATGKPNQWMLPV 532
DB 241 NPKLRRIIIPATGKPNQWMLPV 263

Search completed: December 11, 2003, 14:07:40
Job time : 35.8669 secs

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rabp

Page 1

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OM protein - protein search, using sw method

Run on: December 11, 2003, 14:01:14 / Search time 34.346 Seconds
(without alignment)

2866.029 Million cell updates/sec

Title: US-09-601-667C-1

Perfect score: 2616
Sequence: 1 YERLRRLVHTQXKEYRFP.....RRITYPATKRNQMLPFYX 533

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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2: /cgn2_6/prodata/1/pubpa/PCF_NEM_PUB.pep.*
3: /cgn2_6/prodata/1/pubpa/US06_NEM_PUB.pep.*
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5: /cgn2_6/prodata/1/pubpa/US07_NEM_PUB.pep.*
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11: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
17: /cgn2_6/prodata/1/pubpa/US60_NEM_PUB.pep.*
18: /cgn2_6/prodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	1267.5	48.5	263	9	US-09-347-064-10
2	1267.5	48.5	267	9	US-09-347-064-4
3	1231	47.1	576	12	US-10-083-336A-1
4	1135.5	44.2	252	9	US-09-347-064-8
5	1135.5	44.0	252	9	US-09-347-064-2
6	1135.5	44.0	252	9	US-10-282-993-3
7	1135.5	44.0	252	9	US-10-282-993-1
8	1135.5	44.0	252	9	US-10-282-993-1
9	1135.5	44.0	252	9	US-10-282-993-1
10	1135.5	44.0	252	9	US-10-282-993-1
11	1135.5	44.0	252	9	US-10-282-993-1
12	1135.5	44.0	252	9	US-10-282-993-1
13	1135.5	44.0	252	9	US-10-282-993-1
14	1135.5	44.0	252	9	US-10-282-993-1
15	1135.5	44.0	252	9	US-10-282-993-1
16	1135.5	44.0	252	9	US-10-282-993-1
17	1135.5	44.0	252	9	US-10-282-993-1
18	1135.5	44.0	252	9	US-10-282-993-1
19	1135.5	44.0	252	9	US-10-282-993-1
20	1135.5	44.0	252	9	US-10-282-993-1
21	1135.5	44.0	252	9	US-10-282-993-1
22	1135.5	44.0	252	9	US-10-282-993-1
23	1135.5	44.0	252	9	US-10-282-993-1
24	1135.5	44.0	252	9	US-10-282-993-1
25	1135.5	44.0	252	9	US-10-282-993-1
26	1135.5	44.0	252	9	US-10-282-993-1
27	1135.5	44.0	252	9	US-10-282-993-1
28	1135.5	44.0	252	9	US-10-282-993-1
29	1135.5	44.0	252	9	US-10-282-993-1
30	1135.5	44.0	252	9	US-10-282-993-1
31	1135.5	44.0	252	9	US-10-282-993-1
32	1135.5	44.0	252	9	US-10-282-993-1
33	1135.5	44.0	252	9	US-10-282-993-1
34	1135.5	44.0	252	9	US-10-282-993-1
35	1135.5	44.0	252	9	US-10-282-993-1
36	1135.5	44.0	252	9	US-10-282-993-1
37	1135.5	44.0	252	9	US-10-282-993-1
38	1135.5	44.0	252	9	US-10-282-993-1
39	1135.5	44.0	252	9	US-10-282-993-1
40	1135.5	44.0	252	9	US-10-282-993-1
41	1135.5	44.0	252	9	US-10-282-993-1
42	1135.5	44.0	252	9	US-10-282-993-1
43	1135.5	44.0	252	9	US-10-282-993-1
44	1135.5	44.0	252	9	US-10-282-993-1
45	1135.5	44.0	252	9	US-10-282-993-1

15	280	10.7	247	12	US-10-375-209A-34	Sequence 34, Appl
16	277	10.6	251	12	US-10-127-890-101	Sequence 102, App
17	277	10.4	251	12	US-10-127-890-101	Sequence 102, App
18	272	10.4	251	12	US-10-127-890-101	Sequence 102, App
19	272	10.4	251	12	US-10-127-890-101	Sequence 102, App
20	271.5	10.4	332	9	US-09-765-527-251	Sequence 211, App
21	271	10.4	251	12	US-10-127-890-99	Sequence 99, Appl
22	270	10.3	316	12	US-10-074-596-1	Sequence 1, Appl
23	270	10.3	251	12	US-10-127-890-100	Sequence 100, App
24	269	10.3	251	12	US-10-127-890-105	Sequence 105, App
25	268	10.2	251	9	US-09-765-527-247	Sequence 247, App
26	268	10.2	251	12	US-10-127-890-2	Sequence 2, Appl
27	268	10.2	251	12	US-10-127-890-103	Sequence 103, App
28	268	10.2	251	12	US-10-127-890-106	Sequence 106, App
29	268	10.2	251	12	US-10-127-890-108	Sequence 108, App
30	268	10.2	507	12	US-10-127-890-11	Sequence 11, Appl
31	267	10.2	251	12	US-10-127-890-11	Sequence 11, Appl
32	267	10.2	251	12	US-10-127-890-109	Sequence 109, App
33	265	10.1	251	12	US-10-127-890-107	Sequence 107, App
34	265	10.1	293	9	US-09-765-527-253	Sequence 253, App
35	265	10.1	309	9	US-09-765-527-253	Sequence 253, App
36	264.5	10.1	198	12	US-10-083-336A-3	Sequence 3, Appl
37	264.5	10.1	198	12	US-10-083-336A-7	Sequence 7, Appl
38	264.5	10.1	199	12	US-10-083-336A-5	Sequence 5, Appl
39	264.5	10.1	200	12	US-10-083-336A-10	Sequence 10, Appl
40	264.5	10.1	185	12	US-10-127-890-7	Sequence 7, Appl
41	264.5	10.1	185	12	US-10-127-890-7	Sequence 7, Appl
42	242.5	9.3	188	12	US-10-083-336A-6	Sequence 6, Appl
43	242.5	9.3	188	12	US-10-083-336A-6	Sequence 6, Appl
44	242.5	9.3	189	12	US-10-083-336A-6	Sequence 6, Appl
45	242.5	9.3	190	12	US-10-083-336A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-347-064-10 Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eck, Jürgen
APPLICANT: Schmidt, Arno
TITLE OF INVENTION: Zinc, Holger
TITLE OF INVENTION: Ribosome-inactivating Proteins of the msl-ecce Viscum
TITLE OF INVENTION: Album
CURRENT APPLICATION NUMBER: US/09/347, 064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP99/00009
EARLIER FILING DATE: 1999-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 263
DESCRIPTION: Viscum album
US-09-347-064-10
Query Match 48.5% Score 1267.5; DB 9; Length 263;
Best Local Similarity 91.6%; Pred. No. 1.7e-112;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
QY 270 DVTGSAEPPIVIRGXGKVDVDDPHGQOLWPKSKNDPQOLMTIKKDDYRS 329
DB 1 DVTGSAEPPIVIRGXGKVDVDDPHGQOLWPKSKNDPQOLMTIKKDDYRS 60
QY 330 NSCLITGTYAGVYVIFPCNTAVAEATVQATKNGTIIINPRSLVLAASGKIGTTLT 389
DB 61 NSCLITGTYAGVYVIFPCNTAVAEATVQATKNGTIIINPRSLVLAASGKIGTTLT 120

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OY 390 VOTLDYTLGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 449
DB 121 VQDLYTLGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 179
OY 450 GSIRKX 509
DB 180 GSIRKX 239
OY 510 NPKLRITITIPATKX 532
DB 240 NPKLRITITIPATKX 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
INVENTOR: Beck, Jürgen
TITLE OF INVENTION: Ribosome-inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 48.5% Score 1267.5 DB 9 Length 267
Best Local Similarity 91.5% Pred. No. 123
Matches 241 Conservative 1 Mismatches 120 Indels 1 Gaps 1
OY 270 DDTGASAPPTVIVGKX 329
DB 1 DDTGASAPPTVIVGKX 60
OY 330 NSGCTTGTGTAAGYVIMPCDNTAREATINQIMKXGIIINFSNLYLAASSIGKTTLT 389
DB 61 NSGCTTGTGTAAGYVIMPCDNTAREATINQIMKXGIIINFSNLYLAASSIGKTTLT 120
OY 390 VOTLDYTLGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 449
DB 121 VQDLYTLGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 179
OY 450 GSIRKX 509
DB 180 GSIRKX 239
OY 510 NPKLRITITIPATKX 532
DB 240 NPKLRITITIPATKX 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Patent No. US2003001655A1
GENERAL INFORMATION:
APPLICANT: Oleon, Mark A
INVENTOR: Oleon, Mark A
TITLE OF INVENTION: Ribosome-inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1

TITLE OF INVENTION: Ribonuclease and Methods of Making and Using Thereof
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 576
TYPE: PRT
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match 47.1% Score 1231 DB 12 Length 576
Best Local Similarity 49.1% Pred. No. 61e-128
Matches 263 Conservative 74 Mismatches 179 Indels 20 Gaps 11
OY 9 TQQTGKX 66
DB 48 TQQTGKX 105
OY 67 TQQTGKX 123
DB 106 TQQTGKX 165
OY 124 GH-ROIPGKX 179
DB 166 GH-ROIPGKX 225
OY 180 XINSKX 239
DB 226 RIRKX 285
OY 286 IILAVYRCAPPSQ---FELIRVYVPMFADV-CNDPEYIVIRVGRVGCVDVAD 340
DB 297 DFDGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 356
OY 341 DFDGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 400
DB 357 ACTGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 415
OY 401 ACTGQGLTANQDAPREYITIGFEDICENSKGVSWEFCSSQKXKXMAIYGD 460
DB 417 FRLGKX 476
OY 450 GSIRKX 509
DB 461 GSIRKX 519
OY 477 GSIRKX 532
DB 520 GSIRKX 575

RESULT 4
US-09-347-064-8
Sequence 8, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
INVENTOR: Beck, Jürgen
TITLE OF INVENTION: Ribosome-inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1

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SEQ ID NO 8
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-8

Query Match
Best Local Similarity 44.2%; Score 115.5; DB 9; Length 252;
Best Local Similarity 91.7%; Pred. No. 1,3e-120;
Matches 233; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

QY 1 YERLRATVHQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTN 60
DB 1 YERLRATVHQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTN 60
QY 61 QGDSSTAIADVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDL 120
DB 61 QGDSSTAIADVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDL 119
QY 121 RYAGHRDQIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRX 180
DB 121 RYAGHRDQIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRX 179
QY 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 240
DB 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 239
QY 241 LAIMLFVCGERP 253
DB 241 LAIMLFVCGERP 252

RESULT 5
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eck, Jürgen
INVENTOR: Eck, Jürgen
APPLICANT: Zinke, Holger
INVENTOR: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTOR: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOURCE: Patent in Ver. 2.1
SEQ ID NO: 2
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-2

Query Match
Best Local Similarity 44.0%; Score 115.5; DB 9; Length 252;
Best Local Similarity 91.7%; Pred. No. 1,3e-119;
Matches 231; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

QY 1 YERLRATVHQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTN 60
DB 1 YERLRATVHQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTN 61
QY 61 QGDSSTAIADVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDL 120
DB 61 QGDSSTAIADVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDL 120
QY 121 RYAGHRDQIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRX 180
DB 121 RYAGHRDQIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRX 180

QY 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 240
DB 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 240
QY 241 LAIMLFVCGERP 252
DB 241 LAIMLFVCGERP 252

RESULT 6
US-10-282-935-3
Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
INVENTOR: GIBBIE, VICTOR F.
APPLICANT: SWALLSHAW, JOAN
INVENTOR: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTOR: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: 015D,884US; US/10/282,935
CURRENT FILING DATE: 2002-10-28
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abrus precatorius
US-10-282-935-3

Query Match
Best Local Similarity 41.7%; Score 454.5; DB 12; Length 251;
Best Local Similarity 41.7%; Pred. No. 5,6e-42;
Matches 105; Conservative 34; Mismatches 88; Indels 25; Gaps 6;

QY 9 THQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTNQGXDTA 68
DB 9 THQTGKYEPRITLLRDVSSGFSNIEILRQSTIPVSDAQRFVLVELTNQGXDTA 66
QY 69 AIDVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDLRRVAGH-RD 127
DB 69 AIDVTNLYVVAQAGQSYFLDAPRGAETHLFTGTRKSLFPYGSYXDLRRVAGH-RD 125
QY 120 QIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRXINSGXSF 187
DB 120 QIPGIGDLOISVLAEXGSGSTXQASILLIOMISEARFPILRRKRXINSGXSF 185
QY 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 240
DB 181 INSGASFLPDVYMLELFTSMGQSTQVQSHSTQGVFNPRILALPPGNFVTLNVADV 236
QY 237 VASLAINFVCG 248
DB 237 VASLAINFVCG 247

RESULT 7
US-10-282-935-1
Sequence 1, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
INVENTOR: GIBBIE, VICTOR F.
APPLICANT: SWALLSHAW, JOAN
INVENTOR: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTOR: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: US/10/282,935
CURRENT APPLICATION NUMBER: US/10/282,935

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1 CURRENT FILING DATE: 2002-10-29
2 PRIOR APPLICATION NUMBER: 09/558, 873
3 PRIOR FILING DATE: 2000-03-30
4 PRIOR APPLICATION NUMBER: 60/126, 826
5 PRIOR FILING DATE: 1999-03-30
6 NUMBER OF SEQ ID NOS: 23
7 SOFTWARE: Patent Ver. 2.1
8 SEQ ID NO: 1
9 LENGTH: 267
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
13 US-10-282-935-1

Query Match 14.4%; Score 377.5; DB 12; Length 267;
Best Local Similarity 38.8%; Pred. No. 2.3e-33;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;

13 THQTTGKXFRFTLLADYSSGS-FSNRPL-RGSTIPNSDAPRYALNQGDX 66
14 TAGATVQSYTNFIRVGRILTDGVRHEIFVLPVRVGLFN--QRIIVLSNHAELSV 70
15 67 TAAIDVTNXXVYVAGDQSYELR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
16 71 TAAIDVTNXXVYVAGDQSYELR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
17 124 GH-RDQIPGIXQIOLQSVYAL--KPGGSTRXQARSILILQMSFAARPNPILMRXQ 179
18 131 GNLRENTLGNPFLKALSLVYTGCTQLPLNLSFLICQMSLSEAKRQVIGERNET 190
19 130 XNSGKSFIPDXMYLELFTSGQCGTOYQHSCTGQFNXPRLAIXGNVTLLXNPRVYA 239
20 131 RIRYNRSAFDPESVITLNSWRLTAIQSNQAFAPAPQLGRNSGKSFYVDSILIP 250
21 240 SLALMFVCGERRSS 254
22 251 IIALMYRCAPRESS 265

Db 251 IIALMYRCAPRESS 265

RESULT 8
US-10-127-890-1
Sequence 1, Application US/10127890
Patent No. US20020166398A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESS: McDonalds, Held & Malloy, Ltd
SUITE 500 West Madison Street, 34th Floor
CHICAGO, ILLINOIS
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, Version #1.25
CURRENT FILING DATE: US/10/127,890
FILING DATE: 23-MAY-2002
CLASSIFICATION DATA: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/06/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994

1 APPLICATION NUMBER: US 08/064,691
2 FILING DATE: 12-MAY-1993
3 APPLICATION NUMBER: US 07/988,430
4 FILING DATE: 09-DEC-1992
5 APPLICATION NUMBER: US 07/901,707
6 FILING DATE: 07-NOV-1991
7 FILING DATE: 04-NOV-1991
8 ATTORNEY/AGENT INFORMATION:
9 NAME: McNicholas, Janet M.
10 REGISTRATION NUMBER: 32,918
11 REFERENCE/DOCKET NUMBER: 200-70, P4
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 312/707-8889
14 TELEFAX: 312/707-9155
15 TELE: 650 388-1248
16 INFORMATION FOR SEQ ID NO: 1:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 267 amino acids
19 TOPOLOGY: linear
20 MOLECULE TYPE: protein
21 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
22 US-10-127-890-1

Query Match 14.4%; Score 377.5; DB 12; Length 267;
Best Local Similarity 38.8%; Pred. No. 2.3e-33;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;

13 THQTTGKXFRFTLLADYSSGS-FSNRPL-RGSTIPNSDAPRYALNQGDX 66
14 TAGATVQSYTNFIRVGRILTDGVRHEIFVLPVRVGLFN--QRIIVLSNHAELSV 70
15 67 TAAIDVTNXXVYVAGDQSYELR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
16 71 TAAIDVTNXXVYVAGDQSYELR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
17 124 GH-RDQIPGIXQIOLQSVYAL--KPGGSTRXQARSILILQMSFAARPNPILMRXQ 179
18 131 GNLRENTLGNPFLKALSLVYTGCTQLPLNLSFLICQMSLSEAKRQVIGERNET 190
19 130 XNSGKSFIPDXMYLELFTSGQCGTOYQHSCTGQFNXPRLAIXGNVTLLXNPRVYA 239
20 131 RIRYNRSAFDPESVITLNSWRLTAIQSNQAFAPAPQLGRNSGKSFYVDSILIP 250
21 240 SLALMFVCGERRSS 254
22 251 IIALMYRCAPRESS 265

Db 251 IIALMYRCAPRESS 265

RESULT 9
US-09-792-793A-39
Sequence 3, Application US/09792793A
Patent No. US20020166370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DANA
TITLE REFERENCE: 25020-601D
CURRENT FILING DATE: US/09/792,793A
FILING DATE: 09-NOV-92
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 39
LENGTH: 247
TYPE: PRT

ORGANISM: Trichostanthus killowii

Query Match 11.8%; Score 309.5; DB 10; Length 247;
Best Local Similarity 34.7%; Pred. No. 1e-25; 94; Indels 13; Gaps 8;

Matches 89; Conservative 49; Mismatches 94; Indels 13; Gaps 8;

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us-09-601-667c-1.rpb

Page 5

13 TCKEYFFITLLADYVSSGFSNIPILKOSTIPVSDAQPFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNIRKALPBERKLYDIPILR--SSIPGS--QRYALHITWYADETISVALIDV 66
73 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 130
67 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 126
131 LGIXOLQSYXALXPGSGSTXQASSTILILQWISAAAREPILMRKXINSKGFEPD 190
127 LGIPALDSATITLFTYNNNS--ASALMWLQSTSEARKEITEQIGKRVK--TFIPS 182
191 XYMLELSTMGQOSTVOQ--HSTQVFNPNPKALIXGNFVILXNVRX--VIASIAIML 245
183 LAIISLNSMSALSXQIQIASTNMGQFESPVVILNNQVAVITTVDAVTVSNITALL 241
US-10-375-209A-39
Sequence 39, Application US/10375209A
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kiliowii
US-10-375-209A-39
Query Match 11.8%; Score 308.5; DB 12; Length 247;
Best Local Similarity 34.3%; Pred. No. 1,7e-25; Indels 13; Gaps 8;
Matches 83; Conservative 49; Mismatches 95;
13 TCKEYFFITLLADYVSSGFSNIPILKOSTIPVSDAQPFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNIRKALPBERKLYDIPILR--SSIPGS--QRYALHITWYADETISVALIDV 66
73 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 130
67 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 126
131 LGIXOLQSYXALXPGSGSTXQASSTILILQWISAAAREPILMRKXINSKGFEPD 190
127 LGIPALDSATITLFTYNNNS--ASALMWLQSTSEARKEITEQIGKRVK--TFIPS 182
191 XYMLELSTMGQOSTVOQ--HSTQVFNPNPKALIXGNFVILXNVRX--VIASIAIML 245
183 LAIISLNSMSALSXQIQIASTNMGQFESPVVILNNQVAVITTVDAVTVSNITALL 241
US-10-127-890-6
Sequence 6, Application US/10127890
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Compising Ribosome-Inactivating
NUMBERS OF SEQUENCES: 172
CORRESPONDENCE ADDRESS:
ADDRESSER: McDonalds, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-PC/MS-DOS
SOFTWARE: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,631
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 12,516
TELEPHONE: 312/707-8899
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
MOLECULAR WEIGHT: 27,816
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6
Query Match 11.7%; Score 306.5; DB 12; Length 247;
Best Local Similarity 34.3%; Pred. No. 1,7e-25; Indels 13; Gaps 8;
Matches 82; Conservative 49; Mismatches 95;
13 TCKEYFFITLLADYVSSGFSNIPILKOSTIPVSDAQPFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNIRKALPBERKLYDIPILR--SSIPGS--QRYALHITWYADETISVALIDV 66
73 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 130
67 TXXVYVYQADQOSYFLSDA--PRGAETHLFTGTREXSLPEFGSYXDLERYAGH--RDQIP 126
131 LGIXOLQSYXALXPGSGSTXQASSTILILQWISAAAREPILMRKXINSKGFEPD 190
127 LGIPALDSATITLFTYNNNS--ASALMWLQSTSEARKEITEQIGKRVK--TFIPS 182
191 XYMLELSTMGQOSTVOQ--HSTQVFNPNPKALIXGNFVILXNVRX--VIASIAIML 245
183 LAIISLNSMSALSXQIQIASTNMGQFESPVVILNNQVAVITTVDAVTVSNITALL 241
US-10-280-679B-4
Sequence 4, Application US/10280679B
GENERAL INFORMATION:
APPLICANT: Bion Science Corporation
TITLE OF INVENTION: Scale Biology Transformation Vectors
FILE REFERENCE: LSCC-0109-0503
CURRENT APPLICATION NUMBER: US/10/280,679B

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us-09-601-667c-1.rapb

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
SEQ ID NO: 1
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-127-890-111
Query Match 10.7%; Score 281; DB 12; Length 251;
Best Local Similarity 33.7%; Pred. No. 1,2e-22;
Matches 85; Conservative 34; Mismatches 113; Indels 20; Gaps 7;
QY 8 VTHQTKXEFYFILLRDY--VSSGSPSENIPLROSTIPVSDAQRVLYELINQGX 64
DB 5 VSFSTGATYIYVNLMLRVLKPKGNSHIPLRKKADDPKKA--FVLVALSNDGQ 62
QY 65 SKTALIVTNKYYVAYQAGDSYFLRDPAGAZTLFTGTRXSLPFKSYXDLERYAG 124
DB 125 HRPQPLGIXOL--TGSVYAKLXPGSRTKQASILLITOMISEARF---NPLIMRX 177
QY 122 YRETTDGIETPLRIGIKLDNNINIKYKTBLAGSLVIVQWSEARFTFENQIRNP 181
DB 178 ROKINSKSLPDXVMELETSWQSQSTQVQS--TGVFNNPYRLAIXGNFTLKNYRX 236
QY 182 QQRIR-----PANNTISLKNKGKLSFQIRTSANGWFSVLELRANGKKYVAVDQ 235
DB 237 VYASLALMFC 248
QY 236 VKPKLALIKFC 247

RESULT 15
US-09-792-793A-34
Sequence 34, Application US/09792793A
Patent No. US20020168370A1

GENERAL INFORMATION:
APPLICANT: BIONOLA, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DANA
FILE REFERENCE: 25020-601D
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 34
US-09-792-793A-34
Query Match 10.7%; Score 280; DB 10; Length 247;
Best Local Similarity 32.0%; Pred. No. 1.5e-22;
Matches 79; Conservative 52; Mismatches 98; Indels 18; Gaps 9;
QY 7 RYHQTQKXEFYFILLRDYSSGSPSENIPLROSTIPVSDAQRVLYELINQGX 66
DB 5 RUSGATF--TSGVFLKRLRPLRKYVNIPLRSS--ISGGRYTLHLYNADDT 60
QY 67 TRLDITNYYVAYQAGDSYFLRDPAGAZTLFTGTRXSLPFKSYXDLERYAG 125
DB 61 SVADVTAVYIMGLADDSYFPLASRTKAPVFKAKKVTLYSONERLQGNAG 120
QY 126 -RDOIPLGIXOL--TGSVYAKLXPGSRTKQASILLITOMISEARF---NPLIMRX 184
DB 121 IRENIFLPGPALDSATITLYVTAS--ASALVLLOSTASARKFEQOIGKVDK- 177
QY 185 XSLPDXVMELETSWQSQSTQVQ--HSTDGVNPNYRLAIXGN---FVLIMVRYXV 238
DB 178 -TFLSLATISLNNMALSNOIDASTNNQPSF--VLLIDNNQKVSITNAGRVV 234
QY 239 ASLALMFC 245
DB 235 SVIALLL 241

Search completed: December 11, 2003, 14:48:46
Job time : 35.348 secs

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Page 1

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OW protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 18.4536 Seconds
(without alignments)

1222.073 Million cell updates/sec

Title: US-09-601-667C-1

Sequence: 1 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 533

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:
1: /csm2_6/prodata/1/iaa/5A.COMB.pep.*
2: /csm2_6/prodata/1/iaa/5B.COMB.pep.*
3: /csm2_6/prodata/1/iaa/5C.COMB.pep.*
4: /csm2_6/prodata/1/iaa/6A.COMB.pep.*
5: /csm2_6/prodata/1/iaa/6B.COMB.pep.*
6: /csm2_6/prodata/1/iaa/6C.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2805	95.8	564	3	US-08-776-059-35
2	1267.5	48.5	263	3	US-08-776-059-43
3	1267.5	48.5	264	3	US-08-776-059-33
4	1155.5	44.2	253	3	US-08-776-059-31
5	1109.5	42.4	340	1	US-08-378-761A-77
6	1107.5	42.4	350	1	US-08-378-761A-77
7	1073.5	42.6	350	1	US-08-378-761A-77
8	454.5	17.4	251	4	US-08-538-873-35
9	447	17.1	250	1	US-08-378-761A-71
10	447	17.1	250	1	US-08-485-286-71
11	404.5	15.5	534	2	US-08-356-786-10
12	377.5	14.4	267	1	US-07-991-707-1
13	377.5	14.4	267	1	US-07-998-430-1
14	377.5	14.4	267	1	US-08-218-382-16
15	377.5	14.4	267	1	US-08-443-313-1
16	377.5	14.4	267	1	US-08-443-313-1
17	377.5	14.4	267	1	US-08-477-484-1
18	377.5	14.4	267	2	US-08-646-360-1
19	377.5	14.4	267	2	US-08-318-793D-61
20	377.5	14.4	267	3	US-08-839-765-1
21	377.5	14.4	267	3	US-09-136-389-1
22	377.5	14.4	267	4	US-09-610-838-1
23	377.5	14.4	267	4	US-09-538-873-1
24	377.5	14.4	267	5	US-09-538-873-1
25	377.5	14.4	267	5	US-09-538-873-1
26	377.5	14.4	267	5	US-09-538-873-1
27	377.5	14.4	267	5	US-09-538-873-1

28	373.5	14.3	280	6	US-08-776-059-35
29	342.5	12.3	252	1	US-08-378-761A-74
30	342.5	12.3	252	1	US-08-378-761A-74
31	308.5	11.8	267	1	US-08-485-286-74
32	306.5	11.7	247	1	US-08-485-1138-6
33	306.5	11.7	247	1	US-08-477-484B-6
34	306.5	11.7	247	1	US-08-477-484B-6
35	306.5	11.7	247	3	US-08-646-360-6
36	306.5	11.7	247	3	US-08-646-360-6
37	306.5	11.7	247	3	US-08-646-360-6
38	306.5	11.7	247	3	US-08-646-360-6
39	301.5	11.5	289	1	US-07-923-638-6
40	301.5	11.5	289	2	US-08-482-820-4
41	301.5	11.5	289	3	US-08-482-820-4
42	301.5	11.5	289	3	US-08-482-820-4
43	301.5	11.5	289	3	US-08-482-820-4
44	291	11.1	263	1	US-07-901-707-4
45	291	11.1	263	1	US-07-988-430-4

ALIGNMENTS

Result 1
US-08-776-059-35
Sequence 35, Application US/0876059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, HANS
APPLICANT: ECK, JURGEN
APPLICANT: ECK, AXEL
APPLICANT: ECK, ROGER
APPLICANT: ECK, ROGER
FILE REFERENCE: 674503-3003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: 9510949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 36
SEQUENCE NO. 35
SEQ ID NO 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match 95.8% Score 2505, DB 3, Length 564;
Best Local Similarity 91.9%, Pred. No. 8.1e-274;
Matches 489; Conservative 3%; Indels 2; Gaps 2;

1 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
2 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
3 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
4 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
5 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
6 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
7 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
8 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
9 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
10 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
11 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
12 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
13 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
14 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
15 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
16 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
17 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
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24 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
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26 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
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30 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
31 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
32 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
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39 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
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41 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
42 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
43 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
44 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60
45 YERLALRYHOTGKXKFR.....RLIIYPATGKPNQMLPVX 60

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Page 2

Db 333 GNOIOLMPSKSNNDPNOLWTIKEDGFISSGCLTYGYTGYWIMFDONTAVRENTLW 392
Qy 361 QIYXNGTINPNSNVLVAASSGKIGTITVQTLDTYLGQWLAGNDTAPREVTYGFRL 420
Db 393 QIYXNGTINPNSNVLVAASSGKIGTITVQTLDTYLGQWLAGNDTAPREVTYGFRL 452
Qy 421 CMESXGSWTCTCSGCKOXXMAYGDSIRKONODCTCXRSNQTIVYUSCX 480
Db 453 CMESNGSWTCTCSGCKOXXMAYGDSIRKONODCTCXRSNQTIVYUSCX 511
Qy 481 XSKXGWFVFNEXAILNLKXXXXXVDAQAPPLRRIIYPATGKPNOMLTPV 532
Db 512 GSSGQWVFNEXAILNLKXXXXXVDAQAPPLRRIIYPATGKPNOMLTPV 563
RESULT 2
US-08-776-059-43
Sequence 43; Application US/08776059B
Best local similarity 91.6%; Pctd No. 1;e-114;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776/059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
TYPE: PRT
LENGTH: 263
ORGANISM: Viscum album
US-08-776-059-43

Query Match 48.5%; Score 1267.5; DB 3; Length 263;
Best local similarity 91.6%; Pctd No. 1;e-114;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
Qy 270 DDTVCASBPVRIYGRXGMXVDVDDPDGNGQIOLMPSKSNNDPNOLWTIKEDGFISS 329
Db 1 DDTVCASBPVRIYGRXGMXVDVDDPDGNGQIOLMPSKSNNDPNOLWTIKEDGFISS 60
Qy 330 NSGCLTYGYTAGYVWIMFDONTAVRENTLWQIYXNGTINPNSNVLVAASSGKIGTITL 389
Db 61 NSGCLTYGYTAGYVWIMFDONTAVRENTLWQIYXNGTINPNSNVLVAASSGKIGTITL 120
Qy 390 VQTLDTYLGQWLAGNDTAPREVTYGFRLCMESNGSWTCTCSGCKOXXMAYGDSIRK 449
Db 121 VQTLDTYLGQWLAGNDTAPREVTYGFRLCMESNGSWTCTCSGCKOXXMAYGDSIRK 179
Qy 450 GSIRPKNODDCTCXGSDSVYVINIVSCSXGXKXQWVFNEXAILNLKXXXXXVDAQA 509
Db 180 GSIRPKNODDCTCXGSDSVYVINIVSCSXGXKXQWVFNEXAILNLKXXXXXVDAQA 239
Qy 510 NPKLRRIIYPATGKPNOMLTPV 532
Db 240 NPKLRRIIYPATGKPNOMLTPV 262

RESULT 3
US-08-776-059-33
Sequence 33; Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen

APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776/059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
TYPE: PRT
LENGTH: 264
ORGANISM: Viscum album
US-08-776-059-33
Query Match 48.5%; Score 1267.5; DB 3; Length 264;
Best local similarity 91.7%; Pctd No. 1;e-122;
Matches 241; Conservative 1; Mismatches 19; Indels 1; Gaps 1;
Qy 270 DDTVCASBPVRIYGRXGMXVDVDDPDGNGQIOLMPSKSNNDPNOLWTIKEDGFISS 329
Db 2 DDTVCASBPVRIYGRXGMXVDVDDPDGNGQIOLMPSKSNNDPNOLWTIKEDGFISS 61
Qy 330 NSGCLTYGYTAGYVWIMFDONTAVRENTLWQIYXNGTINPNSNVLVAASSGKIGTITL 389
Db 62 NSGCLTYGYTAGYVWIMFDONTAVRENTLWQIYXNGTINPNSNVLVAASSGKIGTITL 121
Qy 390 VQTLDTYLGQWLAGNDTAPREVTYGFRLCMESNGSWTCTCSGCKOXXMAYGDSIRK 449
Db 122 VQTLDTYLGQWLAGNDTAPREVTYGFRLCMESNGSWTCTCSGCKOXXMAYGDSIRK 180
Qy 450 GSIRPKNODDCTCXGSDSVYVINIVSCSXGXKXQWVFNEXAILNLKXXXXXVDAQA 509
Db 181 GSIRPKNODDCTCXGSDSVYVINIVSCSXGXKXQWVFNEXAILNLKXXXXXVDAQA 240
Qy 510 NPKLRRIIYPATGKPNOMLTPV 532
Db 241 NPKLRRIIYPATGKPNOMLTPV 263

RESULT 4
US-08-776-059-31
Sequence 31; Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776/059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
TYPE: PRT
LENGTH: 253
ORGANISM: Viscum album
US-08-776-059-31
Query Match 44.2%; Score 1155.5; DB 3; Length 253;
Best local similarity 91.7%; Pctd No. 4.9e-122;
Matches 232; Conservative 1; Mismatches 19; Indels 1; Gaps 1;
Qy 1 YERLRVHTQTCXKFERFILLRDIYSSGSPSNIEPLRSGTIPVSDQRFVLEVLN 60

Db 2 YERIKLVHTGTEGFEFTLLADYVSSGSFSENIPLRQSTIPVSDAQRFLVELTM 61
 QY 61 QGKSKTALIDVTNXYVAVQAGDSYFLADAPGAETHLFTGTXXSLSPFGSYXDL 120
 Db 62 QGDSITRALIDVTNXYVAVQAGDSYFLADAPGAETHLFTGTXXSLSPFGSYXDL 120
 QY 121 RYAGHRDQIPGIXOLIOGYALRXPQSTKXASIIILIMISFAPRPPIIAREXOX 180
 Db 121 RYAGHRDQIPGIXOLIOGYALRXPQSTKXASIIILIMISFAPRPPIIAREXOX 180
 QY 181 INSGXSLFDXYMLBLETSMGQSTOVQSHSTGVFNNPRLAIXXGNFTLXNVXVIA 240
 Db 181 INSGXSLFDXYMLBLETSMGQSTOVQSHSTGVFNNPRLAIXXGNFTLXNVXVIA 240
 QY 241 LAIMLFCVGERPS 253
 Db 241 LAIMLFCVGERPS 253

RESULT 5

US-08-378-761A-77
 ; Sequence 77, Application us/08378761A
 ; Patent No. 5635384
 ; GENERAL INFORMATION:
 ; APPLICANT: WALSH, TERENCE A
 ; APPLICANT: HEY, TIMOTHY D
 ; APPLICANT: MORGAN, ALICE ER
 ; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 ; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: ANDREA T. BORUCKI
 ; STREET: 9330 ZIONSVILLE ROAD
 ; CITY: INDIANAPOLIS
 ; STATE: IN
 ; COUNTRY: US
 ; ZIP: 46268
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentia Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/378,761A
 ; FILING DATE: 26-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BORUCKI, ANDREA T
 ; REGISTRATION NUMBER: 33651
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (317) 337-4846
 ; INFORMATION FOR SEQ ID NO: 77:
 ; LENGTH: 540 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-378-761A-77

Query Match

Best Local Similarity 45.28; Seed No. 43e-118; Indels 19; Gaps 10;
 Matches 242; Conservative 79; Identical 19; Gaps 10;

QY 9 THOFTGKYEFTLLRDVYSSGS-FSENIPL-RQSTIPVSDAQRFLVELTMQGXDX 66
 Db 13 TADAVESYTFIRAVSHLTGADVREHIVLPKRVGLPIE--QFTIVLESNABELSV 70
 QY 67 TLAIDVTNXYVAVQAGDSYFLADAPGAETHLFTGTXXSLSPFGSYXDLERYA 123

Db 71 TLAIDVTNXYVAVQAGDSYFLADAPGAETHLFTGTXXSLSPFGSYXDLERYA 130
 QY 124 GHRDQIPGIXOLIOGYALRXPQSTKXASIIILIMISFAPRPPIIAREXOX 180
 Db 131 GRENTEHGTGLEDAISALYYSTGQIPLIASFWCIOMISAAFPYIEGRKTR 190
 QY 181 INSGXSLFDXYMLBLETSMGQSTOVQSHSTGVFNNPRLAIXXGNFTLXNVXVIA 240
 Db 191 INSGXSLFDXYMLBLETSMGQSTOVQSHSTGVFNNPRLAIXXGNFTLXNVXVIA 240
 QY 241 LAIMLFCVGERPS 253
 Db 241 LAIMLFCVGERPS 253
 QY 251 IALVRCAPPESQ---FSLIRFVYNNADV-CMDEPIVHIVRNOLCVDTGEE 305
 Db 251 IALVRCAPPESQ---FSLIRFVYNNADV-CMDEPIVHIVRNOLCVDTGEE 305
 QY 298 FPDGNOIOLWPKSKNDPNQJMTIKEDXTIRNSGCLTYGYTGYVMI FPDGNAVER 357
 Db 306 FPDGNOIOLWPKSKNDPNQJMTIKEDXTIRNSGCLTYGYTGYVMI FPDGNAVER 357
 QY 358 TIMQVXNGTILNPSNVLAAASGIKOTLVOTLDYTLGQWLAGNDAPREVITYGF 417
 Db 366 TIMQVXNGTILNPSNVLAAASGIKOTLVOTLDYTLGQWLAGNDAPREVITYGF 417
 QY 418 BELQMSXGIVYFTKSGXQXNXYLVAGSGIRKXQDQCTEXRGSVSTYVIA 425
 Db 426 KXGICQANSGKWLDCETSEKAEQ-QWALYASGIRKQNDNCITDANKIYVIALS 484
 QY 478 CSXXSXKRWVFTNEXAIIINLKXXXDVQANPRLRIIIPATGKNCNMWLPV 532
 Db 485 GCPASSQQRWFRNDGIIINLVNVLVYRSDPALKQIIVHPHGININQMLPL 539

RESULT 6

US-08-385-286-77
 ; Sequence 77, Application us/08485286
 ; Patent No. 5646026
 ; GENERAL INFORMATION:
 ; APPLICANT: WALSH, TERENCE A
 ; APPLICANT: HEY, TIMOTHY D
 ; APPLICANT: MORGAN, ALICE ER
 ; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 ; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: ANDREA T. BORUCKI
 ; STREET: 9330 ZIONSVILLE ROAD
 ; CITY: INDIANAPOLIS
 ; STATE: IN
 ; COUNTRY: US
 ; ZIP: 46268
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentia Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,286
 ; FILING DATE: 26-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BORUCKI, ANDREA T
 ; REGISTRATION NUMBER: 33651
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (317) 337-4846
 ; INFORMATION FOR SEQ ID NO: 77:
 ; LENGTH: 540 amino acids
 ; TYPE: amino acid

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us-09-601-667c-1.ra1

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match 42.4%; Score 1109.5; DB 1; Length 540;
Best Local Similarity 45.2%; Pred. No. 2.5e-116;
Matches 242; Conservative 79; Mismatches 195; Indels 19; Gaps 10;

QY 9 TQQTGKYEPRFTILRDYVSSGS-FSENIPL-L-RGRTIVSDAQRFVLELNGCKDSX 66
DB 13 TADAVESYTNFIRAVRSHLTGADVHEHIVLPNNVGLFIS--QFPIIVELSNHAEISV 70
QY 67 TAAIDVTNXYVAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVA 123
DB 71 TAAIDVTNXYVAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVA 130
QY 124 GRRDQIPGLXQILGQSYFAL--XPGSGSTKXKASILLIIONISEAARFPIIMKXKQX 180
DB 131 GIRENIELGPELEDAISALYVYSTCTQIPIILRSPFVCIOWISEAARFPIIMKXKQX 190
QY 181 INSGXSLPDXMLETSVGGQSTQVSHDGVFNNKXLAIXXGNFTLXNVRXVIA 240
DB 191 IRYNNRSDPDESVITLSENGRSLTAIDSGNQPASPILOGRNKGKENVIVSLIPI 250
QY 241 LAIMLVGGERSSDVRKAPVLEPIVAD--DTCASAPVAVIYKXAKTQVRDD 297
DB 251 LAIMLVGGERSSDVRKAPVLEPIVAD--DTCASAPVAVIYKXAKTQVRDD 305
QY 298 FHDGNOIOLMPSKANDPNOIITKXITRNSGCLTGYTAQVYVHPDCTVAREE 357
DB 306 FHDGNOIOLMPSKANDPNOIITKXITRNSGCLTGYTAQVYVHPDCTVAREE 365
QY 358 TIWQVWNGTIIINRSNIVLAASSGIGTITVQTLDTLGGWLANVPAAREVITGP 417
DB 366 FHWQIMDNRTIINRSGLVLAASSNGSTRLVQVNIYVAVSQMPLNNQDFVITIGL 425
QY 418 RDLCHESNGSYVETCCSSQXKXALYGGSIIPRONOCCITGGDSVITNIVS 477
DB 426 YGWCQANSKXWLEDTSEKAEQ-QNALYADSGIIPQQRNDCLTDANIKGTIVKILS 484
QY 478 CSXKXQXRVFTNEKALINIKKXXXXDVAKMFKRLRIIYVATGKXQNMFLV 532
DB 485 CGPSSGQRMFKNDGTILNLYGLVDVRRSDPSIKQIIVHFFGMLQNIWPL 539

RESULT 7
US-08-776-059-39
Sequence 39; Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 6/74503-2003
CURRENT APPLICATION NUMBER: US/08/776, 0598
CURRENT FILING DATE: 1999-06-25
EARLIER FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-39

Query Match 41.0%; Score 1073.5; DB 3; Length 235;
Best Local Similarity 51.9%; Pred. No. 7.8e-113;

Matches 217; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY 18 PRFTILRDYVSSGSFSENIPL-RGRTIVSDAQRFVLELNGCKDSXTRAIDVTNXYV 77
DB 1 PRFTILRDYVSSGSFSENIPL-RGRTIVSDAQRFVLELNGCKDSXTRAIDVTNXYV 60
QY 78 VAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVAHQDQIPGLXQIL 137
DB 61 VAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVAHQDQIPGLXQIL 119
QY 138 QSYXALXPGSGSTKXKASILLIIONISEAARFPIIMKXKQILNGKXSLPDXMLE 197
DB 120 QSYXALXPGSGSTKXKASILLIIONISEAARFPIIMKXKQILNGKXSLPDXMLE 179
QY 198 INSGXSLPDXMLETSVGGQSTQVSHDGVFNNKXLAIXXGNFTLXNVRXVIA 253
DB 180 INSGXSLPDXMLETSVGGQSTQVSHDGVFNNKXLAIXXGNFTLXNVRXVIA 235

RESULT 8
US-09-538-873-3
Sequence 3; Application US/09538873
Patent No. 6566500
GENERAL INFORMATION:
APPLICANT: CHITZ, VICTOR F.
APPLICANT: CHITZ, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
FILE REFERENCE: US/09/538, 873
CURRENT APPLICATION NUMBER: US/09/538, 873
CURRENT FILING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 60/126, 926
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 281
TYPE: PRT
ORGANISM: Atrus precatorius
US-09-538-873-3

Query Match 17.4%; Score 454.5; DB 4; Length 251;
Best Local Similarity 41.7%; Pred. No. 6.4e-43;
Matches 105; Conservative 34; Mismatches 88; Indels 25; Gaps 6;

QY 9 TQQTGKYEPRFTILRDYVSSGSFSENIPL-RGRTIVSDAQRFVLELNGCKDSXTRA 68
DB 9 TQQTGKYEPRFTILRDYVSSGSFSENIPL-RGRTIVSDAQRFVLELNGCKDSXTRA 66
QY 69 AIDVTNXYVAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVAHQ 127
DB 67 AIDVTNXYVAYQAGQSYFAR-DAPRGAEL-THTFTGTRKSSLPFGSGYXDLERVAHQ 125
QY 128 QIPGLXQILGQSYFALXKXPGSGSTKXKASILLIIONISEAARFPIIMKXKQILNG 187
DB 126 QIPGLXQILGQSYFALXKXPGSGSTKXKASILLIIONISEAARFPIIMKXKQILNG 185
QY 188 LBDYXMLETSVGGQSTQVSHDGVFNNKXLAIXXGNFTLXNVRXVIA 236
DB 186 LBDYXMLETSVGGQSTQVSHDGVFNNKXLAIXXGNFTLXNVRXVIA 235
QY 237 VIASATMLPVC 248
DB 236 VIASATMLPVC 247

RESULT 9
US-08-378-761A-71
Sequence 71; Application US/08378761A
Patent No. 6339340
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 6/74503-2003
CURRENT APPLICATION NUMBER: US/08/378, 761A
CURRENT FILING DATE: 1999-06-25
EARLIER FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 71
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-378-761A-71

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us-09-601-667c-1.xai

Page 5

APPLICANT: WALSH, TERENCE A
 APPLICANT: HEY, TIMOTHY D
 APPLICANT: MORGAN, ALICE ER
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANDREA T. BORUCKI
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release H.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BORUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBERS: 38272B
 TELECOMMUNICATION INFORMATION:
 INNOVATION FOR SEQ ID NO: 1676
 INNOVATION FOR SEQ ID NO: 1676
 SEQUENCE CHARACTERISTICS: 71:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IS-08-378-761A-71

Query Match	Similarity	47.1%	Score	447	DB 1	Length	250	
Matches	Conservative	105	Matches	34	Indels	26	Gaps	7
Qy	9	THQYTGKGFPRITLLRPLRYSQSSFSNNEIPILRQSTIPSPDAQRVVEITLQCKQSNXTA	66					
Dy	9	TEGASQYKQKQITLALRR-LKQGLHLLPDPF-LLOERRRIVTLENSDTLSLE	66					
Qy	69	ALYNNKYYVVAQAGQSGFPLRARGAERHLEFGCTKSSLPFGQSKLRRPAGH-ND	127					
Dy	67	GLVNNKYYVVAARQSGSPFLRRASSSNPVFTGTD-HSLPFGYGLGLERHAHQSD	125					
Qy	128	QIFGATQYKQLQGLQALRAGSGSTRQASATLITQIMISAPANNILMRKQXINSQSF	187					
Dy	126	QIFELQALTHQISFSGSGNDKERRATLITVQVAAERRYINRVRVSIQTGTF	185					
Qy	188	LPLPYMTELETSQSDTVQSHSTGVPANNPFLAIKGNVTLINVXK	236					
Dy	186	QPGAAHSLHNNK-DMLRQVDSVQDTIRNQ-----VLTNNIRFVYDLSLHP	234					
Qy	237	VIRASATLMEFVC	248					
Dy	235	TVAVATLMEFVC	246					

US-08-485-286-73
 RESULT 10
 Publication US/08485286
 Patent No. 5646026
 Patent No. 5646026 5646119
 GENERAL INFORMATION: TERENCE A
 INVENTOR: HEYTIMOTHY D
 APPLICANT: MORGAN, ALEE ER
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: FRETICATOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
 TITLE OF INVENTION: USING
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS: BOROUCKI
 ADDRESSEE: ANDREA T. BOROUCKI
 STREET: 3310 ZOOVILLS ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: 08/485,286
 APPLICATION NUMBER: US/08/485,286
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 08/378761
 FILING DATE: 25-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BOROUCKI, ANDREA T.
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 382728
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 337-4946
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STANDARDS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-485-286-71

Query Match	11 %	Score 447	DB 1	Length 250
Best Local Similarity	41.7 %	Pred. No. 4,56 ± 42		
Matches 105	Conservative	34 Mismatches	87 Indels	26 Gaps
QY	THQTGKAEKRFETILARDVSGSSSEKVELPLRSGSTFYPDAQRVLVEILNQCKSKSTXA	68		
Db	9 TEGHSGSGGQVIAHREHL-RGLDHLIDVLPQPT-TLQERKRIIVELSGDSITSGIF	66		
OY	63 AIDVNNVYVAAGKQSGSTFLFARPAQAEHLFIPTGTRKASLSPFGSGXDLERVAGH-ED	127		
Db	67 GIVNNVAVARRGSTGSPFRKASASADYVLFPTGDS-HLFPFGTIGLGRNARHQ	125		
OY	128 QIFETIKIGLGVALKAPKSGSPKQKASILLIOWISPAARENVILMRKQXINSQSGSF	187		
Db	126 QIFELDQALIEFFRSGSGMDIEKARTIIVILQVVAARERIVSIRVRVSTQIGTGF	185		
OY	188 LPRXNMLFETSGKQSGSTVYVHSTDSGVFNKKALIXGNFTLVNTXK	236		
Db	146 QPAMNISLNNW-DMLRSGVSGDFFPQV-Q			
OY	237 VPSASLAIMLFPVC	248		
Db	235 TVVNAALMLFVC	246		

```

RESULT 11
US-08-356-786-10
Sequence 10, Application US/08356786
Patent No. 5833319
GENERAL INVENTION:
APPLICANT: Huxton, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Huxton, L. L.
APPLICANT: Rupp, David B.
TITLE OF INVENTION: Biotynthetic Binding Protein for Cancer-
TITLE OF INVENTION: Marker

```

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02109
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: CRP-053
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7000
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 acid
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-356-786-10

Query Match 15.5%; Score 404.5; DB 2; Length 534;
 Best Local Similarity 27.8%; Pred. No. 9.1e-37;
 Matches 142; Conservative 76; Mismatches 170; Indels 123; Gaps 22;

9 TQQTGKRYFRFTLIDVYSSGS-FSENIFLL-RGSTIVSDAGQFVYELTNQGXDK 66
 16 TQAGTVQSYNPIFVAVRGHITGADVREHLPVLRVGLPIN-QRFTLVLSNHALSY 73
 67 TPAIDVNNKYVAVYAGDQSYFLR-DAPRGAR--THFTGTRKSSLPFGSYXDLERYA 123
 74 TLADVTNAYVGVPRAGNSAFHFHNDQDEALHFLFDVQNNRYPAFGVNDLRLQLA 133
 124 GH-RDQIFLGIXQILQSYVAL--RXPQGSTKXKASILLIOWISEARFNPILMXRQ 179
 134 GMRLENITLNGPLEPALSALVYVSTGCTQLPLRASFICIQWISBARFVIGERT 193
 180 XINSGKSLPDXMLETSGQOQSTGVQVFNNEPRLAIXKXNFTLVNRYVIA 239
 194 RIRNRSAPDPSPVITLNSMRSLTAIQSSNQAFASPIQLRNGSKFSVYDSTILP 253
 240 SLAIMLFCVCGEPSSDVRVMPVITRPVYADVTCASBPYRIVGXKXAVVRDDDF 299
 254 IIALMYRCAPPPESQ--FSLIRPVVPFNADVCMDEBQLV-----Q 295
 300 DANOQLMPSKSNNDPQNLWTKRDXITRNSGCLTYG-----Y 339
 296 SGEFLK-----KFGS--TVK--ISCASSGTPANIGMMKQAPGGLKMGKINVT 343
 340 TA-CYV-----MIFCNRVRENT-----KQIVGTLIRK 372
 344 TQGSTVADPFRERAPLSLSANTAHQINNLNRSKATFCARRFGFAYGQCLTVS 403
 373 SNLYAASGIGKGTTLVQTLVYTLQGLWLANDTLPREVTIYGRFLCNESXGSAWE 432
 404 ASI--SSSGGGGS-----GGSGSG-----GSDIQMOSPSLSAS 438
 433 -----TKSSQ--XNXXV-ALVXGDSIR 453

Db 439 LGEVSLTCRASODIGNSLTWLSQHPDGTIX 469

RESULT 12
 US-07-901-707-1
 Sequence 1: Application US/07901707
 Sequence No. 576546
 GENERAL INFORMATION:
 APPLICANT: Bernhard, Susan L.
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Steve F.
 APPLICANT: Lane, Julie A.
 TITLE OF INVENTION: Materials Comprising and Methods of
 Title of Invention: Composition and Use for Ribosome-Inactivating Proteins
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS: O'Toole, Gerstein, Murray &
 ADDRESSEE: Michael J.
 STREET: Two First National Plaza, 20 South Clark
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/901,707
 FILING DATE: 19920619
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5376546 and, 576546
 REFERENCE/DOCKET NUMBER: 271229/30910
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 984-5750
 TELEFAX: (312) 984-5750
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-901-707-1

Query Match 14.4%; Score 377.5; DB 1; Length 267;
 Best Local Similarity 38.8%; Pred. No. 3.4e-34;
 Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;

9 TQQTGKRYFRFTLIDVYSSGS-FSENIFLL-RGSTIVSDAGQFVYELTNQGXDK 66
 13 TQAGTVQSYNPIFVAVRGHITGADVREHLPVLRVGLPIN-QRFTLVLSNHALSY 70
 67 TPAIDVNNKYVAVYAGDQSYFLR-DAPRGAR--THFTGTRKSSLPFGSYXDLERYA 123
 74 TLADVTNAYVGVPRAGNSAFHFHNDQDEALHFLFDVQNNRYPAFGVNDLRLQLA 130
 124 GH-RDQIFLGIXQILQSYVAL--RXPQGSTKXKASILLIOWISEARFNPILMXRQ 179
 134 GMRLENITLNGPLEPALSALVYVSTGCTQLPLRASFICIQWISBARFVIGERT 190
 180 XINSGKSLPDXMLETSGQOQSTGVQVFNNEPRLAIXKXNFTLVNRYVIA 239
 194 RIRNRSAPDPSPVITLNSMRSLTAIQSSNQAFASPIQLRNGSKFSVYDSTILP 250
 240 SLAIMLFCVCGEPSS 254

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us-09-601-667c-1.fai

Page 7

Db 251 IIALMYRCAPPSS 265

```

RESULT 13
US-07-988-430-1
Sequence 1: Application US/07988430
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS: C/O Toole, Gerstein, Murray &
Associates, 1000 N. Dearborn, Suite 1100,
ADDRESS: Bicknell,
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-01-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19910819
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202 and Greta B.
REGISTRATION NUMBER: 35102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1
Query Match
Best Local Similarity 14.4%; Score 377.5; DB 1; Length 267;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
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QY 180 XINSGKSLPDYXMLELSTNSGCOSTQVQSTDSYFNNRXLAIKXGFYTLKXRVYA 239
DB 191 RIRYNRBAPDSVITLNSNGLSTALQSNQCFASBIDQCRNSKRSYDVSLIP 250
QY 240 SLAIMLFVCGCRPSS 254
DB 251 IIALMYRCAPPSS 265
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RESULT 14
US-08-218-303-16
Sequence 16: Application US/08218303
GENERAL INFORMATION:
APPLICANT: Kara, Bhupendra V.
APPLICANT: Hockney, Robert C.
APPLICANT: Pilton, John E.
TITLE OF INVENTION: FERMENTATION PROCESS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Cushman, Dardy & Cushman
CITY: Washington
STATE: Washington
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,303
FILING DATE: 19980816
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,533
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kowals, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PK/3893/94908/MW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3100
TELEFAX: 671423-1944
TELEX: 021220194
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-218-303-16
Query Match
Best Local Similarity 14.4%; Score 377.5; DB 1; Length 267;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
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QY 9 THQTKAYEYRFTLLADRYSSGS-PSNRIPL-RQSTIPVSDQRFVYELTNGQXDX 66
DB 13 TKGIVQSTYNNIRAVRGRLITGADVREHIVLNRGLPIN--QRFIVLSNHAELSV 70
QY 67 TLAIDYNNXVAYVQAGDSYFLR-DAPRGAE--THLFTGRTXSLSPYGSYDLERYA 123
DB 71 TLLDVNNAYVVGKNSAYFPHDQEDPAATLHLPFDVQNRYPFAFGSYDRLQCA 130
QY 124 GH-RDQIPGLXNOLQSYVAL--RXPQGSTXQASLIIQMTSEARPNPIMXHQ 179
DB 131 GNLENIIELGNGPLEBAISALVYSTGQTLPLARSFIIQMTSEARFPYIEGEMT 190
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QY 180 XINSGKSLPDYXMLELSTNSGCOSTQVQSTDSYFNNRXLAIKXGFYTLKXRVYA 239
QY 191 RIRYNRBAPDSVITLNSNGLSTALQSNQCFASBIDQCRNSKRSYDVSLIP 250
QY 240 SLAIMLFVCGCRPSS 254
DB 251 IIALMYRCAPPSS 265
QY 180 XINSGKSLPDYXMLELSTNSGCOSTQVQSTDSYFNNRXLAIKXGFYTLKXRVYA 239
DB 191 RIRYNRBAPDSVITLNSNGLSTALQSNQCFASBIDQCRNSKRSYDVSLIP 250
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QY 240 SLAIMEFYCGERPSS 254
DB 251 IIALWYRCAPPPSS 265

RESULT 15
US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studzika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF INVENTORS: 340
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TEXT: 25-3856 ID NO. 1:
; INFORMATION NUMBER:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-1

Query Match 14.4%; Score 377.5; DB 1; Length 267;
Best Local Similarity 38.8%; Pred.-No. 3.4e-34; Indels 11; Gaps 7;
Matches 99; Conservative 41; Mismatches 104

QY 9 THOTGKXEFRTLEADVSSG--FSNRIPI--RSTPIPSDARPTVHELTGQXDX 66
DB 13 TAGATVGSYTNFIKAVRHELTGADVREHIVLPINVALEPIN--GRFIVELSHAEISV 70
QY 67 TAAIVNNXYVAYAGAGDSYFLR--DAERGA--THEFTGTXSLSPEFGSYDIERA 123
DB 71 TLALDTNAYVYVRAGNSAFPHDNOEDALITHLFTDVNRYTFAPFGYDRLQOLA 130
QY 124 GH-RQIIGIXQLIGSVKAL--KRPQSTEXQASIIILMIOTSEARFPIIMRXRQ 179
DB 131 GNLKREHILNGPLSEHISALHYITSTGDTLFTLANSFIIOTMISENARFPIIGENRT 190

QY 180 XINSAKSLPDXIWMLELTSGQSTGVCHSTGVNRRKRLAIKXGFTLXNRXIA 239
DB 191 RIKYKRSAHDPSTVILHNSGRSLTAIOBNGCAFSPICLQRNRSKRSYIVDSILIP 250
QY 240 SLAIMEFYCGERPSS 254
DB 251 IIALWYRCAPPPSS 265

Search completed: December 11, 2003, 14:11:30
Job time : 19.4536 secs

Thu Dec 11 16:09:50 2003

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:19 ; Search time 8.20622 seconds
(without alignment)

3093.817 Million cell updates/sec

Title: US-09-601-667c-3

Sequence: 1 DDVTCASBPPTVATVGRXGM.....RRIIYPATGKPNQWMLPVX 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616662 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1*
2: p1r2*
3: p1r3*
4: p1r4*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1390	97.2	264	2	PD0019	mistletoe lectin I
2	1279.5	96.4	265	2	JM0090	lectin-I B chain -
3	849.5	64.0	576	1	RLCSD	ricin B precursor
4	822	61.9	263	2	S06330	ricin E - catalor b
5	726.5	54.7	564	1	RLCSAG	agglutinin precursor
6	717	53.0	528	1	TELGA	agglutinin precursor
7	703	51.0	562	2	S16022	abrin-a precursor
8	702	52.9	527	2	S16022	abrin-b precursor
9	702	52.9	527	2	S16022	abrin-d precursor
10	492	37.9	528	2	S22430	agglutinin I, precur
11	492	37.9	528	2	S22430	agglutinin I, precur
12	125.5	9.5	379	2	UC7832	endo-beta-1,2-xylosidase EC 3.2.1.15
13	118.5	8.9	477	1	US0588	endo-beta-1,2-xylosidase EC 3.2.1.15
14	115.5	8.7	477	1	US0588	endo-beta-1,2-xylosidase EC 3.2.1.15
15	104	7.8	383	2	T34603	protease RPI - R
16	101	7.6	548	2	A39094	protease RPI - R
17	93.5	7.0	475	2	T35697	arabinofuranosidase
18	88.5	6.7	451	2	T34988	probable lipoprote
19	86.5	6.5	1067	2	T28653	hypothetical prote
20	85.5	6.4	1708	2	AB1866	hypothetical prote
21	85	6.4	464	2	T35943	hypothetical prote
22	85	6.4	464	2	T35943	hypothetical prote
23	82	6.2	1711	2	AB1883	hypothetical prote
24	81.5	6.1	160	2	UC7822	beta transglutinin
25	79.5	6.0	1693	2	S76086	probable short-chain
26	79	6.0	295	2	H83452	coat protein gpI -
27	79	6.0	661	2	S49901	coat protein gpI -
28	79	6.0	875	2	I40862	coat protein gpI -
29	78.5	5.9	229	2	C43330	gene 7 protein - p

30	78.5	5.9	231	2	E90810	flagellar biosynth
31	78.5	5.9	231	2	A86670	hypothetical prote
32	78.5	5.9	542	2	A49114	protein-tyrosine k
33	78.5	5.9	1683	2	AF2071	WD-40 repeat prote
34	78	5.9	563	2	A88515	polypeptide N-acet
35	77.5	5.9	612	2	T42243	probable polypepti
36	77.5	5.8	231	2	H64850	flagellar hook for
37	77.5	5.8	386	2	AB1996	hypothetical prote
38	77.5	5.7	187	2	S23240	hypothetical prote
39	77.5	5.7	197	2	S23240	hypothetical prote
40	76	5.7	2214	1	A48548	surface-layer glyco
41	75.5	5.7	593	2	S16375	surface-layer glyco
42	75.5	5.7	1231	1	A48490	endo-1,4-beta-xyla
43	75.5	5.7	943	2	S59317	DIP2 protein - yea
44	75	5.7	1197	2	D82696	hypothetical prote
45	75	5.7				

ALIGNMENTS

RESULT 1
PD0019
mistletoe lectin I B chain - Viscum album (fragment)
C/Species: Viscum album
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C/Accession: PD0019
R/Beschreibung, S./Krauspenhaar, R./Mikhailov, A./Stoeva, S./Betz, C./Voelter, Blochem. Biophys. Res. Commun. 247, 367-372, 1998
A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album
A/Reference number: PD0019, NCBI:8908123, PMID:964213
A/Molecule: PD0019, protein
A/Residues: 1764<RSC>
C/Superfamily: ricin, rRNA N-glycosidase homology

Query Match 97.2%, Score 1390, DB 2, Length 264;
Best Local Similarity 92.4%, Pred. No. 1, 9e-117;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	1	DDVTCASBPPTVATVGRXGMVDVDDPDHGNQTOAMPKSNNDPNQMLTKEQHTIR	60
DB	1	DDVTCASBPPTVATVGRXGMVDVDDPDHGNQTOAMPKSNNDPNQMLTKEQHTIR	60
QY	61	MSGLTGYGTAAVYWIPEPCNRPVREATMOVWNTINPRBNVYAAAGTGTTL	120
DB	61	MSGLTGYGTAAVYWIPEPCNRPVREATMOVWNTINPRBNVYAAAGTGTTL	120
QY	121	VQTLDTGGGMAQNTAPREVITVGRDCKWESNKGWYWCSSGXKXKAAALVGD	180
DB	121	VQTLDTGGGMAQNTAPREVITVGRDCKWESNKGWYWCSSGXKXKAAALVGD	180
QY	181	GSIRPNQNDQCTVGRDYSVTINIVSCSXGXQWAFVTEKATLTKKXXXXVDAQ	240
DB	181	GSIRPNQNDQCTVGRDYSVTINIVSCSXGXQWAFVTEKATLTKKXXXXVDAQ	240
QY	241	NRKRPITVATGKPNQWMLPV 263	
DB	241	NRKRPITVATGKPNQWMLPV 263	

RESULT 2
JM0090
lectin-I B chain - European mistletoe
N/Alternate names: MLI
C/Species: Viscum album (European mistletoe)
C/Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
C/Accession: JM0090
R/Beschreibung, S./Krauspenhaar, R./Mikhailov, A./Stoeva, S./Betz, C./Voelter, Blochem. Biophys. Res. Commun. 247, 367-372, 1998
A/Title: Complete amino acid sequence of the B chain of mistletoe lectin I.
A/Reference number: JM0090, NCBI:98289575, PMID:9618256
A/Accession: JM0090

[illegible]

S06330
Ricin E - castor bean (fragment)
N/Contains: Chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
A/Accession: S06330, J05381
A/Reference: 1-69, 'PS', 72-209, 'A', 211-243, 243-250, 'V', 252-263 <RR>
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-263 <LAD>
A/Cross-References: EMBL:M17631; NID:9169714; PIDD:AAA63506.1; FID:9169715
R/Araki, T.; Funatsu, G.
Biochim. Biophys. Acta 911, 191-200, 1987
A/Title: The complete amino acid sequence of the B-chain of ricin E isolated from small
A/Reference: J05381, M01D:8710186; F01D:3801493
A/Accession: J05381
A/Molecule type: protein
A/Residues: 1-69, 'PS', 72-209, 'A', 211-243, 243-250, 'V', 252-263 <RR>
A/Experimental source: seed
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolyase
F/1-263/Product: ricin E chain B #status experimental <ECH>
F/17-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats
F/20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted
F/95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 61.94; Score 823; DB 2; Length 263;
Best Local Similarity 59.25; Pred. No. 4, 36-72;
Matches 154; Conservative 32; Mismatches 72; Indels 2; Gaps 2;
QY 5 CASSEPTVRIYGRXKXVVDVDDFDHGNQIOLMPKSKNDPNQITKEDYTRISNGSC 64
DB 4 CMDEPVIYIVGNGLCVDRGDFPFGNAGIOLMPCSNPDNDQITKEDYTRISNGSC 63
QY 65 LITVGYTAGVYVMEFCNNAVERATVQIWNXGTTINPSSNLVLAASGIKGTTLVQTL 124
DB 64 LITVGYTAGVYVMEFCNNAVERATVQIWNXGTTINPSSNLVLAASGIKGTTLVQTL 123
QY 125 DYTLCQGLAANDPAPREYITVGRFLCHSKSGSWVETFCSSQXQXKXALYGGDSIR 184
DB 124 IYVSGQMLPNTNPTPTTIVGVXGMLQNSGKXWLBDSKSEQ-QMLYDSSIR 182
QY 185 PKORODCLTKRGDSVSTVYNIVSGSXKXKORVFNEXALINLXXXXXVQAQNP-K 243
DB 183 PQORNDCLTTPDANKGVTKLSCGPVSGQWFFKNDGTLINLNGLVLDVRSPPS 242
QY 244 LKRIITVPATGKPNQMLPV 263
DB 243 LKRIITVPATGKPNQMLPV 262
RESULT 5
RCSAG
agglutinin precursor - castor bean
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
A/Accession: A24261, A24210
R/Roberts, L.W.; Lamb, J.F.; Peppin, D.J.C.; Lord, J.M.
J. Biol. Chem. 269, 15682-15686, 1995
A/Title: The primary structure of Ricinus communis agglutinin. Comparison with ricin.
A/Reference: A24261, M01D:8605949; F01D:3993130
A/Accession: A24261
A/Molecule type: rRNA
A/Residues: 1-564 <ROB>
A/Cross-References: GB:M12089; NID:9169700; PIDD:AAA33869.1; FID:9169701
R/Araki, T.; Yoshioaka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti-

A/Reference number: A24210
A/Accession: A24210
A/Molecule type: protein
A/Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V'
C/Comment: This protein has strong agglutinating activity and weak cytotoxicity com
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolyase; lectin; RNA binding;
F/1-24/Domain: signal sequence #status predicted <SIG>
F/124/Domain: agglutinin chain A #status predicted <ACH>
F/32-284/Product: rRNA N-glycosidase B #status experimental <GBH>
F/303-354/Region: rRNA N-glycosidase B #status experimental <GBH>
F/319-361, 365-402, 405-443, 450-485, 488-549/Disulfide bonds: #status predicted
F/319-361, 365-402, 405-443, 450-485, 488-549/Disulfide bonds: #status predicted
F/104, 147, 231, 232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/200, 203/Active site: Glu, Arg #status predicted
F/282-306, 322-341, 365-382, 453-466, 493-509/Disulfide bonds: #status predicted
F/324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F/357, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/356, 557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 54.74; Score 726.5; DB 1; Length 564;
Best Local Similarity 53.34; Pred. No. 1, 9e-62;
Matches 196; Conservative 36; Mismatches 84; Indels 1; Gaps 1;
QY 5 CASSEPTVRIYGRXKXVVDVDDFDHGNQIOLMPKSKNDPNQITKEDYTRISNGSC 64
DB 306 CMDEPVIYIVGNGLCVDRGDFPFGNAGIOLMPCSNPDNDQITKEDYTRISNGSC 365
QY 65 LITVGYTAGVYVMEFCNNAVERATVQIWNXGTTINPSSNLVLAASGIKGTTLVQTL 124
DB 366 LITVGYTAGVYVMEFCNNAVERATVQIWNXGTTINPSSNLVLAASGIKGTTLVQTL 425
QY 125 DYTLCQGLAANDPAPREYITVGRFLCHSKSGSWVETFCSSQXQXKXALYGGDSIR 184
DB 124 IYVSGQMLPNTNPTPTTIVGVXGMLQNSGKXWLBDSKSEQ-QMLYDSSIR 182
QY 185 PKORODCLTKRGDSVSTVYNIVSGSXKXKORVFNEXALINLXXXXXVQAQNP-K 243
DB 426 IYVSGQMLPNTNPTPTTIVGVXGMLQNSGKXWLBDSKSEQ-QMLYDSSIR 484
QY 185 PKORODCLTKRGDSVSTVYNIVSGSXKXKORVFNEXALINLXXXXXVQAQNP-K 244
DB 485 PQORNDCLTTPDANKGVTKLSCGPVSGQWFFKNDGTLINLNGLVLDVRSPPS 544
QY 245 LKRIITVPATGKPNQMLPV 263
DB 545 LKRIITVPATGKPNQMLPV 563
RESULT 6
RCSAG
abrin-a precursor - Indian jicoria (fragment)
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian jicoria)
C/Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
A/Accession: S32429, J02020; A39761, J01432; S24133, S74110, S74111
R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A/Title: Primary structure of three distinct isobands determined by cDNA sequencing
A/Reference number: S32429; M01D:9312798; F01D:8423313
A/Accession: S32429
A/Status: not compared with conceptual translation
A/Molecule type: rRNA
A/Residues: 1-2-528 <HN>
A/Cross-References: GB:M99344; NID:9166224; PIDD:AAA32624.1; FID:9166225
A/Note: the coding region for the sequence shown is preceded by an ATG codon
A/Note: residues 1-8 were derived from the synthesized primer
R/Funatsu, G.; Taguchi, Y.; Kameo, M.; Yankai, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
A/Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein
A/Reference number: J02020
A/Accession: J02020
A/Molecule type: protein
A/Residues: 1-528 <HN>
A/Cross-References: GB:M99344; NID:9166224; PIDD:AAA32624.1; FID:9166225
A/Note: the amino terminal residue forms pyroglutamate carboxylic acid; therefore, we
R/Bensen, G.; Mathiesen, A.; Sundin, A.
J. Biol. Chem. 266, 6848-6852, 1991

[illegible][illegible]

N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 20-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C:Accession: S32430; UCL1399
R:Humg, C.; Lee, M.; Lee, T.; Lin, J.Y.
J: Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isobabins determined by cDNA sequencing.
A:Reference number: S32429; PMID:9332798; PMID:8421313
A:Accession: S32430
A:Molecule type: mRNA
A:Residues: 1-527 <HUN>
A:Cross-references: GB:M68345; NID:9166296; PIDN:AAA3625.1; PID:g166297
R:Kimura, M.; Sumitawa, T.; Punatsu, G.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: UCL1398; PMID:93169023; PMID:7763422
A:Molecule type: cDNA
A:Accession: S32430
A:Residues: 260-281 /D/ 283-290, /N/ 292-349, /FQ/ 352-377, /N/ 379-425, /W/ 427, /D/ 429-430
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosylase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin; F
F/1-250/Product: abrin-b chain A #status predicted <ACH>
F/7-245/Domain: rRNA N-glycosylase homology <RNG>
F/260-527/Product: abrin-b chain B #status experimental <BCH>
F/292-324/325-365, 366-406, 413-448, 452-491, 494-527/Region: 40-residue repeats
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/110/360-370/380-390/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
F/163/166/Active site: Glu, Arg #status predicted
F/246-268/285-304/328-345/416-429/455-477/Diulfide bonds: #status predicted
F/287/311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/499/520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.9%; Score 702; DB 2; Length 527;
Best Local Similarity 51.9%; Pred. No. 4.2e-60;
Matches 134; Conservative 39; Mismatches 83; Indels 2; Gaps 2;

QY	5	CSAS-EPTVTVKRGKXVYVDDDPDQNGQQLMPKSKNDPNQWLTIKXDTIRSNK 63
DB	268	CSRSREPTVTVKRGKXVYVDDDPDQNGQQLMPKSKNDPNQWLTIKXDTIRSNK 327
QY	64	CLTVYVTVAGVYVTFPCONTAVREATTQVTKXGTTIRPSNLVLAASGIGKTTLVQT 123
DB	328	CLTTEGAPRGVYVTFPCONTAVREATTQVTKXGTTIRPSNLVLAASGIGKTTLVQT 387
QY	124	LDVTLGGVLAAGNDIAPREVTIYGFRLQMSKXSVVETGCSXGXVVAALVGGGSI 183
DB	388	NEVLMRGKRGVNTSPVTSISIGSDICMQQSGSNVLAACDNKKEQ-QVALVTDGSI 446
QY	184	RFQKNDQCLTVGRDVSIVTVIVSCSXGXVVAALVLAALVLAALVLAALVLAALV 243
DB	447	KSVQVNTNCLTSKDKQSPVLAACSGNMAQGLPMDNSITNLAHDVMDVYSGDS 506
QY	244	LRRIITVATKRGKQWML 261
DB	507	LKEITLHPTKRGKQWML 524

RESULT 9
S32431
Abirin-d precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C:Accession: S32431; S32408
R:Humg, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J: Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isobabins determined by cDNA sequencing.
A:Reference number: S32429; PMID:9332798; PMID:8421313
A:Accession: S32431
A:Molecule type: mRNA
A:Residues: 1-528 <HUN>

A:Cross-references: GB:M68346
R:Humg, C.; Lee, M.; Lee, T.; Lin, J.Y.
submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-169 /C/ 171-320 /V/ 322-528 <HUN>
A:Cross-references: GB:M68346; rRNA N-glycosylase homology <RNG>
C:Superfamily: ricin; rRNA N-glycosylase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin
The A and B chains are linked by a single disulfide bond, which is essential for
F/1-251/Product: abrin-d chain A #status predicted <ACH>
F/7-246/Domain: rRNA N-glycosylase homology <RNG>
F/261-528/Product: abrin-d chain B #status predicted <BCH>
F/292-324/325-365, 366-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/110/360-370/380-390/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
F/164/167/Active site: Glu, Arg #status predicted
F/200/233/361, 401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted
F/288/312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/500/521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.9%; Score 702; DB 2; Length 528;
Best Local Similarity 51.9%; Pred. No. 4.2e-60;
Matches 134; Conservative 40; Mismatches 82; Indels 2; Gaps 2;

QY	5	CSAS-EPTVTVKRGKXVYVDDDPDQNGQQLMPKSKNDPNQWLTIKXDTIRSNK 63
DB	269	CSRSREPTVTVKRGKXVYVDDDPDQNGQQLMPKSKNDPNQWLTIKXDTIRSNK 328
QY	64	CLTVYVTVAGVYVTFPCONTAVREATTQVTKXGTTIRPSNLVLAASGIGKTTLVQT 123
DB	329	CLTTEGAPRGVYVTFPCONTAVREATTQVTKXGTTIRPSNLVLAASGIGKTTLVQT 388
QY	124	LDVTLGGVLAAGNDIAPREVTIYGFRLQMSKXSVVETGCSXGXVVAALVGGGSI 183
DB	389	NEVLMRGKRGVNTSPVTSISIGSDICMQQSGSNVLAACDNKKEQ-QVALVTDGSI 447
QY	184	RFQKNDQCLTVGRDVSIVTVIVSCSXGXVVAALVLAALVLAALVLAALVLAALV 243
DB	448	KSVQVNTNCLTSKDKQSPVLAACSGNMAQGLPMDNSITNLAHDVMDVYSGDS 507
QY	244	LRRIITVATKRGKQWML 261
DB	508	LKEITLHPTKRGKQWML 525

RESULT 10
S62627
agglutinin I precursor - European elder
C:Species: Sambucus nigra (European elder)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S62627; S62619
R:Van Damme, E.; J.W.; Balle, A.; Rouge, P.; Van Leuven, F.; Peumans, W.J.
J: Biochem. Biotechnol. Biochem. 53, 189-191, 1993
A:Title: The cDNA sequence of the agglutinin I precursor from elderberry (Sambucus n
A:Reference number: S62619; PMID:96202926; PMID:8631119
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VAN>
A:Cross-references: EMBL:U27122; NID:G1141772; PIDN:AAQ4188.1; PID:G1141773
A:Accession: S62619
A:Molecule type: protein
A:Residues: 29-39/309-319 /VA2
C:Superfamily: ricin; rRNA N-glycosylase homology
F/137/283/Domain: rRNA N-glycosylase homology <RNG>

Query Match 37.4%; Score 496; DB 2; Length 570;
Best Local Similarity 42.9%; Pred. No. 1.4e-40;

A45053
proteinase RPT - *Ratobacter faecitabidus*
C:Species: *Ratobacter faecitabidus*
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
C:Accession: A45053
R:Shimoi, H.; Iijima, Y.; Ohta, T.; Tadenuma, M.
J. Biol. Chem. 267: 25189-25195, 1992
A:Title: Molecular structure of *Ratobacter faecitabidus* protease I. A yeast-lytic serine
A:Reference number: A45053; MUID:93094226; PMID:1339445
A:Accession: A45053
A:Status: preliminary
A:Molecule type: DNA, protein
A:Residues: 1525 <SH2>
A:Cross-references: GB:D10753; PIDN:BA01585.1; PID:dl002060; PID:g912440
A:Experimental source: YJM-50
A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

Query Match
Best Local Similarity 7.6%, Score 104; DB 2; length 525;
Matches 32; Conservative 17; Mismatches 45; Indels 12; Gaps 5;

QY 2 DVTCSAEPYVRIYSEKXVYVDRDDPHDQNOIQMPSKNNPNOQMTIKEDTIRSN 61
DB 399 DVT-----TSYVQYQNNCIVPNSDPTDQKQLOVWNCNGTN--AQKSEHDPGTLRIN 450
QY 62 GSCL-ITVGYT-AGYVWIFDQNTVREBATTWQIMXNGTINPRSN 105
DB 451 GRCDDRWAMTNGTEVQLMNCNGH--NQRTLNAGDIVVHAN 494

RESULT 15

A39094
glucan endo-1,3-beta-glucosidase (EG 3.2.1.-) precursor - *Oerskovia xanthineolytica*
C:Species: *Oerskovia xanthineolytica*
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
C:Accession: A39094
R:Shen, S.H.; Chretien, P.; Bastien, L.; Siliaty, S.N.
J. Biol. Chem. 266, 1058-1063, 1991
A:Title: Primary sequence of the glucanase gene from *Oerskovia xanthineolytica*. Express
A:Reference number: A39094; MUID:91093212; PMID:1985933
A:Accession: A39094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1548 <SH2>
A:Cross-references: GB:M60826; GB:M28734; NID:g150444; PIDN:AA025520.1; PID:g150445
C:Keywords: glycosidase; hydrolase

Query Match
Best Local Similarity 7.6%, Score 101; DB 2; length 548;
Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;
QY 22 VVPDDPHDQNOIQMPSKNNPNOQMTIKEDTIRSNGL-ITVGYTGYTMIF 79
DB 434 LVPWADPTDNGVQL--ATCSGAQAQMTGCTGTVRAKGLDPAASGADGTAWIT 491
QY 80 DQNTAVREKTIWQIV---XNGTINPRSNIVLAASGSI---KGTLLVQTLDTLTGGW 132
DB 492 TCN-----GTGAQKVTYSATRALNPDGSKCLDAGSALPDQGVQVLTWCQTERQW 546

Search completed: December 11, 2003, 13:55:40
Job time : 10.2062 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18; Search time 4.53677 seconds
(without alignments)
2736.539 Million cell updates/sec

Title: US-09-601-667c-3

Sequence: 1 DVTCSASEPTRIYGRKSM.....RRIIYPATGRKQNMWLPYX 264

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Databases: SwissProt_41.*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	1290	97.2	264	1 MIB_VISAL	P81830 viscum albu
2	825.2	84.9	576	1 KXCG_NICCO	P02879 ricinus com
3	725.2	84.9	576	1 KXCG_NICCO	P02879 ricinus com
4	717	54.0	528	1 ABRR_ABRP	P11440 abrus prec
5	703	53.0	527	1 ABRR_ABRP	P06677 abrus prec
6	702	52.9	527	1 ABRR_ABRP	P06677 abrus prec
7	494.5	37.3	563	1 NIXN_GAMU	P33183 sambucus ni
8	118.5	8.9	477	1 XNNA_STRLI	P26514 streptomyc
9	104	7.8	525	1 SPI_FABPA	Q05308 xanthoxan
10	101	7.6	548	1 B13E_AFTSP	Q09146 archibacte
11	101	7.6	548	1 B13E_AFTSP	P22222 oerxkova x
12	93.5	7.0	475	1 ABRR_STRKO	O54161 streptomyc
13	79.3	6.8	475	1 ABRR_STRKO	P06463 streptomyc
14	79.3	6.8	475	1 ABRR_STRKO	Q05563 streptomyc
15	78.5	5.9	462	1 KXCG_NICCO	P02879 ricinus com
16	78.5	5.9	462	1 KXCG_NICCO	P02879 ricinus com
17	78.5	5.9	462	1 KXCG_NICCO	P02879 ricinus com
18	78.5	5.9	462	1 KXCG_NICCO	P02879 ricinus com
19	77.5	5.8	462	1 KXCG_NICCO	P02879 ricinus com
20	77.5	5.8	462	1 KXCG_NICCO	P02879 ricinus com
21	76	5.7	2214	1 F01D_CX24	P06482 methanococ
22	76	5.7	2214	1 F01D_CX24	P06482 methanococ
23	75.5	5.7	593	1 CSQ_METFE	P27373 methanococ
24	75.5	5.7	593	1 CSQ_METFE	P27373 methanococ
25	75.5	5.7	593	1 CSQ_METFE	P27373 methanococ
26	75.5	5.7	593	1 CSQ_METFE	P27373 methanococ
27	75	5.7	943	1 D1P2_YEAST	Q07625 mactinactin
28	74.5	5.6	704	1 AKH_BICAC	P06482 methanococ
29	74.5	5.6	704	1 AKH_BICAC	P06482 methanococ
30	74	5.6	704	1 AKH_BICAC	P06482 methanococ
31	73	5.5	501	1 YH92_CAEEL	P06482 methanococ
32	73	5.5	501	1 YH92_CAEEL	P06482 methanococ
33	73	5.5	1764	1 YH92_CAEEL	P06482 methanococ

ALIGNMENTS

RESULT 1	ID	MB_VISAL	STANDARD	ERT	264 AA.
1	1	MB_VISAL	STANDARD	ERT	264 AA.
2	2	MB_VISAL	STANDARD	ERT	264 AA.
3	3	MB_VISAL	STANDARD	ERT	264 AA.
4	4	MB_VISAL	STANDARD	ERT	264 AA.
5	5	MB_VISAL	STANDARD	ERT	264 AA.
6	6	MB_VISAL	STANDARD	ERT	264 AA.
7	7	MB_VISAL	STANDARD	ERT	264 AA.
8	8	MB_VISAL	STANDARD	ERT	264 AA.
9	9	MB_VISAL	STANDARD	ERT	264 AA.
10	10	MB_VISAL	STANDARD	ERT	264 AA.
11	11	MB_VISAL	STANDARD	ERT	264 AA.
12	12	MB_VISAL	STANDARD	ERT	264 AA.
13	13	MB_VISAL	STANDARD	ERT	264 AA.
14	14	MB_VISAL	STANDARD	ERT	264 AA.
15	15	MB_VISAL	STANDARD	ERT	264 AA.
16	16	MB_VISAL	STANDARD	ERT	264 AA.
17	17	MB_VISAL	STANDARD	ERT	264 AA.
18	18	MB_VISAL	STANDARD	ERT	264 AA.
19	19	MB_VISAL	STANDARD	ERT	264 AA.
20	20	MB_VISAL	STANDARD	ERT	264 AA.
21	21	MB_VISAL	STANDARD	ERT	264 AA.
22	22	MB_VISAL	STANDARD	ERT	264 AA.
23	23	MB_VISAL	STANDARD	ERT	264 AA.
24	24	MB_VISAL	STANDARD	ERT	264 AA.
25	25	MB_VISAL	STANDARD	ERT	264 AA.
26	26	MB_VISAL	STANDARD	ERT	264 AA.
27	27	MB_VISAL	STANDARD	ERT	264 AA.
28	28	MB_VISAL	STANDARD	ERT	264 AA.
29	29	MB_VISAL	STANDARD	ERT	264 AA.
30	30	MB_VISAL	STANDARD	ERT	264 AA.
31	31	MB_VISAL	STANDARD	ERT	264 AA.
32	32	MB_VISAL	STANDARD	ERT	264 AA.
33	33	MB_VISAL	STANDARD	ERT	264 AA.

cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.

-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-1- SUBUNIT: Disulfide-linked dimer of A and B chains.

-1- COMPOSITION: The B chain is composed of 216 amino acids, each domain consists of 3 loops.

-1- PTM: THE MAJOR B-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.

-1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.

-1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF. 1, REF. 2 AND REF. 3).

-1- DATABASE: NMR=Protein Spotlight;

NOTE=Issue 31 of February 2003;
WWW=ncicb.org/spotlight/articles/april03.html

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DR EMBL; X03179; CAA26939.1; -
DR EMBL; X02908; CAA37095.1; -
DR EMBL; X02908; CAA37095.1; -
DR PIR; J24092; R1CSD058.1; -
DR PIR; J24092; R1CSD058.1; -
DR PDB; 2AAT; 31-JAN-94.
DR PDB; 1AR3; 31-JAN-94.
DR PDB; 1FEP; 31-OCT-93.
DR PDB; 1IFS; 14-JAN-98.
DR PDB; 1IFT; 14-JAN-98.
DR PDB; 1IFU; 14-JAN-98.
DR PDB; 1RTG; 31-OCT-93.
DR PDB; 1OBS; 16-JUN-97.
DR PDB; 1OBT; 16-JUN-97.
DR PDB; 1BR5; 02-SEP-98.
DR PDB; 1IL3; 16-JAN-02.
DR PDB; 1IL4; 16-JAN-02.
DR PDB; 1IL9; 16-JAN-02.
DR GlycoStatedB; P02879; -
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00386; SHIGARICIN.
DR SMART; SMO0253; Ricin; 2 LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal; 3D-structure.
FT SIGNAL 1 35
FT CHAIN 36 302 RICIN A CHAIN.
FT PEPTIDE 303 314 LINKER PEPTIDE.
FT CHAIN 315 576 RICIN B CHAIN.
FT DOMAIN 321 448 RICIN B-TYPE LECTIN 1.
FT DOMAIN 451 575 RICIN B-TYPE LECTIN 2.
FT REPEAT 331 373 1-ALPHA.
FT REPEAT 374 416 1-BETA.
FT REPEAT 417 448 2-ALPHA.
FT REPEAT 449 497 2-BETA.
FT REPEAT 501 540 2-GAMMA.
FT ACT_SITE 212 212
FT DISULFID 234 318 INTERCHAIN.
FT DISULFID 334 353

Query Match 64.0%; Score 849.5; DB 1; Length 576;
Best Local Similarity 60.6%; Pred. No. 1,9e-76;
Matches 157; Conservative 29; Mismatches 72; Indels 1; Gaps 1;

FT	DISULFID	377	394	
FT	DISULFID	465	478	
FT	DISULFID	504	521	
FT	CARBOHYD	45	45	N-LINKED (GLCNAc...)
FT	CARBOHYD	271	271	/F1D-CAR 00080. (IN MINOR FORM)
FT	CARBOHYD	409	409	N-LINKED (GLCNAc...)
FT	CARBOHYD	449	449	N-LINKED (GLCNAc...)
FT	CONFLICT	76	76	E -> D (IN REF. 3).
FT	CONFLICT	551	551	A -> R (IN REF. 3).
FT	STRAND	43	47	
FT	TURN	49	50	

DB 318 CNDPEYVRLISNGSLCTVDHDFHNNALQWCKSTADNMLTKDNTISNGC 377
65 LITVGTATGTYVMIPDNTAVRENTINQKGTINPSNVVAASGIGVTLTVQTL 124
378 LITVGTGCVVWVWDNPMATDNTQWIDNCTINPSSVVAATSGNCTTLTVQTN 437
125 DVTLCQGLAGNDTPREVTVYGRDLQMSNKGSWVERCKSSQXNXXVLYDQSLR 184
438 IYAVSGWLPNNTPPVTVTVGLVGLQLANSQGVVIEQSSKABO-QVALYADQSLR 496
185 PRONQDGLYKGRDSVTVYINISGXKXQRPVFNEXALMLKXXXXXPDAPKRL 244
497 PQMRNKLITSDNIRETVKILSCPSAQGMWFCNDGTLMLVSLVLDVRAADPSL 556
QY 245 REITVPAKCPKQKMLPV 263
DB 557 KQILLPLHSDPNOIWLPL 575

RESULT 3
ID AGEL_RICCO STANDARD; PRT; 564 AA.
DI AGEL_RICCO
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (P0A) (Contains: Agglutinin A chain (rRNA N-glycosidase) (BC 3.2.2.22); Agglutinin B chain).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
RX NCBI_TaxID=3986;
RN SOURCE FROM N.A.
RS MEDLINE=6059449; PubMed=2999130;
RA Roberts L.M., Lamb F.J., Pappin D.J.C., Lord J.M.;
RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin".
RL J. Biol. Chem. 260:15682-15686(1985).
RN [2]
RP SEQUENCE OF 303-564.
RC TISSUE=Seed;
RA Arai T., Yoshioka Y., Funatsu G.;
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin 150,215-217-225 (castor bean seeds)".
RN Ricinus. Biophys. Acta 612:217-225(1986).
RP SEQUENCE OF 303-337.
RX MEDLINE=60178723; PubMed=6768555;
RA Lin T.T.-S., Li S.S.-L.;
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis".

RL Eur. J. Biochem. 105:453-459(1980).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC -----
 DR EMBL: M12089; AAA33869.1; -
 DR EMBL: S40368; AA22584.1; -
 DR FIC: A24261; RLCBAG.
 DR HSBP: P02879; IBB6.
 DR GYCSULCDB: P08750; -
 DR GYCSULCDB: P08750; Ricin_B_lectin.
 DR Interpro: IPR001574; RIP
 DR Pfam: P00652; Ricin_B_lectin. 6.
 DR Pfam: P00161; RIP_1
 DR PRINTS: P00396; SHIGARICIN.
 DR SMART: SM00458; RICIN. 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN. 2.
 DR PROSITE: PS00275; SHIGA_RICIN. 1.
 KM Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KM Glycoprotein; Lectin; Signal. POTENTIAL.
 KM CHAIN. 2.
 FT PROPEP 231 302 AGGLUTININ, A CHAIN.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 564 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 405 437 1-GAMMA.
 FT REPEAT 450 485 2-ALPHA.
 FT REPEAT 489 528 2-BETA.
 FT REPEAT 531 558 2-GAMMA.
 FT AGGLUTININ 200 200 BY SIMILARITY.
 FT AGGLUTININ 306 306 BY SIMILARITY.
 FT DISULFID 322 306 INVERTED (BY SIMILARITY).
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 352 352 N -> D (IN REF. 2).
 FT CONFLICT 362 362 R -> G (IN REF. 2).
 FT CONFLICT 364 364 F -> T (IN REF. 2).
 FT CONFLICT 364 364 F -> T (IN REF. 2).
 FT CONFLICT 552 552 F -> T (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 VM; D4552A22609759 CMC4;
 Query Match 54.7%; Score 726.5; DB 1; Length 564;
 Best Local Similarity 53.3%; Pred. No. 2.7e-64;
 Matches 138; Conservative 36; Mismatches 84; Indels 1; Gaps 1;

DB 426 IYASQGMPTNNTPPTTIGLXKMLQNSGKYLEDTSEKAO-QMALYADSGIR 484
 QY 185 PRONQDGLTQGDVSTVNTVNSCKXKXGFWFTXKALILKXXXXXVDAQKPKL 244
 DB 485 PQRNRDLCTDANKKTVKILSCPSASQKWFNRKDTILNLVNLVADVRSDDSL 544
 QY 245 RRIITVPATGKQKMLPV 263
 DB 545 KQITVHPKSNLQMLPL 563
 RESURT 4
 ID ABRA_ABRP STANDARD; PRT; 528 AA.
 AC P11340; P28589;
 DT 01-JUN-1989 (Rel. 11, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abirin-a precursor [Contains: Abirin-a A chain (rRNA N-glycosidase)
 DE (EC 3.2.2.22); Abirin-a B chain].
 OS Abirus precatocius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Rosales; Fabaceae; Leguminosae; core eudicots; Rosidae;
 OC Noduliales; Papilionales; Fabaceae; Papilionoideae; Azyzae; Abirus.
 OC NBI_TaxID=3816.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=9133798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabirins determined by cDNA
 RT sequencing. Conservation and significance.";
 RT J. Mol. Biol. 229:263-267(1993).
 RN [2] SEQUENCE OF 1-251.
 RP TISSUE=Seed.
 RA Funsten G., Taguchi Y., Kameosono M., Yanaka M.;
 RT "The complete amino acid sequence of the A-chain of abirin-a, a toxic
 RT protein from the seeds of Abirus precatocius.";
 RT Agric. Biol. Chem. 52:1095-1097(1988).
 RN [3]
 RP SEQUENCE OF 1-251 FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=9101329; PubMed=2016300;
 RA Evensen G., Mathiesen A., Sundan A.;
 RT "Direct molecular cloning and expression of two distinct abirin
 RT A-chains.";
 RN [4] Biol. Chem. 266:6848-6852(1991).
 RP SEQUENCE OF 262-528.
 RX MEDLINE=9237656; PubMed=1505674;
 RA Chen Y.-L., Chow L.-P., Tsegats A., Lin J.-Y.;
 RT "The complete primary structure of abirin-a B chain.";
 RL FEBS Lett. 309:115-118(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
 RX MEDLINE=9533188; PubMed=7608990;
 RA Hake G., Hake T.H., Lin T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
 RT "Crystal structure of abirin-a at 2.14 A.";
 RN [6] Biol. Chem. 270:3333-3337(1995).
 CC -1- FUNCTION: THE CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABIRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC PERCEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.

CC -----1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -----
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CC or send an email to license@sb-ship.ch

DR EMBL; M98344; AAA32624.1; ALT INIT.
DR EMBL; X54872; -; NOT_ANNOTATED_CDS.
DR PIR; S32429; TZLSA.
DR PDB; 1ABR; 07-FEB-95.
DR InterPro; IPR00772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00651; Ricin_A_lectin.
DR PRAS; PR02466; Ricin.
DR SMART; SM00458; RCTN2.
DR PROSITE; PS00275; SHIGG_RICIN; 1.
DR PROSITE; PS00275; SHIGG_RICIN; 2.
KM Glycoprotein; Lectin; 3D-structure; Pyroglutamate carboxylic acid.
FT CHAIN 1 251 ABRIN-A A CHAIN.
FT PEPTIDE 252 261 LINKER PEPTIDE.
FT CHAIN 252 528 ABRIN-B B CHAIN.
FT DOMAIN 273 400 RICIN B-TYPE LECTIN 1.
FT REPEAT 283 325 RICIN B-TYPE LECTIN 2.
FT REPEAT 326 404 1-ALPHA.
FT REPEAT 414 449 2-GAMMA.
FT REPEAT 453 492 2-BETA.
FT REPEAT 495 528 2-GAMMA.
FT ACT_SITE 164 164 BY SIMILARITY.
FT DISULFID 247 269 INTERCHAIN (BY SIMILARITY).
FT DISULFID 286 305 BY SIMILARITY.
FT DISULFID 329 346 BY SIMILARITY.
FT DISULFID 417 430 BY SIMILARITY.
FT DISULFID 456 473 BY SIMILARITY.
FT WDI_RES 361 361 PYROGLUTAMATE CARBOXYLIC ACID.
FT CATHID 481 481 N-LINKED (GLN-...).
FT CONFLICT 202 202 MISSING (IN REF. 2).
FT CONFLICT 298 298 N -> Y (IN REF. 4).
FT CONFLICT 427 427 M -> L (IN REF. 4).
FT CONFLICT 467 467 T -> P (IN REF. 4).
FT CONFLICT 483 483 V -> L (IN REF. 4).
FT STRAND 5 8
FT TURN 10 11
FT HELIX 14 28
FT TURN 32 33
FT TURN 34 35
FT STRAND 36 38
FT TURN 42 43
FT HELIX 47 49
FT STRAND 51 57
FT STRAND 63 69
FT TURN 70 72
FT STRAND 75 79
FT STRAND 83 86
FT TURN 88 89
FT TURN 92 93
FT HELIX 96 107
FT TURN 106 107
FT TURN 113 114
FT TURN 115 119
FT HELIX 124 126
FT STRAND 129 129
FT HELIX 131 142
FT TURN 143 144

FT HELIX 148 167
FT STRAND 168 168
FT HELIX 169 180
FT TURN 181 182
FT STRAND 185 185
FT HELIX 189 196
FT TURN 197 197
FT STRAND 202 202
FT TURN 222 222
FT STRAND 226 231
FT TURN 232 233
FT HELIX 235 239
FT STRAND 240 240
FT STRAND 243 243
FT STRAND 248 248
FT STRAND 268 268
FT STRAND 276 277
FT STRAND 277 284
FT HELIX 284 284
FT STRAND 286 286
FT HELIX 296 297
FT TURN 299 303
FT STRAND 311 313
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FT HELIX 355 355
FT STRAND 357 358
FT TURN 360 361
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FT TURN 367 370
FT STRAND 371 374
FT TURN 380 381
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FT STRAND 385 387
FT STRAND 387 387
FT STRAND 398 399
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FT HELIX 413 415
FT STRAND 417 421
FT TURN 422 423
FT STRAND 424 428
FT TURN 432 433
FT STRAND 435 437
FT HELIX 439 441
FT TURN 441 444
FT STRAND 447 448
FT TURN 450 451
FT STRAND 452 459
FT TURN 464 465
FT STRAND 467 472
FT TURN 474 475
FT STRAND 478 480
FT HELIX 483 484
FT STRAND 486 487
FT TURN 490 492
FT TURN 492 492
FT STRAND 493 501
FT STRAND 501 501

Query Match 54.0%: Score 717; DB 1; Length 528;
Best Local Similarity 52.7%: Pred. No. 2,2e-63;
Matches 136; Conservative 39; Mismatches 81; Indels 2; Gaps 2;
CY 5 CSAS-EPTVARIYORXGXVYVADDDPHGNOIQLPFSKNDPNQJLTKXIDYTRNSG 63

D6 CSSEYRPEVFRIGGRGNCQVDVVGHNGNNIIMKCKDLRENOAMLKSDELTRENKK 328

Q7 269 GSGSYRPETVRIGRRGNQCVDVVGHNGNIIIMRKCKDLENEOAMLSKDPTLRENKK 328

OY CLTVGVTVGYVMIFPDONAVREARITWIVXNKGITINPSNVLLAASSIKGTILVTOT 123

D6 64 :CLTGGVTVGYVMIFPDTSSVAALRYATMINDMGITINPSNLVLHNSRSSKGTLVTOT 388

Q7 329 CTTTGGAASYSYTMIFDTSSAAVALRYATMINDMGITINPSNLVLHNSRSSKGTLVTOT 388

OY 124 LHYTAGCGGLANDVPRAEVIYTGFPLCQSNXXGSVWGFTCSGXOXNXNALVGQSST 183

D6 389 NBYLMRGRTAGRNNTSPPFVSISGISDPLCMQAQCNWMADDBSKKEGD-QMALTYQGSI 447

Q7 184 RKQNDDQLTZLRDSRVSVIYNVICSSXXXSRWFVEFKALINTXXXXDVYAQRNF 243

D6 448 RSVQNMNDCTLSHDHQGSTKITLLMGSCNMAASQRFVANIDISTLYLDWDMDVYGSDRS 507

OY 244 LRRIITYPKENGMML 261
.:.
.:.

D6 508 LKQYLTPFGTRNQHM 525

RESULT 5
ABRC_ABRPR
ID ABRC_ABRPR STANDED; PRT; 562 AA.

P28550;
DI DEC-1992 [Rel. 24, Created]
DT 01-DIC-1992 [Rel. 24, Last sequence update)
DT 28-FEB-2003 [Rel. 41, Last annotation update)
DE ABR_1_Protein
AC AC_1_3_223 Cloning c chain
PF Pfam 000653; Ricin B Chain (TrNA N-glycosidase)
OS Abura predatorii [Indian Isocetes] (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
eucotsids I; Fabales; Papilionoideae; Adreaceae; Astraea; Abruta.
NCBI_TaxId=3816;

RN [1]

NX SEQUENCE FROM N.A.

RC TISSUE=tent,
RX MEDLINE=9126657; PubMed=2050149;
FA KEGG=map04301; MEGALIGN=J.M.Walshydrack.E.J.; Platak.M.;
RT "Proteobiont": genomic cloning, characterisation and the expression of
RL the A-chain in Saccharothra coli." ;
RL Eur. J. Biochem. 198;723-732(1991).

-! FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE COVALENT INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ACTIN TO THE CALIX MEMBERS THAT PRECEDES ANNOTOGISIS. RATING OF ACTIVITY ON THE CALIX MEMBER OF THE N-Glycosidic bond at one amino acid position, number 285.

-! DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETTA, GAMMA).

-! SIMILARTY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

-! SIMILARTY: Contains 2 ricin B-type lectin domains.

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CC FMR; X55667; CAU39202.1; -
DR ER; SI6027; StetZ.
DR D13541; GI134071; -
DR TRIPROTO; IRP000772; Ricin_B_lectin.
DR Interpro; IPRO01574; RIP
DR Pfam; PF00653; Ricin_B_Lectin; 6.
DR pfam; PF00164; RIP_1.
DR PRINTS; PR00396; SHIGARCIN.
DR SMART; SMO0458; RICIN; 2.

DR	PROSITE; PS00731; RGIN B LECTIN 2.
DR	Plant database; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;
KM	STONR
FT	CHAIN 1
FT	PEPTIDE 35 285 ABRIN C A CHAIN (BY SIMILARITY) .
FT	CHAIN 1
FT	PEPTIDE 286 295 LINKER PEPTIDE (BY SIMILARITY) .
FT	CHAIN 1
FT	DOMAIN 326 562 ABRIN C B CHAIN (BY SIMILARITY) .
FT	DOMAIN 307 434 RGIN B-TYPE LECTIN 1.
FT	REPEAT 417 561 RGIN B-TYPE LECTIN 2.
FT	REPEAT 337 339 1-ALPHA.
FT	REPEAT 360 400 1-BETA.
FT	REPEAT 403 405 2-ALPHA.
FT	REPEAT 403 405 2-BETA.
FT	PERMANENT 487 526 2-GAMMA.
FT	PERMANENT 529 562
FT	ACT SITE 198 198 BY SIMILARITY.
FT	DISULFID 281 303 INTERCHAIN (BY SIMILARITY) .
FT	DISULFID 320 339 BY SIMILARITY.
FT	DISULFID 363 380 BY SIMILARITY.
FT	DISULFID 451 464 BY SIMILARITY.
FT	DISULFID 450 567 BY SIMILARITY.
FT	MOD RES 35 35 PHOSPHORYLATED CARBOXYLIC ACID
FT	CARBOND 234 234 N-LINKED (GLNAC. . .) (POTENTIAL).
FT	CARBOND 335 335 N-LINKED (GLNAC. . .) (POTENTIAL).
FT	CARBOND 435 435 N-LINKED (GLNAC. . .) (POTENTIAL).
SO	SEQUENCE 562 AA; 62817 MW; 1E0AB8C7DBA6278 CRC64;
Query Match	53.0%; Score 703; DB 1; Length 562;
Best Local Similarity	51.9%; Pred. No. 58-62;
Matches 141	Conservative 39; Mismatches 83; Indels 2; Gaps 2
QY	5 CSAS-EPPRIIVGRKXGMDVIRDEPDHNGOQLAKESKNDDNPMTLRRTXTSSNS 63
Db	303 CSRPRPIVATIGSDGDCVDYDGDGNNGRLIHWKCDFLENOUWTLRSKPITRSNK 362
QY	64 CLTGTGYAPAYWIIFPCNTVEKATITWQVNGDTINRNENIVLAASSICGTTLTVOT 133
Db	363 CLTTSEVAFPNQNIWICYCSVAELWAEATWLNQNTLINRKALVIAASSSGGTIVTF 422
QY	124 IDVTLLGGMLANDTAAREVETIYVRFDLCNESKGSWYETCSSQXOKXALHYOGSI 193
Db	423 NEHTAGQKTRNNATSPFTYSISGISDLCDMGQSNNMALDCKNNKEQ-QRAYLTDSI 481
QY	184 EPPKRDODCLTKGSDVSVINVS-CSKSKSQGVNYTEKAILIKKKXXXXDVAAQRK 243
Db	482 KSYUNNNCCCTLSHKQCSPIVLAKSCMGASQMRFLPKDGSITYNLHDWDVMDYSBDS 541
QY	244 LRRIIIVATGKGNOML 261
Db	542 ILEIIILHYKGNQIMLV 559
RESULT 6	
THERM_ABRP	STANDARD; FRT; 527 AA.
AC	O06077; P81374;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last annotated update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Abrin b precursor [Comtains: Abrin-b A chain (mRNA N-glycosidase)]
DE	(EC 3.2.2.22); Abrin-b B chain; (oe) (Crab's eye)
OS	Rhus precatorius (Linnaeus Streptomyces; Embryophyta; Tracheophyta;
OC	Eukaryota; Eukarya; Streptophyta; endosymbionts; core eudicots; Rosidae;
OC	eudicots I; Fabales; Papaveraceae; Papilionoideae; Abreae; Abrus.
OX	NBI TaxID=3816;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91332798; PubMed=8421313;
RT	Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y., Primary structure of three distinct isoabserins determined by cDNA

DR	PROSITE; PS00731; RGIN B LECTIN 2.
DR	Plant database; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;
KM	STONR
FT	CHAIN 1
FT	PEPTIDE 35 285 ABRIN C A CHAIN (BY SIMILARITY) .
FT	CHAIN 1
FT	PEPTIDE 286 295 LINKER PEPTIDE (BY SIMILARITY) .
FT	CHAIN 1
FT	DOMAIN 326 562 ABRIN C B CHAIN (BY SIMILARITY) .
FT	DOMAIN 307 434 RGIN B-TYPE LECTIN 1.
FT	REPEAT 417 561 RGIN B-TYPE LECTIN 2.
FT	REPEAT 337 339 1-ALPHA.
FT	REPEAT 360 400 1-BETA.
FT	REPEAT 403 405 2-ALPHA.
FT	REPEAT 403 405 2-BETA.
FT	PERMANENT 487 526 2-GAMMA.
FT	PERMANENT 529 562
FT	ACT SITE 198 198 BY SIMILARITY.
FT	DISULFID 281 303 INTERCHAIN (BY SIMILARITY) .
FT	DISULFID 320 339 BY SIMILARITY.
FT	DISULFID 363 380 BY SIMILARITY.
FT	DISULFID 451 464 BY SIMILARITY.
FT	DISULFID 450 567 BY SIMILARITY.
FT	MOD RES 35 35 PHOSPHORYLATED ACID
FT	CATABOND 234 234 N-LINKED (GLNAC. .) (POTENTIAL).
FT	CATABOND 335 335 N-LINKED (GLNAC. .) (POTENTIAL).
FT	CATABOND 435 435 N-LINKED (GLNAC. .) (POTENTIAL).
SO	SEQUENCE 562 AA; 62817 MW; 1E0AB8C7DBA6278 CRC64;
Query Match	53.0%; Score 703; DB 1; Length 562;
Best Local Similarity	51.9%; Pred. No. 58-62;
Matches 141	Conservative 39; Mismatches 83; Indels 2; Gaps 2
QY	5 CSAS-EPPRIIVGRKXGMDVIRDEDPDNGOQLAKESKNDDNPMTLRRTXTSSNS 63
Db	303 CSRRIPIRVATIGSDGCVIDVDGDGNNGRIIAWKCDELLENOWATLRSKTKIRSNK 362
QY	64 CLTGTGYAPAYWIIFPCNTVEKATITWQVNGDTIINRNINVLAASSGICGTLTVOT 133
Db	363 CLTTSEYAFPNQNIWICYCSVAELTWLEWNTGIINIKSAIVLAASSSGGTLVT 422
QY	124 IDVTLAGQMLANDTAREVETIYVRDLCNESKGSWETCYSSQXOKXNALYGDSI 193
Db	423 NEHFAAGQNRGNNATSPFTYSIGSIDCLQMGQSNNMLADCDNNKEQ-QRAYLTDSI 481
QY	184 EPRKRDODCLTGKDSDVSVINVS-CSKXSQGVNYTEKAILDKKKXXDXDAQANRK 243
Db	482 KSVQNNNCCTLSKHQCSPIVLA-CNVGAQSMRLFRDGISTYVNLHDVMWDVYSDDS 541
QY	244 LRRIIIVATGSKNQMWL 261
Db	542 ILEIIILHYKGNQIMWL 559
RESULT 6	
THERM_ABRP	STANDARD; FRT; 527 AA.
AC	O06077; P81374;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last annotated update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Abrin b precursor [Comtains: Abrin-b A chain (mRNA N-glycosidase)
DE	(EC 3.2.2.22); Abrin-b B chain] (see) (Crab's eye)
OS	Abrus precatorius (Linnaeus Streptomyces; Embryophyta; Tracheophyta;
OC	Eukaryota; Eubacteria; Mesophyllophyta; endocytodians; core eudicots; Rosidae;
OC	eucosids I; Fabales; Papaceae; Papilionoideae; Abroee; Abrus.
OX	NBI TaxID=3816;
RN	[1] _NAME;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91332798; PubMed=8421313;
RT	Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.,
	"Primary structure of three distinct isoabroteins determined by cDNA

RT sequencing. Conservation and significance.";
 J. Mol. Biol. 229:263-267 (1993).
 [2]
 RP SEQUENCE OF 260-527.
 RC TISSUE=Seed.
 RX MEDLINE=3169023; PubMed=7763422;
 RT "Kobayashi, Sumitama T., Funatsu G.;
 RT "The complete amino acid sequences of the B-chains of abrin-a and
 RT abrin-b toxic proteins from *Rhus precatorius*."
 RT Biosci. Biotechnol. Biochem. 57:146-169 (1993).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,124 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- DOMAIN: 1. DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE DIMER CONSISTS OF 2 IDENTICAL SUBUNITS. EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (1st, 2nd, 3rd).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC -----
 DR EMBL, M98345; AAA32625.1; -
 DR PIR, S32430; S32430.
 DR HSSP, P11140; 1ABR.
 DR InterPro, IPR000772; Ricin_B_lectin.
 DR InterPro, IPR001574; RIP.
 DR Pfam, PF00652; Ricin_B_lectin; 6.
 DR SMART, SM00458; RICIN2.
 DR SMART, SM00458; RICIN2.
 DR PROSITE, PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE, PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Pyrolydine carboxylic acid.
 FT CHAIN 1 250
 FT PEPTIDE 251 260
 FT CHAIN 261 527
 FT DOMAIN 272 399
 FT DOMAIN 402 526
 FT REPEAT 322 324
 FT REPEAT 368 400
 FT REPEAT 413 448
 FT REPEAT 452 491
 FT REPEAT 494 527
 FT ACT_SITE 163 163
 FT DISULFID 246 268
 FT DISULFID 328 345
 FT DISULFID 416 429
 FT DISULFID 455 472
 FT MOD_RES 1 1
 FT CARBOHYD 110 110
 FT CARBOHYD 360 360
 FT CARBOHYD 400 400
 FT CONFLICT 282 282
 FT CONFLICT 291 291
 FT CONFLICT 350 351
 FT CONFLICT 378 378
 S -> N (IN REF. 2).
 S -> N (IN REF. 2).

FT CONFLICT 426 426 L -> M (IN REF. 2).
 FT CONFLICT 428 428 Y -> D (IN REF. 2).
 FT CONFLICT 431 431 N -> S (IN REF. 2).
 FT CONFLICT 484 484 R -> K (IN REF. 2).
 FT CONFLICT 491 491 H -> Y (IN REF. 2).
 FT CONFLICT 493 493 H -> Y (IN REF. 2).
 FT CONFLICT 502 502 R -> G (IN REF. 2).
 FT CONFLICT 509 509 E -> Q (IN REF. 2).
 FT CONFLICT 512 512 H -> M (IN REF. 2).
 FT CONFLICT 513 513 H -> M (IN REF. 2).
 SQ SEQUENCE 527 AA; 59114 MW; 1235AE430CEB9494 CIRC64;
 Query Match 52.9%; Score 702; DB 1; Length 527;
 Best Local Similarity 51.9%; Pred. No. 6,76-63;
 Matches 134; Conservative 39; Mismatches 83; Indels 2; Gaps 2;
 QY 5 CSAS-EPTVAIVGRXGVYDVCDPDPDQNOQLMPKSNNDPNQLTWIRKXTRIRNGS 63
 Db 268 CSRSEPTVAIVGRXGVYDVCDPDPDQNOQLMPKSNNDPNQLTWIRKXTRIRNGK 327
 QY 64 CLITGVYAGVYVIMPCNTAVREATTNQTAKXGTTINRSNLTVAASGINKTTLTVOT 123
 Db 328 CLITGVYAGVYVIMPCNTAVREATTNQTAKXGTTINRSNLTVAASGINKTTLTVOT 387
 QY 124 LDVTTGGQMLANDTAPREAVTGPDLCHRNAGSWYECSSGXQXKXALYAGGSGI 183
 Db 388 NEVLMQCMPTCNTNTPFTSTISYSDLCVQAGSNVLTACDNKXEQ-QVALYTDGSI 446
 QY 184 RPKQNDQCLTIGSDVSTVINIVSCSXKXQKRVFTHEXALINIKXXXXPVAQANKR 243
 Db 447 RSVQNTNCTSRKXQSFVLMACSGNAGQKRLFRMDSTVNHDDVMDVRESDES 506
 QY 244 LRLITVYATGPRNQML 261
 Db 507 LKLLIHHYHGRNQML 524
 RESULT 7
 NIGR SANMI ID NIGR SANMI STANDARD; PRT; 563 AA.
 AC P33183; P33184; P93542;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 26-FEB-2003 (Rel. 41, Last sequence update)
 DT 26-FEB-2003 (Rel. 41, Last annotation update)
 DI MIMAT000003 (MIMAT)
 DR (MIMAT) B-glycosidase (Ref. 3, 2, 22); Nigrazin B chain.
 OS Sambucus nigra (European elder).
 OC Burkholderia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxId=4202;
 RN (1)
 RC SEQUENCE FROM N. A.
 RC TISSUE=Bank;15449; PubMed=8647092;
 RX MEDLINE=368217; PubMed=8647092;
 RT "Van Leuven F., Pennane W. J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
 RT from the bark of elderberry (Sambucus nigra)."
 RT Eur. J. Biochem. 237:505-513 (1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Bank;
 RX MEDLINE=94003077; PubMed=8400335;
 RC TISSUE=Bank;
 RX MEDLINE=94003077; PubMed=8400335;
 RT "Gibbes T., Citores L., Petrezeas J.M., Rojo M.A., Iglesias R.,
 RT "Munoz R., Aras F.J., Calonge M.J., Garcia J.R., Mendes E.;
 RT "Isolation and partial characterization of Nigrazin B, a non-toxic
 RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
 RT nigra (L.). Biol. 22:1191-1196 (1993).
 CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH SPECIFICALLY INHIBITS MNAMINATIN
 CC PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL
 CC SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

[illegible]

```

178 YODDS:R:KONQDDGCT:KXAGDSVSTVYINVCSSXXSXGVRFTNEALINIKKXXXXXV 237
Db 475 YODDTR:R:NRSLQALCVTTNGNSNDLIIIIKKQGLF-SQVF:R:NRSDGAIYNPKSRHWYDV 533
Cy 238 AQANPKLRIRIIIVYATKRNQML 261
Db 534 RASWSEKRLIIIFATNAPQDMV 557

RESULT 6
XVNA_STRLI STANDARD: PRT: 477 AA.
AC P26514; P96464;
ID XVNA_STRLI
DT 01-AUG-1992 (Rel. 23, Created)
DT 30-MAY-2000 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 43, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.6) (Xylanase A)
OS Xylaria
OC Streptomyces lividans.
OC Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces; Streptomyces.
OC NCBI_Textid:1916;
LN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RC STRAIN=66 / 1326;
RX MEDLINE=20707433; PubMed=1743511.
RA Sharek F., Roy C., Taguchi N., Morosoli R., Kluepfel D.;
RT "Isolation and characterization of three genes specifying xylanases in Streptomyces lividans"
RL Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 20 AND 140-141.
RC STRAIN=66 / 1326;
RX Sharek F.;
RT Submitted (JUL-1998) to the EMBL/Genbank/DBD databases.
RN [3] DAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
RX MEDLINE=9434223; PubMed=8065533.
RA Deyendenda V., Swenson L., Green R., Wei Y.Y., Morosoli R., Sharek F., Kluepfel D., Deyendenda Z.S.;
RT "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans F xylanase A, a member of the F family of beta-1,4-D-glycanases."
RL J. Biol. Chem. 269:20811-20814(1994).
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major component of plant cell-walls. XLA and XLB seem to act sequentially on the substrate to yield xylobiose and xylose as carbon sources.
CC -1- TISSUE: Xylanase.
CC -1- PATHWAY: Xylanase.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: Contains 1 rich B-type lectin domain.
CC CC
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CC CC
CC EMBL: M64551; AAC26525.1; -
DR EIR: JS05891; OS0589.
DR FDB: 1XMS; 21 MAY-01.
DR FDB: 1EYV; 23 MAY-01.
DR FDB: 1KXU; 19-JUN-02.
DR FDB: 1KMY; 11-SEP-02.
DR InterPro: IPR001000; Glyco_hydro_10.

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DR InterPro: IPR000772; Ricin B lectin.
 DR Pfam: PF00331; Glyco_Hydro_10; 1.
 DR Pfam: PF00652; Ricin B lectin; 3.
 DR PRINTS: PR00134; GUMHYDROLASE10.
 DR SMART: SM00453; Glyco_10; 1.
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
 DR PROSITE: PS00231; Ricin B lectin; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 3D-structure.
 FT SIGNAL 1 41
 FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
 FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
 FT ACT_SITE 169 169 PROTON DONOR.
 FT ACT_SITE 277 277 NUCLEOPHILS.
 SQ SEQUENCE 477 AA; 51162 MW; E14AF337BDC68CC CRC64;
 Query Match 8.9%; Score 118.5; DB 1; Length 477;
 Best Local Similarity 29.1%; Pred. No. 0.000263;
 Matches 39; Conservative 19; Mismatches 63; Indels 13; Gaps 6;
 QY 7 ASBP-----TWIATGKXGVYVDYDDPHDQNGICQMFPSKNDPNOIWTIKKXKTRISN 61
 Db 346 SSBPADGQIKVWG-SGRCIDVPDASTDQIQIMDCSGT--NQWALTAAGALRY 402
 QY 62 G-SCLTGYGTAGVYVMTFPCNTAVREATIQTWKNXGIIINPSNLVLA--SSGIKQT 118
 Db 403 GRCIDAGTNSKVKQVYSCWGDNR--WRINSDSVGVGSLCLAVNGTANGTL 460
 QY 119 LVVQTLDTTLOQW 132
 Db 461 IOLYTGNSGNQR 474

RESULT 9
 SPL_RAFPA STANDARD; PRT; 525 AA.
 AC 005308; (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DI 28523881; Author (EC 3.4.21.-) (REF).
 OS Parabacter faecitabidus
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococciaceae; Parabacteraceae; Parabacter.
 NCBI_TaxID=13243;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
 RC STRAIN-YLM-50;
 RX MEDLINE=9309426; PubMed=1339445;
 RA Shimoi H., Iimura Y., Oota T., Tadenuma M.;
 RT Molecular structure of Parabacter faecitabidus protease I. A yeast-
 RT lytic serine protease having mannose-binding activity.";
 RL J Biol. Chem. 267:25189-25193(1992).
 RP SEQUENCE OF 212-247.
 RX MEDLINE=9238668; PubMed=1776983;
 RA Shimoi H., Tadenuma M.;
 RT "Characterization of Parabacter faecitabidus protease I, a
 RT yeast-lytic serine protease having mannose-binding activity.";
 RL J. Biochem. 110:608-613(1991).
 CC -1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
 CC LYING YEAST CELLS. SIMILAR TO ELASTASE IN ITS SUBSTRATE
 CC SPECIFICITY AND HAS A LECTIN-LIKE AFFINITY FOR MANNOSE.
 CC -1- SUBCELLULAR LOCATION: BE THE NERVE SUBSTRATE FOR RFI.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
 CC -1- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D10753; AAA01595.1; -
 DR FTR: A45053; A45053.
 DR HSRP: P00178; 7GBA.
 DR HSRP: P00178; 7GBA.
 DR InterPro: IPR004235; AL protease.
 DR InterPro: IPR001315; EndopeptidaseA.
 DR InterPro: IPR000772; Ricin B lectin.
 DR InterPro: IPR001254; Ser protease_Try.
 DR Pfam: PF02983; AL protease; 1.
 DR Pfam: PF00652; Ricin B lectin; 3.
 DR PRINTS: PR00861; ALYTIPTASE.
 DR SMART: SM00458; RYCIN; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR PROSITE: PS00231; Ricin B lectin; 1.
 KM Xylanase; serine protease; Mannose-binding; Signal; Zymogen;
 3D-structure.
 FT SIGNAL 1 32
 FT PROPER 33 211 POTENTIAL.
 FT CHAIN 212 525 SERINE PROTEASE I.
 FT DOMAIN 396 525 RICIN B-TYPE LECTIN.
 FT DOMAIN 401 525 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
 FT FOR PROTEASE FUNCTION.
 FT DISULFID 223 239 BY SIMILARITY.
 FT DISULFID 310 320 BY SIMILARITY.
 FT DISULFID 346 346 BY SIMILARITY.
 FT DISULFID 442 442 BY SIMILARITY.
 FT DISULFID 443 472 BY SIMILARITY.
 FT DISULFID 496 514 BY SIMILARITY.
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 270 270 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 525 AA; 55654 MW; DA2BCF7D330EBB61 CRC64;
 Query Match 7.8%; Score 104; DB 1; Length 525;
 Best Local Similarity 30.2%; Pred. No. 0.01; Indels 12; Gaps 5;
 Matches 32; Conservative 17; Mismatches 45;
 QY 2 DYCASAEPYVITIGKXGVYDDPHDQNGICQMFPSKNDPNOIWTIKKXKTRISN 61
 Db 399 DVT-----TSVGVGNQNCIDVPSDPTDQIQVNNQGN--AQVGFPHDQTLRI 450
 QY 63 GSCI-TTYGT-AGVYVMTFPCNTAVREATIQTWKNXGIIINPSN 105
 Db 451 GRCIDAGTNSKVKQVYSCWGDNR--WRINSDSVGVGSLCLAVNGTANGTL 494
 RESULT 10
 E138_RATSP STANDARD; PRT; 548 AA.
 ID 005316;
 DT 03-JUN-1998 (Rel. 36, Created)
 DT 15-OCT-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-
 DE glucan endohydrolase) ((1->3)-beta-glucanase).
 GN GUCI.
 OS Actinobacter sp. (strain YCMD3).
 OC Bacteria; Actinobacteridae; Actinobacteriales;
 OC Micrococciaceae; Micrococciaceae; Arthobacter.
 NCBI_TaxID=167;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Watanabe T., Hasegawa H., Tanaka H., Doi A., Doi K.;
 RT Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
 CC SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC -----
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CC -----
CC EMBL: D21668; BA04892.1; -.
CC HSP: P02879; 2A1.
CC InterPro: IPR000772; Ricin B lectin.
CC Pfam: PF00652; Ricin B lectin. 3.
CC SMART: SMO0458; RICIN, 1.
CC PROSITE: PS0231; Ricin B lectin; 1.
CC K1: HYDROLASE; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
FT SIGNAL 1 36
FT CHAIN 37 548
FT DOMAIN 422 548
FT SEQUENCE 548 AA; 58164 MW; ED6534315750596 CRC64;
SQ
Query March 7.6%; Score 101; DB 1; Length 548;
Best Local Similarity 30.8%; Pred. No. 0.021;
Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;
DB 434 LDVPMADPTDITVQVL-ATCGNAAQQTGRTDITVRALEKCDVARSGTADGNVWIT 491
QY 80 DONTAVRENTIWIW---XNGTINPRSNVLAASGI---KGTTLVQTLDTLGGCW 132
DB 492 TCN-----GTGAKQKTYDASATVLAHNFQSKCKLDAGCAPLDDQKVLQMTGNTQADQW 546
RESULT 11
E13B OERXA STANDARD; PRT; 548 AA.
AC P2222;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-
DE glucan endoglucanase) ((1->3)-beta-glucanase).
DE Desoxya xanthineolase; (1->3)-beta-glucanase).
DE Bacteriophage Actinobacteriophage; Actinomycetales;
CC Micrococciaceae; Promicromonosporaceae; Cellulosimicrobium.
CC NCBI_Taxid=1710;
RM
RN
RS
RT
RT MEDLINE=91093212; PubMed=1985933;
RA Shen S.-H., Chretien P., Bastien L., Siliaty S.N.;
RT "Primary sequence of the glucanase gene from Oerskovia
RT xanthineolytica. Expression and purification of the enzyme from
RT Escherichia coli." J. Biol. Chem. 268:1058-1063 (1993).
RT J. Biol. Chem. 268:1058-1063 (1993).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M60826; AA25520.1; -.
CC HSP: A39094; A39094.
CC HSP: P02879; 2A1.
CC InterPro: IPR000772; Ricin B lectin.
CC Pfam: PF00652; Ricin B lectin; 3.
CC SMART: SMO0458; RICIN, 1.
CC PROSITE: PS0231; Ricin B lectin; 1.
CC K1: HYDROLASE; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
FT SIGNAL 1 36
FT CHAIN 37 548
FT DOMAIN 422 548
FT DOMAIN 430 548
FT DOMAIN 472 548
FT SEQUENCE 548 AA; 58088 MW; 412554AA24C04B CRC64;
SQ
Query March 7.6%; Score 101; DB 1; Length 548;
Best Local Similarity 30.8%; Pred. No. 0.021; 54; Indels 16; Gaps 5;
Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;
DB 434 LDVPMADPTDITVQVL-ATCGNAAQQTGRTDITVRALEKCDVARSGTADGNVWIT 491
QY 80 DONTAVRENTIWIW---XNGTINPRSNVLAASGI---KGTTLVQTLDTLGGCW 132
DB 492 TCN-----GTGAKQKTYDASATVLAHNFQSKCKLDAGCAPLDDQKVLQMTGNTQADQW 546
RESULT 12
ARB5 STFCO STANDARD; PRT; 475 AA.
AC OEA161;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
GN ARFB OR SC05932 OR SC7H1.02.
CC Streptomyces coelicolor.
CC Bacteria; Actinobacteriophage; Actinomycetales;
CC Streptomyces; Streptomyces; Streptomyces.
CC NCBI_Taxid=1902;
RM
RN
RS
RT
RT MEDLINE=2196410; PubMed=1200953;
RC SPRIN-13(2) / M145;
RA Bentley S.D., Chater K.F., Csernok-Farraga A.-W., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.S., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Latke J., Lawley J., Oliver K., O'Neill S.,
RA Rabinowitch S., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Segura K., Singer S., Taylor K.,
RA Warren T., Metcalf A., Woodward A., Barrett B.G., Parkhill J.,
RA Hooton D.A.; Genome sequence of the model actinomycete Streptomyces
RA coelicolor 342. "J. Biol. Chem. 274:41714-41720 (2000).
RT Nature 407:141-147 (2002).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinofuranoside residues in alpha-L-arabinosides.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC -----
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EMBL: A039125; CANA6189.1; --

DR PIR: P03697; 15697; Glyco hydro 62.
DR Interpro: IPR005193; Glyco hydro 62.
DR Interpro: IPR000772; Ricin B lectin.
DR Pfam: PF03664; Glyco hydro 62; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR SMART: SM00458; Ricin B lectin; 1.
DR PROSITE: PS50231; Ricin B lectin; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KM Complete proteome.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
FT DOMAIN 39 166 RICIN B-TYPE LECTIN.
FT DOMAIN 167 50455 NM; 476707F8343C60D CRC64;
SQ SEQUENCE 475 AA; 50045 NM; 476707F8343C60D CRC64;

Query Match 7.0%; Score 93.5; DB 1; Length 475;
Best Local Similarity 27.3%; Pred. No. 0.1; Mismatches 66; Indels 9; Gaps 6;
Matches 35; Conservative 18; Mismatches 66; Indels 9; Gaps 6;

QY 22 VDVRDDDFDNGNQLMPSKNDNQLTKRDXITRNSG-SCITTYGYTA--GYVMI 78
DB 52 LDVLSGSDGALLQLYDCMGST--NQMTSTDTGRLTYGDKLDVPGHATAPRTVQI 109
QY 79 FDCNTAVEATWQIXNGTIINPNSLVL-ANSSG-IKGTITVQTLDTYLGQMLAGN 136
DB 110 WSGSGNQ--WRNSDGVGVSGSLCENAGNGRANGRAVQMTNCGSNQMTGLT 167
QY 137 DPAPEVT 144
DB 168 GTPPTDT 175

RESULT 13
ASPE STRLI STANDARD; FRT; 475 AA.
ID ASPE STRLI
DI 15-DEC-1998 (Rel. 37, Created)
DI 15-DEC-1998 (Rel. 37, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
GN ABPA.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN SOURCE FROM N.A.
RC STRAIN=67220326; PubMed=9148759.
RX MEDLINE=97220326;
RA Vincent P. Sharick F. Dupont C. Morosoli P. Kuepfel D.;
RT "New alpha-L-arabinofuranosidase produced by Streptomyces lividans:
RT cloning and DNA sequence of the abp3 gene and characterisation of the
RT enzyme";
RL Biochem. J. 322:845-852(1997).
RN REVIEWS:
RC STRAIN=66 / 1326;
RA Sharick P.; (1998) In: the EMBL/GenBank/DBJ database.
RL FUNCTION: Has a specific activity of cleaving alpha-L-arabinofuranoside
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-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.

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EMBL: A039125; CANA6189.1; --

DR PIR: P03697; 15697; Glyco hydro 62.
DR Interpro: IPR005193; Glyco hydro 62.
DR Interpro: IPR000772; Ricin B lectin.
DR Pfam: PF03664; Glyco hydro 62; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR SMART: SM00458; Ricin B lectin; 1.
DR PROSITE: PS50231; Ricin B lectin; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KM Complete proteome.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
FT DOMAIN 39 166 RICIN B-TYPE LECTIN.
FT DOMAIN 167 50455 NM; 476707F8343C60D CRC64;
SQ SEQUENCE 475 AA; 50045 NM; 476707F8343C60D CRC64;

Query Match 6.8%; Score 90.5; DB 1; Length 475;
Best Local Similarity 27.3%; Pred. No. 0.2; Mismatches 66; Indels 9; Gaps 6;
Matches 35; Conservative 18; Mismatches 66; Indels 9; Gaps 6;

QY 22 VDVRDDDFDNGNQLMPSKNDNQLTKRDXITRNSG-SCITTYGYTA--GYVMI 78
DB 52 LDVLSGSDGALLQLYDCMGST--NQMTSTDTGRLTYGDKLDVPGHATAPRTVQI 109
QY 79 FDCNTAVEATWQIXNGTIINPNSLVL-ANSSG-IKGTITVQTLDTYLGQMLAGN 136
DB 110 WSGSGNQ--WRNSDGVGVSGSLCENAGNGRANGRAVQMTNCGSNQMTGLT 167
QY 137 DPAPEVT 144
DB 168 GTPPTDT 175

RESULT 14
I163-STRY3 STANDARD; FRT; 1693 AA.
ID I163-STRY3
DI 15-DEC-1998 (Rel. 36, Created)
DI 15-DEC-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical WD-repeat protein s110163.
GN S110163.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96127529; PubMed=8590279;
RX Sano T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 644 to 928 of the genome.";
RL DNA Res. 2:153-166(1995).
RN REVIEWS:
RC STRAIN=66 / 1326;
RA Sharick P.; (1998) In: the EMBL/GenBank/DBJ database.
RL FUNCTION: Has a specific activity of cleaving alpha-L-arabinofuranoside
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: D63999; BAI0064.1; --

DR PIR: S76086; S76086.

```

DR InterPro; IPR001580; WD40.
DR Pfam; PF00400; WD40; 16.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 13.
DR SMART; SM00320; WD40; 16.
DR PROSITE; PS00678; WD REPEATS 1, 8.
DR PROSITE; PS00682; WD REPEATS 2, 3.
DR PROSITE; PS00684; WD REPEATS 3, 5.
DR PROSITE; PS00685; WD REPEATS 4, 7.
DR Hypothetical protein; Repeat; WD repeat; Complete proteome.
FT REPEAT 1068 1042 Repeat; WD 1.
FT REPEAT 1053 1083 WD 2.
FT REPEAT 1094 1124 WD 3.
FT REPEAT 1135 1165 WD 4.
FT REPEAT 1176 1206 WD 5.
FT REPEAT 1217 1247 WD 6.
FT REPEAT 1258 1288 WD 7.
FT REPEAT 1299 1329 WD 8.
FT REPEAT 1340 1370 WD 9.
FT REPEAT 1381 1411 WD 10.
FT REPEAT 1422 1452 WD 11.
FT REPEAT 1463 1493 WD 12.
FT REPEAT 1504 1534 WD 13.
FT REPEAT 1545 1575 WD 14.
FT REPEAT 1586 1616 WD 15.
FT REPEAT 1627 1657 WD 16.
SQ SEQUENCE 1693 AA; 189935 MW; 0977A827A0251CFP CRC64;

Query Match
Best Local Similarity 21.6%; Score 79.5; DB 1; Length 1693;
Matches 58; Conservative 30; Mismatches 97; Indels 83; Gaps 13;

QY 3 VTGASGEPYIVIGXKXKXNDV---RDDPH-----DNOIOLMPSKNNPNQIMTK 53
DB 1234 ITSSSDGTAWWSRHKCLGTHGHGHNHGAHPSLDGQXIVY---STDTATLAT-- 1288
QY 54 RXTIRNSGSLFTY-GYTGYYVMFDGN-----TAVREATIQVXKXGI-TPHS 104
DB 1289 -----KEGTLLIRKHQKXYADAFSDGRVFTVSDQTAQWDMSQDITLLTGS 1342
QY 105 NTVLAASGIXGTLTVQTLDTL-----GQGMKAGNDPAFEVITIGSR 149
DB 1343 HWVKNHAFNAGDRLITVSDKIKALMTTGECEVAVLADHCGVTRGQPSF-- 1393
QY 150 DICWESKSWVETCKSSGONKXKXALYGGGSIKRPQONOCCTGSDSYVTN--- 205
DB 1394 -----DGMIVTGSMDKTKQ-LNNVLS-----KLTVAHGHQDVLNFRS 1433
QY 206 -----IVSCSXKXKXQKRWFT-NEXALL 227
DB 1434 PDSQYIVTASDGTARVWNTRELAVL 1461

RESULT 15
PROT_HUMAN STANDARD; PRT; 4074 AA.
ID: Q8TC29
AC Q8TC29
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Polycystic kidney and hepatic disease 1 precursor (Fibrocystin)
DE (Polycystin) (Tigra)
DE PCKD1 OR PCYT OR TICM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC 111_TIGRID-9606.
RP TRP-1249; ARG-1407; FHR-1664; MET-1741; ARG-1917; GTY-1995; ITS-2311.
RP THR-2957; FHR-3018 AND THR-3553, AND VARIANTS MET-752; CYS-760;
RP ARG-853; VAL-1262; MET-2938; THR-3139; ILE-3960 AND ARG-4048.
RC TISSUE=Kidney;
MEDLINE=21918597; Pubmed=11919560;

RA Ward C.J., Hogan M.C., Rossetti S., Walker D., Sneddon T., Wang X.,
RA Kubly V., Cunningham J.M., Baccalao R., Ishibashi M., Milliner D.S.,
RA Torres V.E., Harris P.C.;
RA "The gene mutated in autosomal recessive polycystic kidney disease
RA encodes a large, receptor-like protein."
RA Nat. Genet. 30:259-269(2002).
RA
RA SEQUENCE FROM N.A. (ISOFORM 1), ALTERNATIVE SPLICING, AND VARIANTS
RA APPD MET-36; VAL-222; LBU-253; HIS-760; SER-1122; THR-1624; THR-2357
RA AND THR-3139.
RA TISSUE=Kidney;
RA MEDLINE=21947447; Pubmed=11898128;
RA Ouchic L.F., Furu L., Nagasawa Y., Hou X., Eggemann T., Ren Z.,
RA Bergmann C., Senderik J., Esquivel E., Zeltner R.,
RA Rudnik-Schoenborn S., Murg M., Sweeney W., Ayner E.D., Zeires K.,
RA Quay-Moodford L.M., Somlo S., Germino G.G.;
RA PCKD1, the polycystic kidney and hepatic disease 1 gene, encodes a
RA novel large protein containing multiple
RA immunoglobulin-like plexin-transcription-factor domains and parallel
RA beta-strand repeats.
RA J. Hum. Genet. 70:1305-1317(2002).
RA
RA SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT THR-1204.
RA TISSUE=fetal kidney;
RA MEDLINE=22074934; Pubmed=12079288;
RA Xiong H., Chen Y., Yi Y., Tsuchiya K., Moeckel G., Cheung J.,
RA Liang D., Tham K., Xu X., Chen X.-Z., Pei X., Zhao Z.J., Wu G.;
RA A novel gene encoding a TIG multiple domain protein is a positional
RA candidate for autosomal recessive polycystic kidney disease."
RA Hum. Mol. Genet. 9:1041-1047(2002).
RA
RA -1- SUBCELLULAR LOCATION: Receptor protein that acts in collecting-duct
RA and biliary differentiation.
RA
RA -1- ALTERNATIVE PRODUCTS:
RA Event:Alternative splicing; Named isoforms:2;
RA Comment:Additional isoforms seem to exist. As a matter of fact,
RA alternatively spliced products seem to fall into two broad
RA groups: one group, which includes the longest continuous ORF but
RA which may also include molecules lacking some middle domains,
RA has a single TM element and is likely to be associated with the
RA plasma membrane. The other group lacks a TM domain and thus its
RA members may be secreted;
RA
RA IsoId:Q8TC29-1; Sequence=Displayed;
RA Name:2;
RA IsoId:Q8TC29-2; Sequence=VSP 003947; VSP 003948;
RA TISSUE SPECIFICITY: Predominantly expressed in fetal and adult
RA kidney. Also present in the adult pancreas, but at much lower
RA levels. Detectable in fetal and adult liver. Rather indistinct
RA signal in fetal brain.
RA
RA -1- DISBASIS: Defects in PCKD1 are the cause of all typical forms of
RA autosomal recessive polycystic kidney disease (ARPKD), a affecting
RA hereditary and severe form of polycystic kidney disease affecting
RA the kidneys and the hepatic duct system. The disease spectrum
RA is heterogeneous, with the most cases presenting during infancy. The
RA fetal phenotypic features classically include enlarged and
RA echogenic kidneys, as well as oligohydramnios secondary to a poor
RA urine output. Up to 50% of the affected neonates die shortly after
RA birth, as a result of severe pulmonary hypoplasia and secondary
RA respiratory insufficiency. In the subset that survives the
RA perinatal period, morbidity and mortality are mainly related to
RA severe systemic hypertension, renal insufficiency, and portal
RA hypertension due to portal-tract fibrosis.
RA
RA -1- SIMILARITY: Contains 9 ERM1 repeats.
RA
RA This Swiss-Prot entry is copyright. It is produced through a collaboration
RA between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA the European Bioinformatics Institute. There are no restrictions on its
RA use by non-profit institutions as long as its content is in no way
RA modified and this statement is not removed. Usage by and for commercial
RA entities requires a license agreement (See http://www.isb-sib.ch/announce/
RA or send an email to license@sib-sib.ch).
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[illegible]

FT	CARBOND	1698	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1764	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1779	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1879	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1883	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1919	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1945	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1959	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	1999	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2114	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2144	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2350	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2385	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2435	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2471	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2509	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2535	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2553	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2593	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2623	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2753	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	2768	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3008	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3140	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3169	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3225	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3488	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3558	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3707	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3722	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3838	N-LINKED	(GLONAC)	(POTENTIAL)
FT	CARBOND	3863	N-LINKED	(GLONAC)	(POTENTIAL)
FT	VASPLJC	3396				

21.
 FTID=VSP 009947.
 Missing (in isocform 2).
 GFFREDKONTY -> VITEBAKISE (in isocform

Search completed: December 11, 2003, 14:09:02
Job time : 5.6201 secs

AC OBLK01;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Lectin chain B isoform 3 (fragment).
 DE Viscum album subsp. coloratum.
 DE Bakariya; Vaidiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Streptophyta; Charophyta; Viscum.
 OC NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21566752; PubMed=11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RL Mol. Cells 12:215-220(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF508919; AAM46937.1; -;
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR SMART; SM00458; RICIN_2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 FT NON_TER 1
 FT TER 263
 SQ SEQUENCE 263 AA; 29071 MW; 396C4ADA860F061D CRC64;

Query Match 77.6%; Score 1029.5; DB 10; Length 263;
 Best Local Similarity 74.5%; Pval No. 6e-99; Indels 1; Gaps 1;
 Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 1 DVTCSASEPTVAVGRKXGVYDQDPHDGKQIQMPKSKNDNDPQWLTIKDXTIRS 60
 DB 1 DVTCTSEPTVAVGRKXGVYDQDPHDGKQIQMPKSKNDNDPQWLTIKDXTIRS 60
 QY 61 NSCLTGYGTAGVYVMIIPDCTAVREAVTIWQIXNGTIIIPRSNLTVAASSGIGTII 120
 DB 61 NSCLTGYGTAGVYVMIIPDCTAVREAVTIWQIXNGTIIIPRSNLTVAASSGIGTII 120
 QY 121 VQTDVTLTGQMLASGMPARAVTIYGFDDCMENSGSVTFCTSGHKQK-FKALYD 180
 DB 121 VQTDVTLTGQMLASGMPARAVTIYGFDDCMENSGSVTFCTSGHKQK-FKALYD 179
 QY 181 GSIRPKQNDQCLTGKRSYSVTINIVSCSXSGQWVFTKEALINLKKXXXXDVAAQ 240
 DB 180 GSIRPKQNDQCLTGKRSYSVTINIVSCSXSGQWVFTKEALINLKKXXXXDVAAQ 239
 QY 241 NPKLRILIIYATGKRNQMLPV 263
 DB 240 NPKLRILIIYATGKRNQMLPV 262

RESULT 5

OBLK03
 ID OBLK03 PRELIMINARY; PRT; 266 AA.
 AC OBLK03;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Lectin chain B isoform 1 (fragment).
 DE Viscum album subsp. coloratum.
 DE Bakariya; Vaidiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OC NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21566752; PubMed=11710524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RL Mol. Cells 12:215-220(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF508917; AAM46935.1; -;
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 5.
 DR SMART; SM00458; RICIN_2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 FT NON_TER 1
 FT TER 266
 SQ SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;

Query Match 71.5%; Score 949; DB 10; Length 266;
 Best Local Similarity 64.5%; Pval No. 1e-40; Indels 4; Gaps 2;
 Matches 177; Conservative 29; Mismatches 56; Indels 4; Gaps 2;

QY 1 DVTCSASEPTVAVGRKXGVYDQDPHDGKQIQMPKSKNDNDPQWLTIKDXTIRS 60
 DB 1 DVTCTSEPTVAVGRKXGVYDQDPHDGKQIQMPKSKNDNDPQWLTIKDXTIRS 60
 QY 61 NSCLTGYGTAGVYVMIIPDCTAVREAVTIWQIXNGTIIIPRSNLTVAASSGIGTII 120
 DB 61 NSCLTGYGTAGVYVMIIPDCTAVREAVTIWQIXNGTIIIPRSNLTVAASSGIGTII 120
 QY 118 TLVQTDVTLTGQMLASGMPARAVTIYGFDDCMENSGSVTFCTSGHKQK-FKALYD 177
 DB 121 TLVQTDVTLTGQMLASGMPARAVTIYGFDDCMENSGSVTFCTSGHKQK-FKALYD 179
 QY 178 YGSGIRPKQNDQCLTGKRSYSVTINIVSCSXSGQWVFTKEALINLKKXXXXDV 237
 DB 180 YGSGIRPKQNDQCLTGKRSYSVTINIVSCSXSGQWVFTKEALINLKKXXXXDV 239
 QY 238 AQAPPLARILIIYATGKRNQMLPV 263
 DB 240 AASPLARILIIYATGKRNQMLPV 265

RESULT 6

OBLK174
 ID OBLK174 PRELIMINARY; PRT; 541 AA.
 AC OBLK174;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Protein A chain (BC 3.2.2.22) (rRNA N-glycosylase) (fragment).
 DE Ricinus communis (castor bean).
 OC Bakariya; Vaidiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosales;
 OC OC NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9238377; PubMed=163311;
 RA Roberts L.M., Tregear J.M., Lord J.M.;
 RT "Molecular cloning of ricin.";
 RT Targeted Diast. Ther. 7:81-97(1992).
 CC -1- CATALYTIC ACTIVITY: ENDORHOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADPOSING ON THE 28S RRNA
 CC SPECIFIC ADPOSING TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; F02878; 1986
 DR HSRP; F02878; 1986
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Interpro; IPR001400; Somatostatin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.


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Db          496 GSRPHQDRKCLTSTNHSQSSIISSCSFSSSGRWYFVNDGTLNLKNGLVNDVKG 555
Qy          240 ANPKLRRIIIPATKRNQWMLPV 263
Db          556 SNPSLHQIILIPATKRNQWML 579

RESULT 9
Q94BW3      PRELIMINARY;  FRT;  580 AA.
ID          094BW3
AC          094BW3;  PRELIMINARY;  19, Created
DT          01-DEC-2001 (TRENBLREL; 19, Last sequence update)
DR          01-DEC-2001 (TRENBLREL; 23, Last annotation update)
DE          Type 2 ribosome-inactivating protein cinnamomin III precursor
DS          Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
OS          Cinnamomum camphora (Camphor tree).
OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OX          NCBI_TaxID=13429;

SEQUENCE FROM N.A.
Yang Q., Gong Z.Z., Liu W.Y.;
RT          Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT          genes encoding cinnamomin proteins and study of their expression
RT          patterns. J. JIM-2001) to the EMBL/GenBank/DBJ databases.
RT          Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC          -1- CATALYTIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC          -1- SIMILARITY. BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR          EMBL; AY039803; AAK82460.1; -.
DR          InterPro; IPR000772; Ricin_B_lectin.
DR          InterPro; IPR001574; RIP.
DR          Pfam; PF00652; Ricin_B_lectin; 6.
DR          Pfam; PF00161; RIP; 1.
DR          PRINTS; PR00396; SHIGARICIN.
DR          SMART; SM00458; RICIN; 2.
DR          PROSITE; PS50231; RICIN_B_LECTIN; 2.
FM          Hydroxylase; Signal; Toxin.
FT          CHAIN 33 580
FT          TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT          CINNAMOMIN III
SQ          SEQUENCE 580 AA; 64421 MW; 940010F0187E558 CRC64;

Query Match          60.7%; Score 805; DB 10; Length 580;
Best Local Similarity 59.1%; Pred. No. 4,2e-75;
Matches 156; Conservative 32; Mismatches 74; Indels 2; Gaps 2;

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AC          09FV22;  01-MAR-2001 (TRENBLREL; 16, Created)
DT          01-MAR-2001 (TRENBLREL; 16, Last sequence update)
DR          01-OCT-2002 (TRENBLREL; 22, Last annotation update)
DE          Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
DS          Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
OS          Cinnamomum camphora (Camphor tree).
OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OX          NCBI_TaxID=13429;

SEQUENCE FROM N.A.
Xie L., Liu W.-Y., Wang E.-D.;
RT          Molecular cloning of cinnamomin A-, B-chain and the expression,
RT          purification, characterization and mutagenesis of the A-chain.
RT          Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DL          Type 2 ribosome-inactivating protein cinnamomin I precursor
CC          -1- CATALYTIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC          -1- SIMILARITY. BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR          EMBL; AF129348; AF069718.2; -.
DR          HSPSP; P02873; 2A1.
DR          InterPro; IPR000772; Ricin_B_lectin.
DR          InterPro; IPR001574; RIP.
DR          Pfam; PF00652; Ricin_B_lectin; 5.
DR          Pfam; PF00161; RIP; 1.
DR          PRINTS; PR00396; SHIGARICIN.
DR          SMART; SM00458; RICIN; 2.
DR          PROSITE; PS50231; RICIN_B_LECTIN; 2.
FM          Hydroxylase; Toxin.
FT          CHAIN 1 549
FT          TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT          CINNAMOMIN III
SQ          SEQUENCE 549 AA; 60648 MW; 02607F8607C44B0 CRC64;

Query Match          58.1%; Score 771.5; DB 10; Length 549;
Best Local Similarity 56.6%; Pred. No 1.2e-71;
Matches 150; Conservative 31; Mismatches 81; Indels 3; Gaps 2;

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Thu Dec 11 16:09:51 2003

us-09-601-667c-3.rspt

Page 6

RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamom proteins and study of their expression patterns";

RL Submitted (JUN-2001) to the EMBL/Genbank/DBD databases.

CC -1- CATALYTIC ACTIVITY: ENOHDICOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC EMBL: AY039801, AK82458.1, 1.

DR InterPro: IPR001574; R1c1n.B.1c1c1n.

DR InterPro: IPR001574; R1c1n.B.1c1c1n.

DR Pfam: PF00652; R1c1n.B.1c1c1n. 5.

DR Pfam: PF00161; R1P.1.

DR DR PRINTS: PR00396; SHIGATOICIN.

DR SMART: SMO0458; R1C1N; 2.

DR PROSITE: PS50231; R1C1N.B.1c1c1n. 2.

KW Hydrolase; S1gnal; Toxin.

FT SIGNAL 1

FT CHAIN 33

FT POTENTIAL. TYPE 2 RIBOSOME-INACTIVATING PROTEIN

FT CINNAMOIN I.

SEQUENCE 581 AA; 64215 MW; 68655F8FB6AD196 CRC64;

[illegible]

```

DR Pfam: PF00652; Ricin_Blectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00346; SHGAPRGIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LETTIN; 2.
DR PROSITE: PS00275; SHGAP_RICIN; 1.
KW Hydrolase; Toxin.
PT NON_TER
PT NON_TER
PT NON_TER
SQ SEQUENCE 528 AA; 58970 MW; 62BD42PB8FEF079 CRC64;
Query Match 52.9%; Score 702; DB 10; Length 528;
Best Local Similarity 51.9%; Pred.No. 2e-64;
Matches 13; Conservative 40; Mismatches 82; Indels 2; Gaps 2;

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[illegible]

Query Match 52.3%, Score 694.5, DB 10, Length 382;

Best Local Similarity 51.8%, Pred. No. 7, 9e-64;

Matches 131, Conservative 37, Mismatches 84, Indels 1, Gaps 1;

QY 9 EFTYRIVGKXGVVDDPHDQNOIQWPSKSNNDPQNLTKKXITRSNGCLTY 68
DB 128 EFTYRIVGKXGVVDDPHDQNOIQWPSKSNNDPQNLTKKXITRSNGCLTY 187
QY 69 GYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOTL 128
DB 188 GYDGVYVWIDCTSAVEPELYEIMDNGITIPKXALVLSAESSMGKLTIVQNDY 247
QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188
DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306
QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248
DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366
QY 249 IYPATGKPNQW 261
DB 367 IWPYTKRPNQW 379

RESULT 14

QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188

DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306

QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248

DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366

QY 249 IYPATGKPNQW 261

DB 367 IWPYTKRPNQW 379

QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188

DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306

QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248

DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366

QY 249 IYPATGKPNQW 261

DB 367 IWPYTKRPNQW 379

QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188

DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306

QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248

DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366

QY 249 IYPATGKPNQW 261

DB 367 IWPYTKRPNQW 379

QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188

DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306

QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248

DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366

QY 249 IYPATGKPNQW 261

DB 367 IWPYTKRPNQW 379

QY 129 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 188

DB 248 GQGLAAGNDTAPFEVITYGFRDLCSNKGSVWETCKSSQXKXWALYGTGSIFR 306

QY 189 QPQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 248

DB 307 TNNCTLSMDHKGSTIVLWCTSNMAGSQRWVFSDGSYSLVDPMVWYKSDPBL 366

QY 64 CLTYGYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 123
DB 348 CLTYGYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 407
QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183
DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466
QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243
DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526
QY 244 LKQIILPBYGNANQW 260
DB 527 LKQIILPBYGNANQW 543

RESULT 15

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

QY 244 LKQIILPBYGNANQW 260

DB 527 LKQIILPBYGNANQW 543

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

QY 244 LKQIILPBYGNANQW 260

DB 527 LKQIILPBYGNANQW 543

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

QY 244 LKQIILPBYGNANQW 260

DB 527 LKQIILPBYGNANQW 543

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

QY 244 LKQIILPBYGNANQW 260

DB 527 LKQIILPBYGNANQW 543

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

QY 244 LKQIILPBYGNANQW 260

DB 527 LKQIILPBYGNANQW 543

QY 124 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 183

DB 408 LDVYTAGVYVWIEDCNFAVEKTIYQIKXNGITIPRSNVLAASSGKGTITVOT 466

QY 184 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 243

DB 467 RPNQNDQCTKXGSDSVYINISGSDCSXKXQVFTFNKXALIKKXKXKXVQANFTLR 526

Thu Dec 11 16:09:51 2003

us-09-601-667c-3.rsp

Qy 240 ANPKLRRIIYPATKPCPCW 260
Db 549 SDPSLOOIIINSTTANPCW 569

Search completed: December 11, 2003, 14:00:59
Job time : 21.3487 secs

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.1263

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18, Search time 26.0864 Seconds

1606.345 Million cell updates/sec

Title: US-09-601-667C-3

Perfect score: 1327

Sequence: 1 DVTGSAEPTVRIVERXKM.....RRIITPATKQNMPLPVX 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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24: /SIDSI/gcgdata/geneseq/emb1/AA2003.DAT*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1291	97.3	264	AAV2597	Mistletoe lectin B
2	1291	97.3	264	AAV2598	Mistletoe lectin B
3	1291	97.3	264	AAV2599	Mistletoe lectin B
4	1291	97.3	264	AAV2597	Mistletoe lectin B
5	1290	97.2	264	AAV2598	Mistletoe lectin B
6	1290	97.2	264	AAV2599	Mistletoe lectin B
7	1290	97.2	264	AAV2597	Mistletoe lectin B
8	1290	97.2	264	AAV2598	Mistletoe lectin B
9	1289	97.1	264	AAV2599	Mistletoe lectin B

10	1289	97.1	265	20	AAV25995	Mistletoe lectin B
11	1286	96.9	264	20	AAV25978	Mistletoe lectin B
12	1286	96.9	264	20	AAV25972	Mistletoe lectin B
13	1286	96.9	264	20	AAV25975	Mistletoe lectin B
14	1286	96.9	533	20	AAV25970	Mistletoe lectin P
15	1286	96.9	533	20	AAV25973	Mistletoe lectin P
16	1286	96.9	533	20	AAV25976	Mistletoe lectin P
17	1277.5	96.3	532	20	AAV25981	Mistletoe lectin B
18	1277.5	96.3	531	20	AAV25979	Mistletoe lectin B
19	1277.5	96.3	532	20	AAV25982	Mistletoe lectin I
20	1277.5	96.3	532	20	AAV25983	Mistletoe lectin I
21	1267.5	95.5	263	19	AAW64662	Prepro mistletoe I
22	1267.5	95.5	264	18	AAW10023	Mistletoe ML B-cha
23	1267.5	95.5	264	20	AAW90126	Mistletoe ML B-cha
24	1267.5	95.5	267	19	AAW64660	Mistletoe rmb pro
25	1267.5	95.5	564	18	AAW10021	Prepro mistletoe I
26	1267.5	95.5	564	20	AAW90127	Mistletoe lectin P
27	1183.5	89.9	267	19	AAW64667	Mistletoe rmb pro
28	1080.5	79.9	263	19	AAW64668	Mistletoe rmb pro
29	1061.5	77.9	263	19	AAW64669	Mistletoe rmb pro
30	1061.5	77.9	263	19	AAW64670	Mistletoe rmb pro
31	949	71.5	266	22	AAW47093	Galactose-recognition
32	851.5	64.2	565	6	AAW50166	Sequence of prepro
33	851.5	64.2	565	22	AAW67890	Castor bean prepro
34	849.5	64.0	574	8	AAW70325	Modified castor bean
35	849.5	64.0	574	10	AAW94793	Sequence of ricin
36	849.5	64.0	576	18	AAW25977	DNA sequence of r1
37	849.5	64.0	576	20	AAW58592	Castor bean ricin
38	849.5	64.0	576	21	AAW58593	Ricinus communis
39	849.5	64.0	576	21	AAW58594	Ricinus communis
40	849.5	64.0	576	22	AAW58595	Castor bean prepro
41	849.5	64.0	576	22	AAW58596	Prepro ricin
42	844.5	63.6	565	7	AAW60220	Ricinus communis
43	840.5	63.6	262	10	AAW90020	Ric B chain of ricin D
44	840.5	63.6	262	10	AAW90020	Ric B chain of ricin D
45	833.5	62.8	576	8	AAW70326	Sequence of Ricin

ALIGNMENTS

AAV2597
AAV25987 standard; Protein: 264 AA.

AAV25987;
18-OCT-1999 (first entry)

Mistletoe lectin B2 protein fragment.

Mistletoe lectin; actinonin; immunostimulant; A-chain; MHA; immunity;

lymphocyte 28S subunit; non-cytotoxic; T-cell activation; immune response;

lymphocyte-producing macrophage; uncontrolled cell growth; treatment;

caner; cytotoxicity; antigen; isotom; lectin B2.

Vaccum album.

DE19804210-A1.

03-FEB-1999; 96DB-1004210.

03-FEB-1999; 96DB-1004210.

(BIOG-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelker W, Wolters P;

WPI: 1999-44535/38.

N-PDB; AA209111.

PT Preparation of mistletoe lectins in heterologous systems,
PT particularly for use as anticancer agents and immunostimulants
XX
XX
XX Claim 9; Fig 9b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Mistletoe lectins (I) and its fragments are used to treat
CC lymphokine-producing macrophages, so stimulate immunity (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly of the
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B2 protein.
XX
XX Sequence 264 AA:
SQ
Query Match 97.3%; Score 1291; DB 20; Length 264;
Best Local Similarity 92.4%; Pred. No. 2,5e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTGSAEPTVRIYVGRKXKVDVDDDFHGNQIOLAFSKSNDPQOLATIRKDTIRS 60
DB 1 DDTGSAEPTVRIYVGRKXKVDVDDDFHGNQIOLAFSKSNDPQOLATIRKDTIRS 60
QY 61 NSCLTGYTAGVYVWIFPCNTAVREATTIWMXNGTINPRSNVLAASSGIGKTTLT 120
DB 61 NSCLTGYTAGVYVWIFPCNTAVREATTIWMXNGTINPRSNVLAASSGIGKTTLT 120
QY 121 VQTLDTLGGWLAAGNDTAPREVITVGFRLCHESNYSVWVETCSQXQXWALYSD 180
DB 121 VQTLDTLGGWLAAGNDTAPREVITVGFRLCHESNYSVWVETCSQXQXWALYSD 180
QY 181 GSIRKQNDQCLTVGRDSVSTVINIVSCSXXSGQVFTFEXAIIINLXXXXDVAAQ 240
DB 181 GSIRKQNDQCLTVGRDSVSTVINIVSCSXXSGQVFTFEXAIIINLXXXXDVAAQ 240
QY 241 NPKLRITIIYPATGKPNOMLFPV 263
DB 241 NPKLRITIIYPATGKPNOMLFPV 263
RESULT 2
AAZ5988
ID AAZ5988 standard; Protein: 264 AA.
XX
XX AAZ5988:
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B3.
XX
XX Viscum album.
XX
XX DE1904210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOG-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P, Sciefel T, Voelter W, Welters P;
XX
XX WPI; 1999-44535/38.
DR N-PEDB; AA209112.
XX
XX Preparation of mistletoe lectins in heterologous systems,
PT particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 10b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Mistletoe lectins (I) and its fragments are used to treat
CC lymphokine-producing macrophages, so stimulate immunity (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly of the
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B3 protein.
XX
XX Sequence 264 AA:
SQ
Query Match 97.3%; Score 1291; DB 20; Length 264;
Best Local Similarity 92.4%; Pred. No. 2,5e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTGSAEPTVRIYVGRKXKVDVDDDFHGNQIOLAFSKSNDPQOLATIRKDTIRS 60
DB 1 DDTGSAEPTVRIYVGRKXKVDVDDDFHGNQIOLAFSKSNDPQOLATIRKDTIRS 60
QY 61 NSCLTGYTAGVYVWIFPCNTAVREATTIWMXNGTINPRSNVLAASSGIGKTTLT 120
DB 61 NSCLTGYTAGVYVWIFPCNTAVREATTIWMXNGTINPRSNVLAASSGIGKTTLT 120
QY 121 VQTLDTLGGWLAAGNDTAPREVITVGFRLCHESNYSVWVETCSQXQXWALYSD 180
DB 121 VQTLDTLGGWLAAGNDTAPREVITVGFRLCHESNYSVWVETCSQXQXWALYSD 180
QY 181 GSIRKQNDQCLTVGRDSVSTVINIVSCSXXSGQVFTFEXAIIINLXXXXDVAAQ 240
DB 181 GSIRKQNDQCLTVGRDSVSTVINIVSCSXXSGQVFTFEXAIIINLXXXXDVAAQ 240
QY 241 NPKLRITIIYPATGKPNOMLFPV 263
DB 241 NPKLRITIIYPATGKPNOMLFPV 263
RESULT 3
AAZ5994
ID AAZ5994 standard; Protein: 265 AA.
XX
XX AAZ5994:
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 variant protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B3.
XX
XX Viscum album.
XX
XX DE1904210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX
 XX
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209118.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 16B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B3 protein.
 XX
 XX Sequence 265 AA;
 XX
 XX Query Match 97.3%; Score 1291; DB 20; Length 265;
 XX Best Local Similarity 92.4%; Pred. No. 2.5e-136;
 XX Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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 XX 1 DDVTCASAPETVAIVGKXKVVQEDDFHDSQICQLMPSKSNNDPQQLMTIKEDXTIRS 60
 XX 1 DDVTCASAPETVAIVGKXKVVQEDDFHDSQICQLMPSKSNNDPQQLMTIKEDXTIRS 60
 XX 61 NSGCLTGYTAGVYWMFDCNTAVRATIQIWDGIIINPASNVLAAASGIKETILT 120
 XX 61 NSGCLTGYTAGVYWMFDCNTAVRATIQIWDGIIINPASNVLAAASGIKETILT 120
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 XX 121 VQILDYLLGQGLAGNDTAPREVITYGFDLCQESNKSQVWETCSXQXKXWALYGD 180
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCSXXKXQVWFFNEKALINLXXXXXADVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCSXXKXQVWFFNEKALINLXXXXXADVQA 240
 XX 241 NPKLRRIITYPATCKNQWMLPV 263
 XX 241 NPKLRRIITYPATCKNQWMLPV 263
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 XX RESULT 4
 XX AA25993
 XX ID AA25993 standard; Protein; 265 AA.
 XX
 XX AA25993;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B2 variant protein fragment.
 XX
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B2.
 XX
 XX Viscum album.

XX DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209117.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 15B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B2 protein.
 XX
 XX Sequence 265 AA;
 XX
 XX Query Match 97.3%; Score 1291; DB 20; Length 265;
 XX Best Local Similarity 92.4%; Pred. No. 2.5e-136;
 XX Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 XX
 XX 1 DDVTCASAPETVAIVGKXKVVQEDDFHDSQICQLMPSKSNNDPQQLMTIKEDXTIRS 60
 XX 1 DDVTCASAPETVAIVGKXKVVQEDDFHDSQICQLMPSKSNNDPQQLMTIKEDXTIRS 60
 XX 61 NSGCLTGYTAGVYWMFDCNTAVRATIQIWDGIIINPASNVLAAASGIKETILT 120
 XX 61 NSGCLTGYTAGVYWMFDCNTAVRATIQIWDGIIINPASNVLAAASGIKETILT 120
 XX 121 VQILDYLLGQGLAGNDTAPREVITYGFDLCQESNKSQVWETCSXQXKXWALYGD 180
 XX 121 VQILDYLLGQGLAGNDTAPREVITYGFDLCQESNKSQVWETCSXQXKXWALYGD 180
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCSXXKXQVWFFNEKALINLXXXXXADVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCSXXKXQVWFFNEKALINLXXXXXADVQA 240
 XX 241 NPKLRRIITYPATCKNQWMLPV 263
 XX 241 NPKLRRIITYPATCKNQWMLPV 263
 XX
 XX RESULT 5
 XX AA25986
 XX ID AA25986 standard; Protein; 264 AA.
 XX
 XX AA25986;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B1 protein fragment.
 XX
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.
XX Viscum album.
XX DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welbers P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209110.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 8B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MMA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen production of
XX the same type. The method of the invention allows the production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B1 protein.
SQ Sequence 264 AA;
Query Match 97.2%; Score 1290; DB 20; Length 264;
Best Local Similarity 92.4%; Pred. No. 3.2e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTYCSASEPTVRIYGRXKGVVDDDFPDNDQIQMPSSNNNDPQGLTTIKEDYTIIS 60
DB 1 DDTYCSASEPTVRIYGRXKGVVDDDFPDNDQIQMPSSNNNDPQGLTTIKEDYTIIS 60
QY 61 NSGCLTGYTGAGYVWIFPCNTAVREATTIWIQINXGIIINPNSNVLVLAASGIGKTLT 120
DB 61 NSGCLTGYTGAGYVWIFPCNTAVREATTIWIQINXGIIINPNSNVLVLAASGIGKTLT 120
QY 121 VQTLDTLGGQMLAGNDTAFREYTIYGRDLQMSNXSVVETCKSSGXKXWALYGD 180
DB 121 VQTLDTLGGQMLAGNDTAFREYTIYGRDLQMSNXSVVETCKSSGXKXWALYGD 180
QY 181 GSIRPKNOQDCLTSGDVSFTVINIVSCGASGSGRWFTBQALINLKGGLADVAQA 240
DB 181 GSIRPKNOQDCLTSGDVSFTVINIVSCGASGSGRWFTBQALINLKGGLADVAQA 240
QY 241 NPKLRITIIYPATGKQWMLPV 263
DB 241 NPKLRITIIYPATGKQWMLPV 263
RESULT 5
ID AAY25590
XX AAY25990;
XX 18-OCT-1999 (first entry)

XX Mistletoe lectin B5 protein fragment.
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MMA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX Viscum album.
XX DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welbers P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209114.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 12B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MMA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B5 protein.
SQ Sequence 264 AA;
Query Match 97.2%; Score 1290; DB 20; Length 264;
Best Local Similarity 92.4%; Pred. No. 3.2e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTYCSASEPTVRIYGRXKGVVDDDFPDNDQIQMPSSNNNDPQGLTTIKEDYTIIS 60
DB 1 DDTYCSASEPTVRIYGRXKGVVDDDFPDNDQIQMPSSNNNDPQGLTTIKEDYTIIS 60
QY 61 NSGCLTGYTGAGYVWIFPCNTAVREATTIWIQINXGIIINPNSNVLVLAASGIGKTLT 120
DB 61 NSGCLTGYTGAGYVWIFPCNTAVREATTIWIQINXGIIINPNSNVLVLAASGIGKTLT 120
QY 121 VQTLDTLGGQMLAGNDTAFREYTIYGRDLQMSNXSVVETCKSSGXKXWALYGD 180
DB 121 VQTLDTLGGQMLAGNDTAFREYTIYGRDLQMSNXSVVETCKSSGXKXWALYGD 180
QY 181 GSIRPKNOQDCLTSGDVSFTVINIVSCGASGSGRWFTBQALINLKGGLADVAQA 240
DB 181 GSIRPKNOQDCLTSGDVSFTVINIVSCGASGSGRWFTBQALINLKGGLADVAQA 240
QY 241 NPKLRITIIYPATGKQWMLPV 263
DB 241 NPKLRITIIYPATGKQWMLPV 263
RESULT 7
ID AAY25996

ID AAY25996 standard; Protein; 265 AA.
AC AAY25996;
DN 18-OCT-1999 (first entry)
XX Mistletoe lectin B5 variant protein fragment.
DE Mistletoe lectin B5 variant protein fragment.
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KM ribozyme 265 subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KM cancer; cytotoxicity; antigen; isoform; lectin B5.
XX Viscum album.
CS DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-44535/38.
XX N-PSDB; AAZ09120.
XX Preparation of mistletoe lectins in heterologous systems.
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 18B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MA)
XX of the mistletoe lectin binds to, and inactivates, the 26S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
SQ Sequence 265 AA;
Query Match 97.2%; Score 1290; DB 20; Length 265;
Best Local Similarity 92.4%; Pval: No. 3,2e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTVCASSEPTVRIYGRKXKXVDVDDPDHGNQICLPFSKSNDDPNQMTIKKXTGIS 60
DB 1 DDTVCASSEPTVRIYGRKXKXVDVDDPDHGNQICLPFSKSNDDPNQMTIKKXTGIS 60
QY 61 NSGCLTYGTAGYVNIIPDCNVAVERATIMQINXGTTINPNSNVLAASSGKGTIT 120
DB 61 NSGCLTYGTAGYVNIIPDCNVAVERATIMQINXGTTINPNSNVLAASSGKGTIT 120
QY 121 VQILDYTLGQWLANQDPAARETITIGFRDLCHSNKSGSWWETLDSQKGMALYSD 180
DB 121 VQILDYTLGQWLANQDPAARETITIGFRDLCHSNKSGSWWETLDSQKGMALYSD 180
QY 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXAILNLKXXXXXVQA 240
DB 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXAILNLKXXXXXVQA 240
QY 241 NPKLRITITTPATKRNQWMLPV 263
DB 241 NPKLRITITTPATKRNQWMLPV 263

DB 241 NPKLRITITTPATKRNQWMLPV 263
RESULT 8
ID AAY25992 standard; Protein; 265 AA.
AC AAY25992;
DN 18-OCT-1999 (first entry)
XX Mistletoe lectin B1 variant protein fragment.
DE Mistletoe lectin B1 variant protein fragment.
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KM ribozyme 265 subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KM cancer; cytotoxicity; antigen; isoform; lectin B1.
XX Viscum album.
CS DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-44535/38.
XX N-PSDB; AAZ09116.
XX Preparation of mistletoe lectins in heterologous systems.
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 14B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MA)
XX of the mistletoe lectin binds to, and inactivates, the 26S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B1 protein.
SQ Sequence 265 AA;
Query Match 97.2%; Score 1290; DB 20; Length 265;
Best Local Similarity 92.4%; Pval: No. 3,2e-136;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 DDTVCASSEPTVRIYGRKXKXVDVDDPDHGNQICLPFSKSNDDPNQMTIKKXTGIS 60
DB 1 DDTVCASSEPTVRIYGRKXKXVDVDDPDHGNQICLPFSKSNDDPNQMTIKKXTGIS 60
QY 61 NSGCLTYGTAGYVNIIPDCNVAVERATIMQINXGTTINPNSNVLAASSGKGTIT 120
DB 61 NSGCLTYGTAGYVNIIPDCNVAVERATIMQINXGTTINPNSNVLAASSGKGTIT 120
QY 121 VQILDYTLGQWLANQDPAARETITIGFRDLCHSNKSGSWWETLDSQKGMALYSD 180
DB 121 VQILDYTLGQWLANQDPAARETITIGFRDLCHSNKSGSWWETLDSQKGMALYSD 180
QY 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXAILNLKXXXXXVQA 240
DB 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXAILNLKXXXXXVQA 240

Db 181 GSIRKXNDQCLTSGRDSVSTVINIVSCSGSGSRMVFTEGAILNLKQPLAMDVQA 240
QY 241 NPKLRRIIYPATKRNQWMLPV 263
Db 241 NPKLRRIIYPATKRNQWMLPV 263

RESULT 9

AAV25989 standard; Protein; 264 AA.

AAV25989;

18-OCT-1999 (first entry)

Mistletoe lectin B4 protein fragment.

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; ribosome 268 subunit; non-cytotoxic; T-cell activation; immune response; lymphokine-producing macrophages; uncontrolled cell growth; treatment; cancer; cytotoxicity; antigen; isoform; lectin B4.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA209113.

Preparation of mistletoe lectins in heterologous systems,

particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 11B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments which have antitumor and immunostimulatory activity. The A-chain (MIA) of the mistletoe lectin binds to, and inactivates, the 268 subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly of cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to a co-administered antigen (tumour-associated, bacterial or viral). The method allows production of mistletoe lectins and their fragments in many different isoforms and on a large scale at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a mistletoe lectin B4 protein.

Sequence 264 AA;

Query Match 97.1%; Score 1289; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 4,26-136; Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTTCASAPPTVIRIVGKXKVDPPDDPHDQDGLAPSKSNDPQNLWTIKEDTIS 60
Db 1 DDTTCASAPPTVIRIVGKXKVDPPDDPHDQDGLAPSKSNDPQNLWTIKEDTIS 60
QY 61 NSCLTIVGYAGYVWIPCNLTVKRACTIWMKNGTINPNSNLVLAASGIGTIT 120
Db 61 NSCLTIVGYAGYVWIPCNLTVKRACTIWMKNGTINPNSNLVLAASGIGTIT 120

QY 121 VQTLDTLGGGWLGNDRAPREVITYGRFLCMESNKSXSWVETCKSGKQXWALYCD 180
Db 121 VQTLDTLGGGWLGNDRAPREVITYGRFLCMESNKSXSWVETCKSGKQXWALYCD 180
QY 181 GSIRKXNDQCLTSGRDSVSTVINIVSCSGSGSRMVFTEGAILNLKQPLAMDVQA 240
Db 181 GSIRKXNDQCLTSGRDSVSTVINIVSCSGSGSRMVFTEGAILNLKQPLAMDVQA 240
QY 241 NPKLRRIIYPATKRNQWMLPV 263
Db 241 NPKLRRIIYPATKRNQWMLPV 263

RESULT 10

AAV25995 standard; Protein; 265 AA.

AAV25995;

18-OCT-1999 (first entry)

Mistletoe lectin B4 variant protein fragment.

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; ribosome 268 subunit; non-cytotoxic; T-cell activation; immune response; lymphokine-producing macrophages; uncontrolled cell growth; treatment; cancer; cytotoxicity; antigen; isoform; lectin B4.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA209119.

Preparation of mistletoe lectins in heterologous systems,

particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 17B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments which have antitumor and immunostimulatory activity. The A-chain (MIA) of the mistletoe lectin binds to, and inactivates, the 268 subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly of cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to a co-administered antigen (tumour-associated, bacterial or viral). The method allows production of mistletoe lectins and their fragments in many different isoforms and on a large scale, at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a variant mistletoe lectin B4 protein.

Sequence 265 AA;

Query Match 97.1%; Score 1289; DB 20; Length 265;

Best Local Similarity 92.4%; Pred. No. 4,26-136; Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTTCASAPPTVIRIVGKXKVDPPDDPHDQDGLAPSKSNDPQNLWTIKEDTIS 60
Db 1 DDTTCASAPPTVIRIVGKXKVDPPDDPHDQDGLAPSKSNDPQNLWTIKEDTIS 60

DT 18-OCT-1999 (first entry)
 XX Mistletoe lectin B chain MLB consensus protein sequence 1.
 DE Mistletoe lectin B chain MLB consensus protein sequence 1.
 XX Mistletoe lectin B chain MLB consensus protein sequence 1.
 KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; MLB; B-chain.
 XX Viscum album.
 OS Viscum album.
 XX Key Location/Qualifiers
 FH Misc-difference 18 /label= Asn, Ser
 FT Misc-difference 21 /label= Cys, Arg
 FT Misc-difference 56 /label= Gly, Asn
 FT Misc-difference 95 /label= Gly, Asp
 FT Misc-difference 157 /label= Gly, Gln
 FT Misc-difference 166 /label= Val, Asp
 FT Misc-difference 170 /label= Gln, Lys
 FT Misc-difference 173 /label= Gly or none
 FT Misc-difference 174 /label= Arg, Lys
 FT Misc-difference 195 /label= Cys, Ser, Val
 FT Misc-difference 212 /label= Ala, Gly
 FT Misc-difference 214 /label= Ser, Gly
 FT Misc-difference 215 /label= Gly, Ser
 FT Misc-difference 224 /label= Gly, Tyr
 FT Misc-difference 231 /label= Asn, Ser, Thr, Lys
 FT Misc-difference 232 /label= Ser, Gly
 FT Misc-difference 233 /label= Leu, Pro
 FT Misc-difference 234 /label= Ala, Met
 FT Misc-difference 235 /label= Met, Val
 FT Misc-difference 264 /label= Pro, Phe
 FT DE19804210-A1.
 XX 12-AUG-1999.
 PD 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARANEWITTEL GMBH.
 XX Morris P. Stiefel T. Voelker W. Walters P.
 XX MPI, 1999-44535/38.
 DR Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Claim 3, Page 28; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLB)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity, (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response against bacterial or viral pathogens. This method allows production of
 CC mistletoe lectin and its individual chains in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin B chain (MLB)
 XX described in the invention.
 SQ Sequence 264 AA;
 Query Match 96.9%; Score 1286; DB 20; Length 264;
 Best Local Similarity 100.0%; Pred. No. 96-116;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPTGASAPPTVIRVGRKXGVYVDDPHQNGQOLWPKSNMPQWATIKEDTIRS 60
 DB 1 DPTGASAPPTVIRVGRKXGVYVDDPHQNGQOLWPKSNMPQWATIKEDTIRS 60
 QY 61 NSGCLTYGYGTAGYVMIFCNTAVREATTQIKXNGTIIIPRSNLVLAASGKXTLT 120
 DB 61 NSGCLTYGYGTAGYVMIFCNTAVREATTQIKXNGTIIIPRSNLVLAASGKXTLT 120
 QY 121 VQTLDTYTLQGMALAGNDIARREVTYGFEDLCMESKGVVETGSCQNNXNALIGD 180
 DB 121 VQTLDTYTLQGMALAGNDIARREVTYGFEDLCMESKGVVETGSCQNNXNALIGD 180
 QY 181 GSIRKONDDCLTKRDSVSTYINIVSCSXXSXGQFVETNEKALINLKKXXVQQA 240
 DB 181 GSIRKONDDCLTKRDSVSTYINIVSCSXXSXGQFVETNEKALINLKKXXVQQA 240
 QY 241 NPLRLRIITYPATGKQNMWLPV 263
 DB 241 NPLRLRIITYPATGKQNMWLPV 263
 RESULT 13
 ID AAY25975
 AC AAY25975
 XX AAY25975;
 XX 18-OCT-1999 (first entry)
 DE Mistletoe lectin B chain MLB consensus protein sequence 2.
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; MLB; B-chain.
 XX Viscum album.
 OS Viscum album.
 XX Key Location/Qualifiers
 FH Misc-difference 18 /label= Asn, Ser
 FT Misc-difference 21 /label= Cys, Arg
 FT Misc-difference 56 /label= Gly, Asn
 FT Misc-difference 95 /label= Gly, Asp
 FT Misc-difference 157 /label= Gly, Gln
 FT Misc-difference 166 /label= Val, Asp

FT Misc-difference 170 /label= Gln, Lys
 FT Misc-difference 173 /label= Gly or none
 FT Misc-difference 174 /label= Arg, Lys
 FT Misc-difference 195 /label= Cys, Ser, Val
 FT Misc-difference 211 /label= Ala, Gly
 FT Misc-difference 212 /label= Gly, Ala
 FT Misc-difference 214 /label= Ser, Gly
 FT Misc-difference 215 /label= Gly, Ser
 FT Misc-difference 224 /label= Gly, Tyr
 FT Misc-difference 231 /label= Asn, Ser, Thr, Lys
 FT Misc-difference 232 /label= Ser, Gly
 FT Misc-difference 233 /label= Leu, Pro
 FT Misc-difference 234 /label= Ala, Met
 FT Misc-difference 235 /label= Met, Val
 FT Misc-difference 264 /label= Pro, Phe
 FT DE19804210-All.
 FT 12-AUG-1999.
 FT 03-FEB-1998; 98DE-1004210.
 FT 03-FEB-1998; 98DE-1004210.
 FT (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 FT Morris P, Stiefel T, Voelter W, Welters P;
 FT WPI; 1999-44535/38.
 FT Preparation of mistletoe lectins in heterologous systems,
 FT particularly for use as anticancer agents and immunostimulants
 FT Claim 6; Page 31; 78pp; German.
 FT This invention describes a novel mistletoe lectin (I) and its fragments
 FT which have antitumor and immunostimulant activity. The A-chain (MMA)
 FT of the mistletoe lectin binds to and activates the T-cell subset of
 FT lymphokine-producing macrophages, so stimulate immunity (I) and its
 FT fragments are used to treat uncontrolled cell growth (particularly of
 FT tumors) and if they lack cytotoxicity, to increase the strength of the
 FT immune response, particularly to a co-administered antigen
 FT (mistletoe lectin, bacterial or viral). The method allows production of
 FT mistletoe lectin, and its individual chains, in many different isoforms
 FT free of a large scale, at any time of the year. Recombinant products are
 FT free of contaminants present in natural mistletoe extracts. This sequence
 FT represents a conserved sequence of the mistletoe lectin B chain (MNB)
 FT described in the invention.
 SQ Sequence 264 AA:

Query Match 96.3%; Score 1286; DB 20; Length 264;
 Best Local Similarity 100.0%; Pred. No. 9e-136;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 DVTGASAEPTVRIVGKXKXVDVDDPHDNGQIQLPKSKSNDPVOGLMTIKEDYTIIS 60
 |||

Db 1 DVTGASAEPTVRIVGKXKXVDVDDPHDNGQIQLPKSKSNDPVOGLMTIKEDYTIIS 60
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 AC AAY25970;
 XX 18-OCT-1999 (first entry)
 DT 18-OCT-1999 (first entry)
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 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MMA; immunity;
 XX ribozyme 26S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform.
 OS Viscum album.
 XX
 FH Key Location/Qualifiers
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 FT Misc-difference 66 /label= Ile, Val
 FT Misc-difference 74 /label= Leu, Ala
 FT Misc-difference 107 /label= Asp, Arg or none
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 XX
 ED 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
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 PR 03-FEB-1998; 98DE-1004210.
 XX
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 PI Morris P. Stiefel T, Voelter W, Welters P.
 XX
 DR WPI; 1999-445335/38.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 FT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 1, Page 25-26; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of the
 CC cancers) and if they lack cytotoxicity, to increase the strength of the

CC immune response, particularly to a co-administered antigen
 CC (antitumour, antiviral or viral). The method allows production of
 CC mistletoe lectin and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX
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 Best Local Similarity 100.0%; Positives 246-115;
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 DT 18-OCT-1999 (first entry)
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 DE Mistletoe lectin protein consensus sequence 2.
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 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KM ribosome 28S subunit; macrophage; T-cell activation; immune response;
 KM lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform.
 XX
 OS Viscum album.
 XX
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 15 /label= Asp, Gln
 FT Misc-difference 63 /label= Gly, Gln
 FT Misc-difference 66 /label= Ile, Val
 FT Misc-difference 107 /label= Leu, Ala
 FT Misc-difference 107 /label= Asp, Arg, none
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XX DE19804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DB-1004210.
XX 03-FEB-1998; 98DB-1004210.
XX (BIOG-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P, Stiefel T, Voelter W, Welters P;
XX WPI: 1999-445335/38.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 4, Page 28-29; 78pp; German.
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC derived from toxins present in natural mistletoe extracts. This sequence
CC represents a consensus sequence of the mistletoe lectin described in the
XX specification.
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DB 330 NSGCTTYGTRAGVYVAFPCNTAFKATITQIKXGIIINPSNLVLAASGKIKTIT 389
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Job time : 27.0864 secs

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 17.0129 seconds
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2896.029 Million call updates/sec

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Searched: 684280 seqs, 185983659 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1267.5	95.5	267	9	US-09-347-064-4 Sequence 4, Appl 1
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4	182	11.5	440	15	US-10-156-761-14970 Sequence 5, Appl 1
5	182	11.5	440	15	US-10-156-761-14970 Sequence 9724, A
6	136.5	10.3	658	15	US-10-156-761-8170 Sequence 8170, Ap
7	136.5	10.3	658	15	US-10-156-761-8170 Sequence 8170, Ap
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12	117.5	8.9	480	9	US-09-770-621-5 Sequence 4, Appl 1
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14	117.5	8.9	480	9	US-09-770-621-5 Sequence 4, Appl 1
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17	104	7.8	41	15	US-10-137-077-18 Sequence 18, Appl 1
18	104	7.8	45	15	US-10-137-077-19 Sequence 19, Appl 1
19	98	7.4	41	15	US-10-137-077-20 Sequence 20, Appl 1
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21	81	6.1	278	15	US-10-128-714-3037 Sequence 3037, Ap
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24	78	5.9	1781	14	US-10-092-751-25 Sequence 25, Appl 1
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44	70.5	5.3	696	15	US-10-128-714-3506 Sequence 3506, Ap
45	70.5	5.3	696	15	US-10-128-714-3506 Sequence 8506, Ap

ALIGNMENTS

US-09-347-064-10	Sequence 10, Application US/09347064A
1	Patent No. US20020045208A1
2	GENERAL INFORMATION:
3	APPLICANT: Eck, Jurgen
4	APPLICANT: Schmidt, Arno
5	APPLICANT: Schmidt, Arno
6	TITLE OF INVENTION: Ribonuclease Inhibiting Proteins of the m1stlesee Virus
7	TITLE OF INVENTION: Ribonuclease Inhibiting Proteins of the m1stlesee Virus
8	FILE REFERENCE: 09282-5
9	CURRENT APPLICATION NUMBER: US/09/347, 064A
10	EARLIER FILING DATE: 1999-07-02
11	EARLIER APPLICATION NUMBER: PCT/EP99/00009
12	EARLIER FILING DATE: 1998-01-02
13	EARLIER APPLICATION NUMBER: EP 97 10 0012.0
14	EARLIER FILING DATE: 1997-01-02
15	EARLIER APPLICATION NUMBER: EP 97 10 0012.0
16	INVENTOR: Schmidt, Arno
17	INVENTOR: Schmidt, Arno
18	INVENTOR: Schmidt, Arno
19	SOFTWARE: Present in ver. 2.1
20	SEQ ID NO 10
21	LENGTH: 263
22	TYPE: PRP
23	ORGANISM: Virus album
24	US-09-347-064-10
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Page 2

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RESULT 2
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Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
INVENTOR: Schmidt, Irwin J.
APPLICANT: Schmidt, Irwin J.
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EXAMINER APPLICATION NUMBER: PCT/EP98/00009
EXAMINER FILING DATE: 1998-01-02
EXAMINER APPLICATION NUMBER: 1998-01-02
EXAMINER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Vascum album
US-09-347-064-4

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Qy 241 NPKLRRIITYPATGKPNQWMLPV 263
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RESULT 3
US-10-083-336A-1
Sequence 1, Application US/1008336A
Patent No. US2003018665A1
GENERAL INFORMATION:
INVENTOR: Olson, Mark A.
APPLICANT: Mallard, Charles B.
APPLICANT: Byrne, Michael P.
APPLICANT: Wannenmacher, Robert W.

TITLE OF INVENTION: Racin Vaccines and Methods of Making and Using Thereof
FILE REFERENCE: 01-58
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 576
TYPE: PRT
ORGANISM: Rictinus communis
US-10-083-336A-1

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Qy 185 PKONODCLTXGRDSVTVIVISCSXXSXCRVFTNEXALINTKXXXXXVQAQNPFL 244
Db 185 PKONODCLTXGRDSVTVIVISCSXXSXCRVFTNEXALINTKXXXXXVQAQNPFL 244
Qy 497 PQGNNDNLTSDSIHRETVVILISGPASSQGRVFPNDGTLINTLSGLVLDVAPSPFL 556
Db 497 PQGNNDNLTSDSIHRETVVILISGPASSQGRVFPNDGTLINTLSGLVLDVAPSPFL 556
Qy 245 RRIITYPATGKPNQWMLPV 263
Db 557 RRIITYPATGKPNQWMLPV 263

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Patent No. US20030092109A1
GENERAL INFORMATION:
INVENTOR: Goldstein, Irwin J.
APPLICANT: Goldstein, Irwin J.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom L
FILE REFERENCE: 07-13
CURRENT APPLICATION NUMBER: US/10/137,077
EXAMINER APPLICATION NUMBER: 2002-05-02
EXAMINER FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/254,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Xizicinus communis
US-10-137-077-17

Query Match 13.6%; Score 180; DB 15; Length 44;
Best Local Similarity 75.0%; Pred. No. 5,4e-13;
Matches 33; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 12 VAIYGRKGVYVADDDDFHGNQIQLPKSKNDPQQLTKRDTIRANSKC 55
Db 1 VAIYGRKGVYVADDDDFHGNQIQLPKSKNDPQQLTKRDTIRANSKC 44

RESULT 5
US-10-074-527-5
Sequence 5, Application US/10074527

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Publication No. US2002014426A1
GENERAL INFORMATION:
APPLICANT: Olandt, Peter J.
APPLICANT: Meyers, Rachel B.
APPLICANT: Galvin, Katherine A.
APPLICANT: Nidhiyasingh, Ramanathan
TITLE OF INVENTION: Uses of Glycosyltransferase and
FILE NUMBER: MP001-018PRCPLM)
CURRENT APPLICATION NUMBER: US/10/074,527
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/269202
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NOS:
LENGTH: 145
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-5

Query Match	12.2%;	Score 162;	DB 14;	Length 145;
Best Local Similarity	32.13%;	Pred. No. 2-8e-10;		
Matches	44;	Conservative 18;	Mismatches 61;	Indels 14;
				Gaps 4;
QY	11	TVRIIVKXGKATVDYRDDDFHDPGNQIQLMPKSKNNDFNQIWTI--KEDQTIIS--NSGC	64	
Db	7	LTIVGIVGKATVDYRDDDFHDPGNQIQLMPKSKNNDFNQIWTI--KEDQTIIS--NSGC	66	
QY	65	LTIVGIVGATGVYMLFPCQVITRATVQIIMKNGIIN-----RSVLTI--AASGKIG	116	
Db	67	LIVNANSPGSEKLYIQCSASNDQNGKELANDGILGNKILIMLVNIVQIVLVKDSITQNG	126	
QY	117	TVLEPOTLIDYLTAGGWL	133	
Db	127	TVLIVYCSGSGRNQWL	143	

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US-10-156-761-14970
? Sequence 14970, Application us/10156761
? Publication No. US20030110018A1
? GENERAL INFORMATION:
?   APPLICANT: OHSKI, SAROSHI
?   APPLICANT: OHSKI, SAROSHI
?   APPLICANT: ISHIKAWA, JUN
?   APPLICANT: ISHIKAWA, JUN
?   APPLICANT: HORIKAWA, HIROSHI
?   APPLICANT: SHIBA, TADAYOSHI
?   APPLICANT: SAKAKI, YOSHIYUKI
?   APPLICANT: HATTORI, WAKAHARA
?   FILING INVENTOR: NOVOI POLYNUCLEOTIDES
?   FILING INVENTOR: NOVOI POLYNUCLEOTIDES
?   CURRENT APPLICATION NUMBER: US/10/156,761
?   CURRENT FILING DATE: 2002-05-23
?   PRIOR APPLICATION NUMBER: JP 2001-204089
?   PRIOR FILING DATE: 2001-05-30
?   PRIOR APPLICATION NUMBER: JP 2001-272697
?   PRIOR FILING DATE: 2001-08-02
?   NUMBER: US2003 ID NOS: 15105
?   SEQ ID NO 14970
?   LENGTH: 420
?   TYPE: PRT
?   ORGANISM: Streptomyces avermitilis
?   US-10-156-761-14970

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Query Match      11.5%   Score 153   DB 15:
Best Local Similarity 30.5%   P-idx. No. 1,2=68
Matches      43,   Conservative      19,   Mismatches 69,   Indels      10,   Gaps      5

CY      1 DD--VTCGSAEPTIVRKKXVVYVDDDFDNDGIDQMPKSKNDNPQNLTKIKDQDTI 58

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Db 284 DDKVTKTQSSSGGAPATLAKCVIVAGSSSSNANAPVLY--CNGQTQAQKWTVASPGL 341
Cy 59 RSNESCL--TGYTATGYVWVTPDCNRARENTIWIQNTGIIIFRSN--VYLAAISOI 114
Db 342 RALRGKCLDPTETNGVAGSFT--WYTPADIDVFNPKNCIDLTQTSNRA 359
Cy 115 KGTLLTVAQIDLTQSGMID 135
Db 400 NGRILQIWSGSGAANRKNKG 420

RESULT 7
US-10-156-761-9724
; Sequence 9724, Application US/10156761
; Publication No. US20030119018A1
; SERIAL INFORMATION:
; APPLICANT: OHTSU, SAPOSHI
; APPLICANT: IYEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, YASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9724
; SEQ ID NO 9724

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01 ORGANISM: Streptomyces avermitilis
02 US-10-156-761-9724
03
04 Query Match      10 38; Score 136.5; D2 15; Length 658;
05 Best Local Similarity 31.48; Pired. No 1,156-06;
06 Matches 38; Conservative 17, Mismatches 57, Indels 9; Gaps 5
07
08 17 RKNQVAVRDDPFNDNQIQWMSKSNDFDPLWT-IKEDTITRSNGCLTLY-GTNG 73
09
10 Db 539 QSRQCALPYNNTTSTQELW-DQNGNSQWVYTSRKEVLVGNKCLDAVNLGTNG 596
11
12 QY 74 YVFFICGNTANREATINQIKNGGTTINRPSNLVLA--SSGKGTITVYQCLDYLTSOG 131
13
14 Db 597 TKVIMDGNQGNK--WNISGGLTNVNAQLCLAVYAAFRNISTSLVWACGCRGNK 654
15
16 QY 132 W 132
17
18 Db 655 W 655

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RESULT 8
US-10-156-761-8170
/ Sequence 8170, Application US/10156761
/ Publication No. US20030115018A1
/ GERMAN INFORMATION: SATOSHI
/ APPLICANT: OMEKA, HARUO
/ APPLICANT: IKEDA, SATOSHI
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ CURRENT APPLICATION NUMBER: US/10156, 761
/ CURRENT FILING DATE: 2002-05-28
/ PRIORITY APPLICATION NUMBER: JP 2001-204089
/ PRIORITY FILING DATE: 2001-05-30

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/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SHOT ID NO: 973
/ LENGTH: 536
/ TYPE: PRF
/ ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
  Score 121.5; DB 15; Length 536;
  Best Local Similarity 29.0%; Pred. No. 5.8e-05;
  Matches 36; Conservative 16; Mismatches 57; Indels 15; Gaps 5;

QY 22 VVVRDDPHGNCQIQMPKSNNDPQMLTIKXDTIRNSG--SCUTTY--GYTGYVM 77
DB 418 IDAVDQTPAKTKIEIWDG---GGMQAVITITAGSRLKXGTCCLADYNGTISGKTQ 474
QY 78 IPDCNFAVEKTIWQKXGTTIRNSNLYV-----ASSGKIKTITVQTLDTYTCOG 131
DB 475 LYTCNGANOK--WSINPQIVTQSGICLDTGSDQSGVAVGTALEMTONGANQO 532
QY 132 WLAG 135
DB 533 WLAG 536

RESULT 9
US-09-973-457-5
/ Sequence 5, Application US/09973457
/ Patent No. US20020164746A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapeller-Libermann, Rosana
/ TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
/ FILE REFERENCE: 1046-03-001
/ CURRENT FILING DATE: 2001-10-09
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/238,849
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 135
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
  Score 119.5; DB 10; Length 135;
  Best Local Similarity 29.1%; Pred. No. 1.6e-05;
  Matches 41; Conservative 18; Mismatches 61; Indels 21; Gaps 8;

QY 14 IYKXGKXVDY--RDDEPHGNCQIQMPKSNNDPQMLTI---KRXDTIRNSG--CLTT 67
DB 7 IGANTGCLDVNGSSSKSDNPVQMDCHGQ--NQMLGTYNESGALRINSDELCTIV 64
QY 68 YGTAGYVMIPDCNFAVE--EATIQWKNXGTTIRNSNLYVLAASSGKIKTITVQTL 125
DB 65 NG-----TTLVSCDGTGKXNDQKQWVXKGTIRNPK--NSKGYVDSG-----LCIDVND 113
QY 126 YTLGGQWLAGNDTAPREVTIY 146
DB 114 GKRYQWLTGCSGSDAPQKWIIF 134

RESULT 10
US-10-074-527-6
/ Sequence 6, Application US/10074527
/ Patent No. US2002014446A1
/ GENERAL INFORMATION:
/ APPLICANT: Olandt, Peter J.
/ APPLICANT: Meyers, Rachel E.

QY 9 EPTVRIYKXGKXVDYRDDEPHGNCQIQMPKSNNDPQMLTIKXDTIRNSGCL--T 66
DB 520 QGTGVSQVLAAGKCLDVNGSSSKSDNPVQMDCHGQ--DCKSGTAKRYVSDQSGALCQDPT 577
QY 67 YGTAGYVMIPDCNFAVEATITQW---XNXTIRNSN--LVLAASSGKIKTITV 120
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Db 578 SAS7DARAKIQUJONCH-----GTAAGRSYNSINSTSDVWVTLAAKCLDVTGNSSANGRRAPQ 632Z

Qy 121 VQTLDYVTLQGM 132

Db 633 TMSCTGANNCH 644

RESULT 12
 US-09-770-621-5
 Sequence 5, Application US/09770621
 Patent No. US20010024815A1
 GENERAL INFORMATION:
 APPLICANT: M. de la, Arja
 APPLICANT: Pemasper, Juri
 APPLICANT: Pemasper, Richard
 APPLICANT: Lapito, Rajia
 APPLICANT: Pabolino, Maria
 APPLICANT: Summen, Patrick
 APPLICANT: Lantinen, Taina
 TITLE OF INVENTION: Production and Secretion of Proteins of
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESS: STEIN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.,
 STREET: 1100 New York Ave., N.W. Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770,621
 FILING DATE:
 PRIORITY INFORMATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/590,563
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/392,412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/282,001
 FILING DATE: 29-JUL-1994
 PRIORITY INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050 0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 480 amino acids
 STRAINDRUGS: amino acid
 TOPOLOGY: linear US20010024815A1 Relevant
 MOLECULE TYPE: peptide
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: AM50

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Query Match      8.9%; Score 117.5; DB 9; Length 480;
Best Local Similarity 31.4%; Pred. No. 0.00014;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3
QY 22 VYADVDHFDGNCGLVMSKSNNDNQLWTIKEDITIRKNS-CITTYGYTGYVYMFED 80
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 379 IDVPKNGKMLDTGVQLVDCSSGS - NCQWYTSASGEPRIPNKKCLDAGSSNGAVQIYS 436

Qy 81 CNAIVREALTIQIQKXGKITIPSPSYLVAASSGKTKITLVQ 122

Db 437 CMGAGNOK - MELADGTLVGVSGCLDVGAGTNGKTRIQ 476

RESULT 13
 US-09-770-621-4
 Sequence 4, Application US/09770621
 Patent No. US20010024815A1
 GENERAL INFORMATION:
 APPLICANT: N tcyi, Arja
 APPLICANT: Vessanper, Jari
 APPLICANT: Tegelstr, Richard
 APPLICANT: Pihonen, Marja
 APPLICANT: Suominen, Pirkko
 APPLICANT: Lahnenen, Taina
 TITLE OF INVENTION: Production and Secretion of Proteins of
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEEN, KESSLER, GOLDBSTEIN & FOX, P.L.L.C.
 1000 New York Ave., N.W. Suite 600
 City, Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: IBM DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770, 621
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/590, 563
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/332, 412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/282, 001
 FILING DATE: 29-OUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050_0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2640
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-770-621-4

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Query Match      8.9%; Score 11.075; DB 9; Length 492;
Best Local Similarity 31.4%; Pctid: No. 0.0015;
Matches 32; Consensitive 16; Mismatches 49; Indels 5; Gaps 3
OY 22 UPBBDQFHDNDQIQAPMSKANDNDQWITIRKDXIRISGS -CTTGYAGTGYAAYIED 80
Db 379 IDPVSQADQIQVLCVCHSSG -NQWITTSSEFRIKNDLADGSSNGAVQVLS 436
OY 81 CTAFAEATVQIKKXGIIINPSRLTALASSGKOTITLIVQ 122

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DB 437 CMGANOK--WEIRADGTTIVGVSSGLCDLVGGSTNGTRIQ 476

RESULT 14
US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M ryl, Arja
INVENTOR: M ryl, Arja
APPLICANT: Venkatesh, Jari
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
TITLE OF INVENTION: Production and secretion of proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIA TYPE: CD-ROM
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hagist, Lawrence B.
REGISTRATION NUMBER: 15,081
ADDRESS: 10000 N. 10th Ave., Suite 100
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MODIFIER TYPE: peptide
POSITION IN SEQUENCE:
CHROMOSOME/SEGMENT: AMS0
US-09-770-621-7

Query Match 8.9%; Score 117.5; DB 9; Length 492;
Best Local Similarity 31.4%; Pred. No. 0.00015;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3;
DB 22 VVRRDDDFHDSNQQLMPSKSNNDPNQLWTKRDXITRNSGS-CLTVGYTAGYVNIIFD 80
379 IDVPKNTALDGTQVQLDCHSGS--NOQWTVSSGSEFRIFANKCLDAGSSNGAVVQLIS 436
QY 81 CNTAVRATITWIKXGTTINPNSNVLAASSGIKETITLTVQ 122

DB 437 CMGANOK--WEIRADGTTIVGVSSGLCDLVGGSTNGTRIQ 476

RESULT 15
US-10-286-993-4
Sequence 4, Application US/10286993
Publication No. US2003014853A1
GENERAL INFORMATION:
APPLICANT: Venkatesh, Jari
INVENTOR: Venkatesh, Jari
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
TITLE OF INVENTION: Production and secretion of proteins in filamentous
FILE REFERENCE: 1716, 0340004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13/20,804
PRIOR APPLICATION NUMBER: US/09/120,804
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: ECT/PI97/00037
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent version 3.0
SEQ ID NO 4
LENGTH: 492
TYPE: PRT
ORGANISM: Actinobacteria flexuosa
US-10-286-993-4
Query Match 8.9%; Score 117.5; DB 12; Length 492;
Best Local Similarity 31.4%; Pred. No. 0.00015;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3;
DB 22 VVRRDDDFHDSNQQLMPSKSNNDPNQLWTKRDXITRNSGS-CLTVGYTAGYVNIIFD 80
379 IDVPKNTALDGTQVQLDCHSGS--NOQWTVSSGSEFRIFANKCLDAGSSNGAVVQLIS 436
QY 81 CNTAVRATITWIKXGTTINPNSNVLAASSGIKETITLTVQ 122
DB 437 CMGANOK--WEIRADGTTIVGVSSGLCDLVGGSTNGTRIQ 476

Search completed: December 11, 2003, 14:48:46
Job time : 17.0129 secs

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OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18; Search time 16.5067 seconds
(without alignment)

3093.817 Million cell updates/sec

Title: US-09-601-667C-4

Perfect score: 2791

Sequence: 1 YERLRRTVHQTGEYFRP.....RRITTPMGKNGMMLPVP 531

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 76:1
2: PIR2:1
3: PIR3:1
4: PIR4:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1339.5	48.0	264	2	PD0019
2	1329	47.6	265	2	JM0090
3	1304	46.7	576	1	RICSD
4	1275	45.7	254	2	PD0018
5	1259.5	45.1	528	1	TRISA
6	1214.5	43.5	562	2	S16022
7	1213.5	43.5	528	2	S12431
8	1197	42.9	527	2	S12430
9	1191.5	42.7	554	1	RICSD6
10	947.5	33.9	520	2	S62637
11	947.5	33.9	520	2	S62637
12	462	16.6	251	2	C19751
13	344.5	12.3	286	2	S25560
14	336.5	12.1	245	2	UC4840
15	337.5	12.1	286	2	UC4840
16	327	11.7	247	2	UC5032
17	326	11.7	247	2	RLTWT
18	325	11.6	247	2	JM00393
19	325	11.6	289	2	UC5606
20	305.5	10.9	316	2	OT0753
21	291.5	10.4	277	2	S22454
22	289.5	10.2	282	2	S22454
23	289.5	10.2	282	2	S22454
24	280	10.0	250	2	JM0108
25	249.5	8.9	328	2	A19817
26	215	7.7	313	2	S17757
27	213.5	7.6	261	2	JM0401
28	208	7.5	294	2	S28421
29	180.5	6.5	253	2	S28539

ALIGNMENTS

RESULT 1

PD0019 mistletoe lectin I B chain - Viscum album (fragment)

C:Species: Viscum album

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: PD0019

R:Schneidberg, S.; Krauspenhar, R.; Mithailov, A.; Stoeve, S.; Betzel, C.; Voelter, B.; Biophys. Res. Commun. 251: 337-342, 1998

A:Accession: PD0019

A:Reference number: PD0018, PMID:98308123; PMID:9642133

A:Molecule type: protein

A:Residues: 1-264 <ESC>

A:Superfamily: ricin; RNA N-glycosidase homology

Query Match 48.0%; Score 1339.5; DB 2; Length 264;

Best local similarity 95.8%; Pred. No. 5.3e-98;

Matches 252; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

DB 265 DVTGASAEPTVYVNGNNDVDDDDPDNDQIUMPSGNDPDQITKEDGHS 328

DB 1 DVTGASAEPTVYVNGNNDVDDDDPDNDQIUMPSGNDPDQITKEDGHS 60

QY 329 NSGCLTYGTAGVYVIMPDQNFARENTHWINGNTIIPRSMVLAASGKGTIT 388

DB 61 NSGCLTYGTAGVYVIMPDQNFARENTHWINGNTIIPRSMVLAASGKGTIT 120

QY 389 VQTLDTLGGQMLANDPAEVTYVTRDLMESGSGVAVETCVSSQND-EMALYD 447

DB 121 VQTLDTLGGQMLANDPAEVTYVTRDLMESGSGVAVETCVSSQND-EMALYD 180

QY 448 GSTRPNQDCTGCRBSVYTVVSGSASGQVPTMGQILNMGANDPA 507

DB 181 GSTRPNQDCTGCRBSVYTVVSGSASGQVPTMGQILNMGANDPA 240

QY 508 NPKLRRIITYPATKRPQNMV 530

DB 241 NPKLRRIITYPATKRPQNMV 263

RESULT 2

Mistletoe lectin I B chain - European mistletoe

C:Species: Viscum album (European mistletoe)

C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: JM0090

A:Reference number: JM0090, PMID:96285955; PMID:9618256

A:Accession: JM0090

A:Molecule type: protein
A:Residues: 1-265 <SOL>
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: glycoprotein
F:61.96.136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 47.6%; Score 1329; DB 2; Length 265;
Best Local Similarity 95.5%; Freq. No. 3,6e-97;
Matches 252; Conservative 2; Mismatches 8; Indels 2; Gaps 2;

QY 269 DQVTCASAPPTVAIVGNMVCVDRDDPHENQIQIAMSNSKNDPNQIWTIKEDGTRIS 328
1 DQVTCASAPPTVAIVGNMVCVDRDDPHENQIQIAMSNSKNDPNQIWTIKEDGTRIS 60

QY 329 NSGCLTWTGAGVAVWIPCKTAVKATVWIMQWNGTIIIPRSNIVLAASGQNGTTLT 388
61 NSGCLTWTGAGVAVWIPCKTAVKATVWIMQWNGTIIIPRSNIVLAASGQNGTTLT 120

QY 389 VQTLDTYTLGQMLAANDAFREVTIYGPDIQESNNGSVWETCVSSQNOQPMALYED 447
121 VQTLDTYTLGQMLAANDAFREVTIYGPDIQESNNGSVWETCVSSQNOQPMALYED 180

QY 448 GSIRPNQDQCLTGSDSYSTVNTVSCASGSGQWFTNBTALINIKYGLANDYDQA 507
181 GSIRPNQDQCLTGSDSYSTVNTVSCASGSGQWFTNBTALINIKYGLANDYDQA 240

QY 508 NPKLRRIIYATGKQNM-LPV 530
241 NPKLRRIIYATGKQNM-LPV 264

Db

RESULT 3
R15SD D precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext. change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Iadim, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2395712
A:Accession: A24041
A:Residues: 1-576 <RNA>
A:Cross-references: GB:X03179; NID:q21082; PIDN:CAA2639.1; PID:q21083
R:Regear, J.W.; Roberts, L.W.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <RNA>
A:Cross-references: GB:X2908; NID:q21084; PIDN:CAA37095.1; PID:q21085
R:Regear, J.W.; Roberts, L.W.; Lord, J.N.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Reference number: A24614; MUID:8519479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75/'D', 77-550/'R', 552-576 <LJM>
A:Cross-references: GB:X02388; NID:q21077; PIDN:CAA26330.1; PID:q21078
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Iadim, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2395712
A:Accession: A24041
A:Residues: 1-576 <RNA>
A:Cross-references: GB:X2908; NID:q21084; PIDN:CAA37095.1; PID:q21085
R:Regear, J.W.; Roberts, L.W.; Lord, J.N.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Reference number: A24614; MUID:8519479; PMID:3838723
A:Accession: A24614
A:Molecule type: protein
A:Residues: 36-97/'Q', 99-109/'S', 111-269/'D', 272-283/'L', 285-288, 290-302 <YOS>
A:Note: This paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tyrosophat

A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', 386-576 <RA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Accession: A03374
A:Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'I'
527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LI', 573-574, 'F', <FNU>
A:Note: This paper, one of a series, summarizes the experimental details for the det
R:Ready, M.P.; Kim, Y.; Robertus, J.D.
Protein 10, 270-278, 1991
A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechan
A:Reference number: A48237; MUID:91352006; PMID:1881883
R:Kutchen, E.; Robertus, J.D.
Protein 10, 270-278, 1991
A:Contents: annotation; X-ray crystallography; 2.5 angstroms
A:Reference number: A48238; MUID:91352005; PMID:1881882
R:Kutchen, E.; Robertus, J.D.
Protein 10, 270-278, 1991
A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; MUID:91352004; PMID:1881881
A:Contents: annotation; X-ray crystallography; 2.5 angstroms
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains. W
no the cell of the A chain inhibitor protein synthesis. It is a disulfide-linked dimer of
C:Superfamily: ricin rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding;
P:1-35/Domain: signal sequence #status predicted <Sig>
P:36-302/Product: ricin D chain A #status experimental <ACh>
P:315-373/Domain: rRNA N-glycosidase homology <RNA>
P:315-373/Product: ricin D chain B #status experimental <BCh>
F:345, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:115, 158, 249, 244/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:234, 318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
F:326, 349, 350/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimen
F:348, 569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match 46.7%; Score 1304; DB 1; Length 576;
Best Local Similarity 51.0%; Freq. No. 1e-94;
Matches 233; Conservative 81; Mismatches 161; Indels 20; Gaps 11;

QY 9 THGTGGERFRITLIDYSSG-PSNRPL-ROGIRPSQADGPIVLEMGQSDGI 66
48 HGAATGYNIRAVAGRLTITADVREHPLVPRVGLPIN-QEIVLDSNNAELAV 105

QY 67 TNAIDTLYVAVYQADDSYFLR-LAPRAE-LHLEFGT-TSSSLPFGSYPLDERVA 122
106 TNAIDTLYVAVYQADDSYFLR-LAPRAE-LHLEFGT-TSSSLPFGSYPLDERVA 165

QY 123 GH-RDQIFGIDQLQSTALAE--PGSRTQASRILLIIONTEARPNILMAAQ 178
166 GH-RDQIFGIDQLQSTALAE--PGSRTQASRILLIIONTEARPNILMAAQ 225

QY 179 GUNGBELHNGPDLERLALNLYISGTOPLPLARSLICITSDAPKPYLIGMRT 238
226 RLRNRSAPDPEVTLEMSKRLSTALQSNQAFSPLOLRQNSRPSVYDILIR 285

QY 239 SLALMFFGGERSSDYVWPLVPIVAD--DYVCSASPTVAIVGNMVCVDRDD 295
286 IIAIYVYCAPSPSSQ---ESLILIFVYVNPAAV-CDPEPTVAIVGNMVCVDRDD 340

QY 296 DPHNQIQIAMSNSKNDPNQIWTIKEDGTRISNSCLTWTGAGVAVWIPCKTAVK 355

Best Local Similarity 47.7%; Pred. No. 2,9e-91;
Matches 254; Conservative 89; Mismatches 162; Indels 29; Gaps 8;

QY 9 TQOTTGSEYFPPTLLADYVSSGSPENIEPLRGSTIPVSDQRFVLELTWQGGDSTA 68
DB 9 TQATTQSQYKQPTLAKRRL-RGGLHIDIPVLPDPT-TLQERNKATVTELSNSESIEV 66
QY 69 AIDPTLVYVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 127
DB 69 AIDPTLVYVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 127
DB 67 GIDVTNAYVVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 126
QY 128 IFLADIDQLOSVVAFPPGSGSTFQKRSILILQKISEAARFNPIMAAQYNSGASFL 187
DB 127 IFLQALQTHAISFPKSGANDKERRKTLVLIQWAEARFRYSNNVVASIQYTAHQ 186
QY 188 PDVYMLEETISWGQSTQVQSHTDGVP-ANPRLALPFGNFTLVNVDVYASLALMFLV 246
DB 187 PDVYMLEETISWGQSTQVQSHTDGVP-ANPRLALPFGNFTLVNVDVYASLALMFLV 246
QY 237 TASHALMEFCQGRSSSDRYKRYFVIRPYADDTGAS-EPYRIVQGNQWCHDPPQDQ 235
DB 237 TASHALMEFCQGRSSSDRYKRYFVIRPYADDTGAS-EPYRIVQGNQWCHDPPQDQ 235
QY 236 DEHDQVQQLMPKSNNDPQVLTIRKGTIRKNSGCLTGYGTAGVYVMIPOCNVAYE 355
DB 293 GYHNGRILIMKCKRLEKQKRLKSKIRKNSGCLTGYGTAGVYVMIPOCNVAYE 352
QY 356 ATTQVQNGTILNPSNUTLASGICGTTLTCTGLTCTGCGTANQNPAPREVTIYG 415
DB 353 ATTQVQNGTILNPSNUTLASGICGTTLTCTGLTCTGCGTANQNPAPREVTIYG 412
QY 416 PDLCMESNGSVVETCVSSQONQNALYDGSIRPKQNDQCLTCGRDSVTVINIVS 475
DB 413 YEDLCMAQGSNVMADQDNKKKQCMALYDGSIRPKQNDQCLTCGRDSVTVINIVS 472
QY 476 CSAGSSQGVVTFNEGALINKNGLANDVQANPLRILITVATGKQNGML 528
DB 473 CSAGSSQGVVTFNEGALINKNGLANDVQANPLRILITVATGKQNGML 525

RESULT 6

S16022
abrin-c precursor - Indian licorice

N/Contains: rRNA N-glycosidase (EC 3.2.2.22)

C/Species: Abrus precatorius (Indian licorice)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext-change 20-Aug-1999

R/Mod: X.A. Long, J.M.; Mawryczak, E.J.; Platak, M.

Eur. J. Biochem. 198, 723-732, 1991

A/Title: Preprobrin: genomic cloning, characterization and the expression of the A-chain

A/Reference number: S16022; MIMD:91265957; PMID:2050149

A/Accession: S16022

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-562 <MO>

A/Cross-references: BMLX5667; MIMD:916094; PMID:3324201; PMID:916085

C/Comment: The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid

F/35-285/Product: abrin-c chain A #status predicted <CH>

F/35-562/Product: abrin-c chain B #status predicted <CH>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

Best Local Similarity 47.8%; Pred. No. 1.1e-87;
Matches 250; Conservative 89; Mismatches 175; Indels 9; Gaps 7;

QY 9 TQOTTGSEYFPPTLLADYVSSGSPENIEPLRGSTIPVSDQRFVLELTWQGGDSTA 68
DB 9 TQATTQSQYKQPTLAKRRL-RGGLHIDIPVLPDPT-TLQERNKATVTELSNSESIEV 100
QY 69 AIDPTLVYVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 127
DB 69 AIDPTLVYVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 127
DB 101 GIDVTNAYVVAQAGQSVFELADPAGAEHLFTCTGSSLPKSGYDLPKRYEER-EPQ 160
QY 128 IFLADIDQLOSVVAFPPGSGSTFQKRSILILQKISEAARFNPIMAAQYNSGASFL 187
DB 161 IFLQALQTHAISFPKSGANDKERRKTLVLIQWAEARFRYSNNVVASIQYTAHQ 220
QY 188 PDVYMLEETISWGQSTQVQSHTDGVP-ANPRLALPFGNFTLVNVDVYASLALMFLV 246
DB 221 PDVYMLEETISWGQSTQVQSHTDGVP-ANPRLALPFGNFTLVNVDVYASLALMFLV 280
QY 247 CQERSSSDRYKRYFVIRPYADDTGAS-EPYRIVQGNQWCHDPPQDQ 305
DB 281 CQERSSSDRYKRYFVIRPYADDTGAS-EPYRIVQGNQWCHDPPQDQ 336
QY 306 DEHDQVQQLMPKSNNDPQVLTIRKGTIRKNSGCLTGYGTAGVYVMIPOCNVAYE 365
DB 337 GYHNGRILIMKCKRLEKQKRLKSKIRKNSGCLTGYGTAGVYVMIPOCNVAYE 366
QY 366 ATTQVQNGTILNPSNUTLASGICGTTLTCTGLTCTGCGTANQNPAPREVTIYG 415
DB 397 GYHNGRILIMKCKRLEKQKRLKSKIRKNSGCLTGYGTAGVYVMIPOCNVAYE 456
QY 416 PDLCMESNGSVVETCVSSQONQNALYDGSIRPKQNDQCLTCGRDSVTVINIVS 475
DB 457 GYHNGRILIMKCKRLEKQKRLKSKIRKNSGCLTGYGTAGVYVMIPOCNVAYE 456
QY 476 CSAGSSQGVVTFNEGALINKNGLANDVQANPLRILITVATGKQNGML 528
DB 517 CSAGSSQGVVTFNEGALINKNGLANDVQANPLRILITVATGKQNGML 559

RESULT 7

S32431
abrin-d precursor - Indian licorice (fragment)

N/Contains: rRNA N-glycosidase (EC 3.2.2.22)

C/Species: Abrus precatorius (Indian licorice)

C/Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #ext-change 01-Aug-1997

R/Mod: X.A. Long, J.M.; Mawryczak, E.J.; Platak, M.

Eur. J. Biochem. 198, 723-732, 1991

A/Title: Primary structure of three distinct isobabins determined by cDNA sequencing

A/Reference number: S32431; MIMD:9132758; PMID:8421313

A/Accession: S32431

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-528 <MO>

A/Cross-references: GB:098346

R/Mod: X.A. Long, J.M.; Mawryczak, E.J.; Platak, M.

Eur. J. Biochem. 198, 723-732, 1991

A/Title: Primary structure of three distinct isobabins determined by cDNA sequencing

A/Reference number: S32431; MIMD:9132758; PMID:8421313

A/Accession: S32431

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-169 <MO>

A/Cross-references: GB:098346

C/Comment: The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid

F/35-285/Product: abrin-c chain A #status predicted <CH>

F/35-562/Product: abrin-c chain B #status predicted <CH>

F/317-359/Domain: rRNA N-glycosidase homology <RG>

F/200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/247-269,286-305,329-346,417-430,456-473/Dsulfide bonds: #status predicted
 F/248,317/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/300,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 43.5%; Score 1213.5; DB 2; Length 528;
 Best Local Similarity 47.8%; Pred. No. 1,26-87;
 Matches 250; Conservative 90; Mismatches 174; Indels 9; Gaps 7;

OY 9 THQTGEYFRFTLLRDYSSGSFSENEIPRLRGSTIPVSDAGRFVLEVTNQGSDSITA 68
 DB 9 TEGATSGYQGFLEALRQL-TGGLEHIDPLEPDT-TVERNRKTYTELSENSEISIEV 66
 OY 69 AIDYNNYVYVAGQDGYFLRDAFPAQETFLFTGTSSSLPFGNSYFLERYAGH-RDQ 127
 DB 67 GIDYNNYVYVIRKASQSLFLRDAFPAQETFLFTGTSSSLPFGNSYFLERYAGH-RDQ 126
 OY 128 IPIGIDQLQSVYALFPFGSSTRTQASLIILQWTSKARFPLVRAQYINSQSFL 187
 DB 127 IPIGIDQLQSVYALFPFGSSTRTQASLIILQWTSKARFPLVRAQYINSQSFL 186
 OY 127 ISGLQALTAISPLRSGASMDKEXKRLTVIYIOWSEARVRYISNVGVSIRGTAFQ 186
 DB 186 PDVYMLEETSGQSGTQVGHSTGVF-NPRLALPFGNPFVTVWADYVIALMFLV 246
 OY 187 PDPMILSENNDNLSCGVQSGVQDTFENNVLISINRQFVYVDSLSHTVAVALMLFV 246
 DB 247 GERRSSDVRWMLVIRPVADDTCSAS-BPVYIVGRNKCVDYRDDPHDQIOL 305
 OY 247 GERRSSDVRWMLVIRPVADDTCSAS-BPVYIVGRNKCVDYRDDPHDQIOL 305
 DB 247 GERRSSDVRWMLVIRPVADDTCSAS-BPVYIVGRNKCVDYRDDPHDQIOL 302
 OY 306 WPKSNNDPNQMLTKRQDGTIRNSGCLTGYTQVYVWIPFCNTVREATVQWNG 365
 DB 303 WKCKRLEENQMLTKRQDGTIRNSGCLTGYTQVYVWIPFCNTVREATVQWNG 362
 OY 366 TIIPRSNLYVLAASSGKGTLLVOTLDYTLGGQMLAGNDAPREVTIYFRLQWNSG 425
 DB 363 TIIPRSNLYVLAASSGKGTLLVOTLDYTLGGQMLAGNDAPREVTIYFRLQWNSG 422
 OY 426 GSWVETCVSSQNGKALYDGSIRFQKQDQCLFCGSDYSTVITNVCSSAGSQRM 485
 DB 423 GSWVETCVSSQNGKALYDGSIRFQKQDQCLFCGSDYSTVITNVCSSAGSQRM 482
 OY 486 VFTNEGATLNLKGLMDVYVAGNPLRRIIIPATGKPNQWL 528
 DB 483 LFRNDGSIYVLDHMDVYVAGNPLRRIIIPATGKPNQWL 525

RESULT 8
 S32430
 A:Protein precursor - Indian licorice (fragment)
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Fabaceae)
 C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 A:Accession: S32430; JCI399
 R:Huang, C.H.; Lee, M.C.; Lin, T.C.; J. Mol. Biol. 229, 263-267, 1993
 A:Title: Primary structure of three distinct isoenzymes determined by cDNA sequencing. CD
 A:Reference number: S32429; PMID:93137798; PMID:842113
 A:Accession: S32430
 A:Molecule type: RNA
 A:Residues: 1-527 <RND>
 A:Cross-references: GB:W98345; NID:G166296; PTD:AAA2625.1; PTD:G166297
 A:Keywords: rRNA N-glycosidase
 A:Experimental source: seed
 A:Supplemental: rRNA N-glycosidase homology
 A:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F
 F/1-243/Product: abrin-b chain A #status predicted <KCH>
 F/1-243/Domain: rRNA N-glycosidase homology <RNG>

F/260-527/Product: abrin-b chain B #status experimental <RCH>
 F/262-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F/74,113,194,195/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
 F/110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/110,360/Active site: Gln, Arg #status predicted
 F/153,160/Active site: Gln, Arg #status predicted
 F/345,466,429,435-472/Dsulfide bonds: #status predicted
 F/287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/409,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 42.9%; Score 1197; DB 2; Length 527;
 Best Local Similarity 47.2%; Pred. No. 2,46-86;
 Matches 247; Conservative 91; Mismatches 175; Indels 10; Gaps 8;

OY 9 THQTGEYFRFTLLRDYSSGSFSENEIPRLRGSTIPVSDAGRFVLEVTNQGSDSITA 68
 DB 9 TEGATSGYQGFLEALRQL-TGGLEHIDPLEPDT-TLGRNRKTYTELSENSEISIEV 66
 OY 69 AIDYNNYVYVAGQDGYFLRDAFPAQETFLFTGTSSSLPFGNSYFLERYAGH-RDQ 127
 DB 67 GIDYNNYVYVIRKASQSLFLRDAFPAQETFLFTGTSSSLPFGNSYFLERYAGH-RDQ 126
 OY 128 IPIGIDQLQSVYALFPFGSSTRTQASLIILQWTSKARFPLVRAQYINSQSFL 187
 DB 127 IPIGIDQLQSVYALFPFGSSTRTQASLIILQWTSKARFPLVRAQYINSQSFL 185
 OY 186 PDVYMLEETSGQSGTQVGHSTGVFNPRLALPFGNPFVTVWADYVIALMFLV 246
 DB 186 PDPMILSENNDNLSCGVQSGVQDTFENNVLISINRQFVYVDSLSHTVAVALMLFV 245
 OY 247 GERRSSDVRWMLVIRPVADDTCSAS-BPVYIVGRNKCVDYRDDPHDQIOL 305
 DB 247 GERRSSDVRWMLVIRPVADDTCSAS-BPVYIVGRNKCVDYRDDPHDQIOL 301
 OY 306 WPKSNNDPNQMLTKRQDGTIRNSGCLTGYTQVYVWIPFCNTVREATVQWNG 365
 DB 303 WKCKRLEENQMLTKRQDGTIRNSGCLTGYTQVYVWIPFCNTVREATVQWNG 361
 OY 366 TIIPRSNLYVLAASSGKGTLLVOTLDYTLGGQMLAGNDAPREVTIYFRLQWNSG 425
 DB 363 TIIPRSNLYVLAASSGKGTLLVOTLDYTLGGQMLAGNDAPREVTIYFRLQWNSG 421
 OY 426 GSWVETCVSSQNGKALYDGSIRFQKQDQCLFCGSDYSTVITNVCSSAGSQRM 485
 DB 423 GSWVETCVSSQNGKALYDGSIRFQKQDQCLFCGSDYSTVITNVCSSAGSQRM 481
 OY 486 VFTNEGATLNLKGLMDVYVAGNPLRRIIIPATGKPNQWL 528
 DB 483 LFRNDGSIYVLDHMDVYVAGNPLRRIIIPATGKPNQWL 524

RESULT 9
 R32429
 A:Protein precursor - castor bean
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Ricinus communis (castor bean)
 C:Date: 31-Dec-1993 #sequence_revision 16-Dec-1993 #text_change 16-Jul-1999
 A:Accession: A24210
 R:Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; J. Biol. Chem. 260, 15682-15686, 1985
 A:Title: The primary structure of Ricinus communis agglutinin. Comparison with ricin
 A:Reference number: A24261; PMID:86059449; PMID:2999130
 A:Accession: A24210
 A:Molecule type: protein
 A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V'

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Page 6

C.Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to C. parvum.
C.Specificity: ricin, rRNA N-glycosidase homology
C.Keywords: duplication, glycoprotein, glycosidase, hydrolase, lectin, RNA binding, seed
P.1-24/Domains: signal sequence <status predicted <SIG>
P.35-230/Product: agglutinin chain A homology <ACH>
P.35-231/Domains: rRNA N-glycosidase homology <RNG>
P.303-561/Product: agglutinin chain B <status experimental <EBH>
P.310-381,352-402,405-423,450-485,486-528/Conserved sequence repeats
P.104,117,221,235/Binding site: Substrate (Tyr, Tyr, Glu, Asn) <status predicted
P.500,203/Active site: Glu, Arg <status predicted
P.324-336,338-348,351-382,453-465,492-509/Disulfide Bonds: Asp, Gln, Asn <status predicted
P.427,437/Binding site: carboxylate (Asn) (covalent) <status experimental
P.336,557/Binding site: N-acetylglucosamine (Asp, Asn) <status predicted

Query Match	42.7%;	Score 1191.5;	DB 1;	Length 564;
Best Local Similarity	47.6%;	Pred. No. 7.2e-86;		
Matches 254;	Conservative 84;	Mismatches 177;	Indels 19;	Gaps 10;

```

Oy      9 THOTGGEYRRITLFDYVSSSS--FNEIPIL--PGSTIPVSPARFVLEITMOGMSI 66
Db      37 TAAATVSYNINIAFRSHLITADVHEIPILSNVGLPIS--GRITVLEISHNELSV 94
Oy      67 TAAIDVTMLYYVAQAGDSIFLR--DAPGAE--TLLPHTGTRS--SEFSPYSIDLEKKA 122
Db      95 TLLADVTMLAAVAGVQVLAALF---PGSGTSPHAFSLITLMOISBAARPNIMLAEQY 154
Oy      123 GHGDDIPIAGIDILQGYLAF---PGSGTSPHAFSLITLMOISBAARPNIMLAEQY 179
Db      155 GLSENTELGGPELMALYYSTGCTGPIFLARSFVNCIMTSEARFOYICSEMR 214
Oy      180 INSGASFLPYVYMLETFSMOQSTOVASHETGVFNNPILAPISGFVTLINTEVDIAS 239
Db      215 IYRNRSAPSPVYITLSEMSRSLTALDSSNGASAPSPLOQENSSAPVYIDSLIPI 274
Oy      240 LALNF.PVOGSGRESSDVRWYVYHPIPLD---DYCCASAPSPYITVYRWKCVDRDD 296
Db      275 IALNYRARPSSG-----FSLHIVYVHFNRADY--CMDEPILVIVYRNGLCVDVTGER 329
Oy      297 PFGDNOILQWPSKSNDDPVOAMITIKDDITFNSGSCITVYGAVGYMLFPCVYVFEA 356
Db      330 PFOANDILQWPKSGSTVNOAMLRDITIRSKGCTIISGSPROCVYVYNTCTAVGA 389
Oy      359 ITWQINGWCTITNPSNLYVAASGSKGTLTVQVTDLYLQCGMLANQTPAAREVITV 416
Db      390 TFMQIDNRKRTITNPSGYSWASNSGCTIKVLYQVNLNQQQLNPOGFTTIVYL 449
Oy      411 RLCQMSQWVWETQVSSQOONQKALYQSGAPRPNQDQCTCMGDSVSVYVINYGC 476
Db      450 YXKQILQANSQKWLDECTSEKAEQWALYADSGIPEPQOONQCTLTDMANKITVYLKSC 509
Oy      477 YAGSGSGQWPFNTBZALILMKGLADVYQAGNPKIRKIIITVPATGSPNQMLTPV 530
Db      510 GPASGSGQWPKNDQDTLILNKGSLVYDPRSDSSIKGIIIVYHFGNQQMLPE 563

```

RESULT 10
S62627
agglutinin I precursor - European elder
C.Species: Sambucus nigra (European elder)
C.Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #ext_change 20-Aug-1999
C.Accession: S62627, S62619
R.van Damme, E.J.M.; Barre, A.; Rongey, P.; van Leuven, P.; Pennaers, N.J.
Eur. J. Biochem. 235, 188-197, 1996
A.Title: The Neuro(1,6h2-6)-Gal/GalNAc-Binding Lectin from elderberry (Sambucus nigra)
A.Reference Number: S62619, MIMD:96202926, PMID:863119
A.Accession: S62627
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-570 (<VNA>
A.Cross-references: EMBL:U071122; NID:G1141772; PTDN:PAC49158.1; PDB:G1141773
A.Accession: S62619

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-39/309-119 <RA>
C:Superfamily: rctin: rRNA N-glycosidase homology
E:37-283/Domain: rRNA N-glycosidase homology <RMG>

Query Match	33.9%	Score 947.5;	DB 2;	Length 570;
Best Local Similarity	40.7%;	Pred. No. 1 2e-66;		
Matches 220;	Conservative 82;	Mismatches 206;	Indels 33;	Gaps 15;

QY 8 VTHQTG-EEFRFTLLRDVSSGSFS-EIPLRSTIPSDAQFVLVELTNGGDS 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 37 VSFNLTGADYIEPFLPALOKVIIGNHAFDLPLVNLNES-QVSDSRFVLVPLTNPSGDT 95

Cy 66 ITAAIDVNTLVAVNAQGDPSYFLRDAPRGAEHLFTGTRSSLPPFGSYDLERYAGH- 124
 : | | | | | | | : | | | | : | | | |

Db 96 VTTAIDVNLTIVVAFFSSNGKSIYPFSGGSTAVQRNLLPDTTGELNFIGNYSLSERGVGF 155

```

Oy      125 RDGIPFG---IDQLIOSVTALRFEGSGSTRTQASLILIQMSAAEFNPILMRQAQYIN 181
          | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db      156 RYVILPGPKSLDQAISSLRTYTLNGDTKPLAGGLVVIQMSAAAFRYIELRITST 215

```

QY 182 SGASPLPDVWMLLELESWGGOOSTYQHSS-TDGVENNPRIALPFGNVTLLNVRDY--IA 238
 : : : : : : : : : : : : : : : : : :
 Db 216 DASEFTFDLTLMSMENNNSSMSSEIQAPPGGAFAGVQLRDERNNSEIVTNFRRLBELT 275

Qy 239 SLAIMEVCGEPPSS-----DYYNPLVIRPYIA--DVTCSASEPTYRIVGRNGMC 289
:::| | | : : : | | | | : :
Db 276 YIVLLETCAPVTSSSYNNALDAQ--ITKMPFRGGEYEKKVCYVEVTRIRISGNDGLC 332

Oy 290 VDVRRDDPFDGNGIQGLMPKSKNNNDNQWLTIKPDGTISNGSLTTGYTAGYYWMLFDC 349
||| : ||| : ||| : ||| : ||| :
Db 333 VDPFRYGHYIDGNPVQLRP--CGNECQQLMFRITDGIIRLGGCL-----TASSSWMLYDC 385

QY 350 NTAVREATIQWNGNIIINPRSNIVLAASSGIGKTLVQTLDTYVLQGGWAGNDIAPR 400
 ||| : ||||| : ||| : |||
 Db 386 NTTPPEAIKWVSDIGITINHSGLVLTAPQAAESTALSLENNIIHAARQGWWG-DVEPL 444

[illegible]

QY 468 STVINIVSCASGSGGQRTVFNEGALINLNGMLNDVADANPELRRIIYPAGQKQNM 52

D5 505 SDLVILKCE-GSGNQRRVFNTNGTISNPAKLMDVADVDLSRKIIILYRPTGNPAQM 563

QY	528	L	528
		:	
DB	564	I	564

RESULT 11
S06330
Ricin F - castor bean (fragment)

N/Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
C:Accession: S06330: J05381

R, Ladach, B. F.; Murray, E. B.; Halling, A. C.; Halling, R. C.; Hildebrand, N.; Plant Mol. Biol. 9, 287-295, 1987

A1 Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis protein

A1 Reference number: S06330

A:Accession: S06330
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-263 <IAD>

References: EMBU:MI7631; MID:G169714; EUD:MA463508.1; EUD:G160722
R:Araki, T.; Funatsu, G.
Biochim. Biophys. Acta 911, 191-200, 1987
Title: The complete amino acid sequence of the B-chain of ricin E isolated

A:Reference number: JC5381; MUID:87101186; PMID:380193
A:Accession: JC5381
A:Molecule type: protein

RESULT 11

S06330
Ricin E - castor bean (fragment)

C:Species: Ricinus communis (castor bean)

C/Accession: S06330; JC5381
 Title: Murray, F.F.; Halling, A.C.; Halling, K.C.; Tilakaratne, N.; Lo

Plant Mol. Biol. 9, 287-295, 1987

A;Reference number: S06330
A;Accession: S06330

A;Molecule type: mRNA

A; Cross-references: EMBL:M17631; NID:g169714; PIDN:AAA63506.1; PID:g169715

Biochim. Biophys. Acta 911, 191-200, 1987

A/Reference number: JC5381; PMID:87201186; PMID:3804733
A/Accession: JC5381

m/molecule type: protein

A/Residues: 1-69, 'P', 'S', '72-209, 'A', '211-241, '243-250, 'V', '252-263 <ABA>
A/Experimental source: seed
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
F/1-263/Product: ricin B chain B #status experimental <BC>
F/10-359/60-100/103-143/148-183/187-228/232-263/Region: 40-residue repeats
F/10-359/60-100/103-143/148-183/187-228/232-263/Region: 40-residue repeats
F/195/115/Binding site: carboxylate (Asn) (covalent) #status experimental
Query Match 31.9%; Score 891.5; DB 2; Length 263;
Best Local Similarity 62.5%; Pred. No. 1.1e-62;
Matches 162; Conservative 34; Mismatches 62; Indels 1; Gaps 1;
QY 273 CSASEPTVAVSNMCDVDRDDFDQNGQIQMPKSKNPPNQMLTKDGTIRSNASC 332
DB 4 CNDPEPTVAVSNMCDVDRDDFDQNGQIQMPKSKNPPNQMLTKDGTIRSNASC 63
QY 333 LTTVGTAGVYVAFEDCNVREANTVQIMKNGTINPSSNIVAAASGIRKTTVPTQL 392
DB 64 LTTVGTAGVYVAFEDCNVREANTVQIMKNGTINPSSNIVAAASGIRKTTVPTQL 123
QY 393 DTLTGQWLAGVETAPREVITVIGRDLCSNNGSVWVETCVSSQGNQRMALVGSIRP 452
DB 124 ITAVSQWLPNTNTPPTVITVIGRDLCSNNGSVWVETCVSSQGNQRMALVGSIRP 183
QY 453 KQNDQCLTCGRDVSFTVINTVSCSGSGGQWVETVSGAIIINIKKGLANDVAQANP-KL 511
DB 184 QQNDQCLTCGRDVSFTVINTVSCSGSGGQWVETVSGAIIINIKKGLANDVAQANP-KL 243
QY 512 RRTITVATKRNQWLEFV 530
DB 244 KQITVATKRNQWLEFV 262

RESULT 12
C39761
abrin (clone 7.2) precursor - Indian jicorice (fragment)
N/Contexts: rRNA N-glycosidase (BC 3.2.2.22)
C/Species: Abrus precatorius (Indian jicorice)
C/Date: 21-Feb-1992 #sequence, revision 31-Dec-1993 #ext. change 20-Aug-1999
R/Accession: C39761, S14471, S14471, S14471, S14471, S14471, S14471, S14471
J. Biol. Chem. 266:6848-6852, 1991
A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A/Reference number: A39761; MUID:51201359; PMID:2026300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EV>
R/Bvensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A/Description: Direct molecular cloning of two distinct abrin A-chains.
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 'M', '1-251 <EV>
A/Cross-references: EMBL:X54872; NID:g16088; PIRN:CA38654.1; PID:g16089
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycosidase; hydrolase; lentin; toxin
F/1-251/Product: abrin (clone 7.2) chain A #status predicted <AC>
F/74/113/Domain: rRNA N-glycosidase homology <RNG>
F/74/113/195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/164/167/Active site: Glu, Arg #status predicted
Query Match 16.5%; Score 462; DB 2; Length 251;
Best Local Similarity 44.4%; Pred. No. 6.3e-25;
Matches 107; Conservative 38; Mismatches 92; Indels 4; Gaps 4;

QY 9 TQGTGEEYFRTITLADYVSSGSFNEPIPLAGSTIPISDQGFVLTNMGQDSITPA 68
DB 9 TQGTGEEYFRTITLADYVSSGSFNEPIPLAGSTIPISDQGFVLTNMGQDSITPA 68
QY 69 AIDVTNLVAVAGQDSYFLNDAPGAFETLFTGTRSLTPGSGYDLEFRAQH-FQ 127
DB 69 AIDVTNLVAVAGQDSYFLNDAPGAFETLFTGTRSLTPGSGYDLEFRAQH-FQ 127

DB 67 GIDVTNAYVAVNRASQGVFNDAPASSTVILPTGTRVSLRSDGYDLERMAHQTRQ 126
QY 128 IPIGIDQLQSVTLAPFGSGSTRQASSTILIIOMISEKARFPLWRARQYNSGASPL 187
DB 127 ISIGQMLTRHAPLSGASNDKARATLIVIOSEKARFPLWRARQYNSGASPL 186
QY 188 PDVYMLKETSNGQSTQVGHSTQGFNNRILALPQNFVTLTV-RDVYSLATMLFV 246
DB 187 PDVYMLKETSNGQSTQVGHSTQGFNNRILALPQNFVTLTV-RDVYSLATMLFV 246
QY 247 C 247
DB 247 C 247
RESULT 13
S25560
rRNA N-glycosidase (BC 3.2.2.22) momordin II - balsam apple
C/Species: Momordica balsamina (balsam apple)
C/Date: 25-Feb-1994 #sequence, revision 03-Aug-1995 #ext. change 20-Aug-1999
R/Accession: S25560, M
Nucleic Acids Res 20, 4662, 1992
A/Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is a
A/Reference number: S25560; MUID:93027170; PMID:1408772
A/Accession: S25560
A/Molecule type: mRNA
A/Status: preliminary
A/Cross-references: EMBL:U12175; NID:g19525; PIRN:CAAT816.1; PID:g19526
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: glycosidase; hydrolase
F/27-264/Domain: rRNA N-glycosidase homology <RNG>
Query Match 12.3%; Score 344.5; DB 2; Length 286;
Best Local Similarity 34.8%; Pred. No. 1.5e-19;
Matches 88; Conservative 54; Mismatches 92; Indels 19; Gaps 9;
QY 13 TGEYFPTILIRVYSSGSFNEPIPLAGSTIPISDQGFVLTNMGQDSITPA 69
DB 33 TATVYFET--EPPATLPSPKRYDIPPLVST--ISISRRFTLIDLSVAVETISVA 86
QY 70 ITMTLVAVAVAGQDSYFLNDAPGAFETLFTGTRSLTPGSGYDLEFRAQH-FQ 127
DB 87 ITMTLVAVAVAGQDSYFLNDAPGAFETLFTGTRSLTPGSGYDLEFRAQH-FQ 127
QY 128 IPIGIDQLQSVTLAPFGSGSTRQASSTILIIOMISEKARFPLWRARQYNSGASPL 187
DB 146 IDIGPLASATLTLFVYNAQSAFA--LTVLQTTAEKAPFYERHAKVY--ATNFK 201
QY 188 PDVYMLKETSNGQSTQVGHSTQGFNNRILALPQNFVTLTV-RDVYSLATMLFV 246
DB 202 PNAITSLKQNSKQPIPLAGSTIPISDQGFVLTNMGQDSITPA 68
QY 246 VCEFRPSSDPAV 258
DB 262 L-MSAATNDKDP 273
RESULT 14
JC4840
rRNA N-glycosidase (BC 3.2.2.22) trichogangula - snake gourd
C/Species: Trichosanthes anguina (snake gourd)
C/Date: 15-Aug-1995 #sequence, revision 24-Oct-1997 #ext. change 05-Dec-1997
R/Accession: JC4840, J07071, J07071, J07071, J07071, J07071, J07071, J07071
R/Chow, L.P.; Kano, M.; Yan, D.I.; Wang, S.H.; Ueno, Y.; Tsugita, A.
A/Title: Snake gourd rRNA N-glycosidase homology <RNG>
A/Accession: JC4840
A/Molecule type: protein
A/Residues: 1-132, 'S', '134-245 <CHO>
A/Experimental source: seed

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18, Search time 5.1251 seconds

2736.539 Million cell updates/sec

Title: US-09-601-667C-4

Perfect score: 2791

Sequence: 1 YERLRRLVHTQTCGEYFRP.....NRITVPAKGNOMLPPV 531

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1339.5	48.0	264	1 MBL_VISAL	P081830 viscum albu
2	1304	46.7	526	1 RIE1_RICCO	P028175 ricinus com
3	1283	45.1	528	1 ABR1_ABRP	P11440 abrus prec
4	1259.5	45.1	528	1 ABR1_ABRP	P11440 abrus prec
5	1244.5	43.5	552	1 ABR1_ABRP	P11440 abrus prec
6	1197	42.9	537	1 ABR1_ABRP	P06077 abrus prec
7	1191.5	42.7	564	1 AGGL_RICCO	P06750 ricinus com
8	895.5	32.1	563	1 NIGB_SANNI	P33181 sambucus ni
9	350	12.5	282	1 RIE2_BYD1	P98184 bryonia dio
10	344.5	12.3	286	1 RIE2_BYD1	P293139 momordica b
11	327.5	11.7	294	1 RIE1_TRIAN	P293139 momordica b
12	326	11.7	289	1 RIE1_TRIAN	P09988 crichosanth
13	325	11.6	289	1 RIE1_TRIAN	P24478 crichosanth
14	318.5	11.1	286	1 RIE1_TRIAN	P24478 crichosanth
15	318.5	11.1	286	1 RIE1_TRIAN	P24478 crichosanth
16	294.5	10.6	350	1 RIE1_BYD1	P33181 sambucus ni
17	291.5	10.4	277	1 RIE1_BYD1	P33181 sambucus ni
18	284.5	10.2	286	1 RIE1_BYD1	P33181 sambucus ni
19	280	10.0	280	1 RIE1_BYD1	P33181 sambucus ni
20	249.5	8.9	278	1 RIE1_BYD1	P33181 sambucus ni
21	215	7.7	313	1 RIE1_BYD1	P33181 sambucus ni
22	213.5	7.6	261	1 RIE1_BYD1	P33181 sambucus ni
23	208	7.5	264	1 RIE1_BYD1	P33181 sambucus ni
24	180.5	6.5	253	1 RIE1_BYD1	P33181 sambucus ni
25	180.5	6.5	253	1 RIE1_BYD1	P33181 sambucus ni
26	178.5	6.4	253	1 RIE1_BYD1	P33181 sambucus ni
27	177.5	6.2	252	1 RIE1_BYD1	P33181 sambucus ni
28	168.5	5.4	310	1 RIE1_BYD1	P33181 sambucus ni
29	165.5	5.1	293	1 RIE1_BYD1	P33181 sambucus ni
30	142.5	5.0	236	1 RIE1_BYD1	P33181 sambucus ni
31	140	5.0	236	1 RIE1_BYD1	P33181 sambucus ni
32	138.5	5.0	236	1 RIE1_BYD1	P33181 sambucus ni
33	127	4.6	315	1 SLTA_BP119	P08026 bacterioph

ALIGNMENTS

RESULT 1	MBL_VISAL	STANDARD	PRT	264 AA.
1	MBL_VISAL	STANDARD	PRT	264 AA.
2	MBL_VISAL	STANDARD	PRT	264 AA.
3	MBL_VISAL	STANDARD	PRT	264 AA.
4	MBL_VISAL	STANDARD	PRT	264 AA.
5	MBL_VISAL	STANDARD	PRT	264 AA.
6	MBL_VISAL	STANDARD	PRT	264 AA.
7	MBL_VISAL	STANDARD	PRT	264 AA.
8	MBL_VISAL	STANDARD	PRT	264 AA.
9	MBL_VISAL	STANDARD	PRT	264 AA.
10	MBL_VISAL	STANDARD	PRT	264 AA.
11	MBL_VISAL	STANDARD	PRT	264 AA.
12	MBL_VISAL	STANDARD	PRT	264 AA.
13	MBL_VISAL	STANDARD	PRT	264 AA.
14	MBL_VISAL	STANDARD	PRT	264 AA.
15	MBL_VISAL	STANDARD	PRT	264 AA.
16	MBL_VISAL	STANDARD	PRT	264 AA.
17	MBL_VISAL	STANDARD	PRT	264 AA.
18	MBL_VISAL	STANDARD	PRT	264 AA.
19	MBL_VISAL	STANDARD	PRT	264 AA.
20	MBL_VISAL	STANDARD	PRT	264 AA.
21	MBL_VISAL	STANDARD	PRT	264 AA.
22	MBL_VISAL	STANDARD	PRT	264 AA.
23	MBL_VISAL	STANDARD	PRT	264 AA.
24	MBL_VISAL	STANDARD	PRT	264 AA.
25	MBL_VISAL	STANDARD	PRT	264 AA.
26	MBL_VISAL	STANDARD	PRT	264 AA.
27	MBL_VISAL	STANDARD	PRT	264 AA.
28	MBL_VISAL	STANDARD	PRT	264 AA.
29	MBL_VISAL	STANDARD	PRT	264 AA.
30	MBL_VISAL	STANDARD	PRT	264 AA.
31	MBL_VISAL	STANDARD	PRT	264 AA.
32	MBL_VISAL	STANDARD	PRT	264 AA.
33	MBL_VISAL	STANDARD	PRT	264 AA.

FT VARIANT 231 231 N -> S OR T.
FT VARIANT 231 233 NGL -> KXP.
FT VARIANT 232 235 GLAM -> SLWV.
SQ SEQUENCE 264 AA; 28981 MW; 7D0DC326CC6F5M4 CRC64;
Query Match 48.0%; Score 1339.5; DB 1; Length 264;
Best Local Similarity 95.8%; Pred. No. 1.7e-99;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
Db 1 DDTCSASEPTVAIVGNMGRVDYRDPDHNGQQLMPSKNNDRNQLTIEGDTIS 60
QY 269 DDTCSASEPTVAIVGNMGRVDYRDPDHNGQQLMPSKNNDRNQLTIEGDTIS 328
Db 1 VDTLDTLQGLMAGNDTAPREVTIYGFEDLQENSGSVWETCVSSQONQ-FMALYD 447
QY 329 VDTLDTLQGLMAGNDTAPREVTIYGFEDLQENSGSVWETCVSSQONQ-FMALYD 388
Db 61 NOSCLITTYGAGVYVWIFPCNTAVREATIMQIMNGTIIIPRSNVLAASSQIKGTLT 120
QY 389 VDTLDTLQGLMAGNDTAPREVTIYGFEDLQENSGSVWETCVSSQONQ-FMALYD 447
Db 121 VDTLDTLQGLMAGNDTAPREVTIYGFEDLQENSGSVWETCVSSQONQ-FMALYD 507
QY 448 GSIRPRNODCLTCGDSYGVYVNIYSCSGSGQPRYFEGATILKRCIAMDYDQ 180
Db 181 GSIRPRNODCLTCGDSYGVYVNIYSCSGSGQPRYFEGATILKRCIAMDYDQ 240
QY 508 NPKLRRIIYPATGKNQMLPV 530
Db 241 NPKLRRIIYPATGKNQMLPV 263

RESULT 2
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
AC P02879; P02880; STANDARD; PRT; 576 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-SEP-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor [contains: Ricin A chain (RNA N-glycosidase)
DB (EC 3.2.2.22); Ricin B chain).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids; Malvales; Malvaceae; Euphorbiaceae; Ricinus.
OC MBL_TaxId=3986;
RN 1; MBL_TaxId=3986;
RP SEQUENCE FROM N.A.
RX MEDLINE=86067244; PubMed=2399712;
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
Weaver R.F.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
communis";
RL Nucleic Acids Res. 13:8019-8033(1985).
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=9218016; PubMed=1171405;
RA Tregear J.W., Roberts L.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
RL ricin gene and three lectin pseudogenes";
RL Plant Mol. Biol. 18:515-528(1992).
RN 3;
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=3838723;
RA Lamb A., Roberts L.M., Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin";
RL J. Biol. Chem. 265:2701(1985).
RN 1;
RP SEQUENCE OF 36-302.
RA Yoshitake S., Funatsu G., Funatsu M.;
RT "Isolation and sequences of peptide peptides, and the complete
RL sequence of the chain of ricin-D";
RL Agric. Biol. Chem. 42:1267-1274(1978).
RN 15;
RP SEQUENCE OF 315-576.

RA Funatsu G., Kimura M., Funatsu M.;
RT "Primary structure of ricin D-chain";
RL Agric. Biol. Chem. 43:2221-2224(1979).
RN 6;
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1368517;
RA Kimura Y., Kusunoku H., Tada M., Takagi S., Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant";
RL Agric. Biol. Chem. 54:157-162(1990).
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RP MEDLINE=21480122; PubMed=11595654;
RA Olmes S., Kozlov J.V.;
RT "Ricin";
RL Toxicol. 39:1723-1728(2001).
RN 181;
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=87165983; PubMed=3558397;
RA Morfitt W., Vallatrance J.E., Monzingo A.F., Ernst S.R., Katzin B.,
Rueber B., Xuong N.H., Hamlin R., Roberts J.D.;
RT "The three-dimensional structure of ricin at 2.8 A";
RL J. Biol. Chem. 262:5398-5403(1987).
RN 9;
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=91352004; PubMed=1881861;
RA Katzin B.J., Collins E.J., Roberts J.D.;
RT "Structure of ricin A-chain at 2.5 A";
RL Proteins 10:251-259(1991).
RN 101;
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1881882;
RA Rueber B., Roberts J.D.;
RT "Structure of ricin B-chain at 2.5-A resolution";
RL Proteins 10:260-269(1991).
RN 11;
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=7990130;
RA Weston S.A., Tucker A.D., Thatcher D.R., Darbyshire D.J.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution";
RL J. Mol. Biol. 244:410-422(1994).
RN 112;
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
RX MEDLINE=96374222; PubMed=8780513;
RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svahn M.C., Roberts J.D.;
RT "The structure and activity of an active site substitution of ricin A
RL chain";
RL Biochemistry 35:11098-11103(1996).
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RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9068280;
RA Yan X., Hollis T., Swinch M., Day F., Monzingo A.F., Milne G.M.,
Roberts J.D.;
RT "Structure-based identification of a ricin inhibitor";
RL J. Mol. Biol. 266:1043-1049(1997).
RN 114;
RP MEDLINE=93165632; PubMed=1287657;
RA Kin Y., Roberts J.D.;
RT "Analysis of several key active site residues of ricin A chain by
RL mutagenesis and X-ray crystallography";
RL Protein Eng. 5:775-779(1992).
RN 1;
RP FUNCTION: Ricin is highly toxic to animal cells and to a less
CC extent to plant cells. The A chain is responsible for inhibiting
CC protein synthesis through the catalytic inactivation of 60S
CC ribosomal subunits. It acts as a glycosidase that removes a
CC specific adenine residue from an exposed loop of 28S ribosomal
CC rRNA. The B chain is involved in the binding of elongation
CC factors. The two chains make a stable support protein
CC complex. The A chain can inactivate the support protein
CC per minute, thus inactivating them faster than the cell can make
CC new ones. A single A-chain molecule can therefore kill an animal

CC		call. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.
CC	-1	CATALYTIC ACTIVITY: Endolytolytic cleavage of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC	-1	SUBUNIT: Disulfide-linked dimer of A and B chains.
CC	-1	COMPOSITION: Consists of two homologous subdomains ('alpha, beta domain').
CC	-1	PNU: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 27.
CC	-1	SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSE-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC	-1	SIMILARITY: Contains 2 rich B-type lectin domains.
CC	-1	CATION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1., REF.2 AND REF.3).
CC	NH2	NAME: Ribose-binding protein Spd203pht.
CC	-1	MW: http://www.embl.org/spoilight/articles/spc1l03.html .
CC	--	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL	X03179; CAA26399.1; -
CC	EMBL	X52088; CAA37095.1; -
CC	EMBL	X02388; CAA26230.1; -
CC	EMBL	A12892; CAA01058.1; -
CC	PIR	A24041; RLCSO.
DR	PDB	ZAAI; 3I-JAN-94.
DR	PDB	IARG; 3I-JAN-94.
DR	PDB	1N9P; 3I-OCT-93.
DR	PDB	1IKS; 14-JUN-98.
DR	PDB	1IFU; 14-JUN-98.
DR	PDB	1RCQ; 3I-OCT-93.
DR	PDB	1OB8; 16-JUN-97.
DR	PDB	1OB1; 02-SEP-98.
DR	PDB	1B86; 02-SEP-98.
DR	PDB	1IJ3; 16-JUN-92.
DR	PDB	1IY4; 16-JUN-92.
DR	GISAID	PR02975.
DR	GISAID	IPR001574; RIP.
DR	InterPro	IPR001574; Ricin_B_lectin.
DR	InterPro	IPR00652; Ricin_B_lectin; 6.
DR	Pfam	PF00161; RIP; 1.
DR	PRINTS	PR00396; SHIGARICIN.
DR	SMART	SMO0458; RICIN; 2.
DR	FROSIT	PSS00231; RICIN_B_LECTIN; 2.
DR	FROSIT	PSS00275; SHIGA_RICIN; 1.
DR	Prosite	PS00275; SHIGA_RICIN; 1.
DR	GLITE	Glite definition: Hydrophobic protein synthesis inhibitor; Toxin; Repeat; Glycylglycyl; Lectin; 3D-structure.
KM	SIGNAL	1 35 signal; 3D-structure.
FT	CHAIN	36 302 RICIN A CHAIN.
FT	PEPTIDE	303 314 LINKER PEPTIDE.
FT	CHAIN	315 576 RICIN B CHAIN.
FT	DOMAIN	321 448 RICIN-B-TYPE LECTIN 1.
FT	REPEAT	451 575 RICIN-B-TYPE LECTIN 2.
FT	REPEAT	331 373 1-ALPHA.
FT	REPEAT	377 416 1-BETA.
FT	REPEAT	416 446 1-ALPHA.
FT	REPEAT	462 497 2-ALPHA.
FT	REPEAT	501 540 2-BETA.
FT	REPEAT	543 570 2-GAMMA.
FT	ACT_SITE	212 212 INTERCHAIN.
FT	DISULFID	294 318
FT	DISULFID	334 353

FT	DISULFID	377	394	
FT	DISULFID	465	478	
FT	DISULFID	504	521	
FT	CARBOHYD	45	45	
FT	CARBOHYD	271	271	
FT	CARBOHYD	409	409	
FT	CARBOHYD	449	449	
FT	CONFLICT	76	76	
FT	CONFLICT	551	551	
FT	STANDARD	43	47	
FT	TURN	49	50	
Query Match		46.7%	Score 1304	DB 1
Best Local Similarity		51.0%	Freq. No. 38-96	Length 576;
Matches 2733	Conservative	61	Matches 161	Indels 20
				Gaps 11
QY	9	THOQTGEFFEFITLLADNVSSS--FENFELPL-RQSTIVPDADQRYVLELNQGGQSI	66	
DB	48	TAGATGSSYTNFIAVAGRLTGTADVDEHIEVLNRCVGLPIN--QRFIIYELSHAEISLV	105	
QY	67	TAAIDVNYLYVAAQYQGGSYFAR-DAPKQAR--THLPTQT--TRSSLPFNSYDLSEYA	122	
DB	106	TGADVVNYVYVGRKASGAFPHFDEQDEALHTLTVONARITFAAPKRNPLIMBQD	165	
QY	123	GG-DOGPGGLDQIQSYSTAF--PGSGTRAPSLITLIONSPARKRNPLIMBQD	178	
DB	166	GNFENIEHNGNPLEBASLYAVYGTGQIPLASSTICLIONSPARKROYLEGHWT	225	
QY	179	YINSGAFPLDYVLELTSTGQGGQGVQSHSDVNNPRLALIPDNVPLINWADIA	238	
DB	226	RIRYKRSASADPSYITLNSGHSITLAIQESNGQASAPSTOLQRANSGFVSVDYSLIP	285	
QY	293	SLAINEPVGSGPSSDVRWELVIRPYAD--DVTGASAPFTRVYKNNQGNURD	295	
DB	286	ILNLYVIRKQAPSSQ----FSLIRVYVKNNDI--GMPEPIYRLVHNGLVQVADG	340	
QY	296	DFPDNGQIQWMSKNNPNQNLWTREKDGTRNSGSCITLYGTYGVYVLPDQNAARE	355	
DB	341	REFNQNADIQMFCSCWTDANDNLWIKEDNTISNGKCLITYGSGVYVYIDQNTAAD	400	
QY	356	ATVQIWGNQNTINFSNMLVLAASGIRKQTLVTVQTLDTLQGNLGNADNAPAEVITYG	415	
DB	401	ATKQWQMNQNTINFSNMLVLAASGIRKQTLVTVQNTINAVSQWELTNVQVITYVIG	460	
QY	416	PRQTKNSGNSWYTCVSSQGNFALAYGHSITLIPKNNQDCLCTGDSVYVITNS	475	
DB	461	LYGLCLQNSGQGVWIEDSSFKRAQOMALYDQSIIFQNRDHCITSDNSITFEVYKILS	520	
QY	476	CSAGSSQGRWYTBGAIINIKNGIADVAQANXKRELIITVYATGAPKNNQWLPV	530	
DB	521	CGPSSQGRWFKQNDQITINIVYSGVLVDPAASDLSIKQILVPLHSGPNQIWLPL	575	
RESULT 3				
ML	MLA VISAL	STANDARD;	PRT:	254 AA.
AC	P81346;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosylase) (EC 3.2.2.22).			
OS	Yucca album (Boraginaceae) (Euphorbia)			
CC	Yucca album (Boraginaceae) (Euphorbia)			
CC	Sanitales; Santalaceae; Viscum.			
NCBI	Taxid=972;			
NCBI	[1]			
SEQUENCE.				
STRAIN=	subsp. album;			
NCBI	MEDLINE=97134561; PubMed=8980141;			

RA	Soletier M., Stoeva S., Schwaborn C., Wilhelm S., Stetel T.,
RA	Voelter M.,
RT	"Complete amino acid sequence of the A chain of mistletoe lectin I,"
RT	FEBS Lett. 399:153-157(1996).
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC	SYNTHESIS BY BLOCKING THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC	SUBUNIT. THIS BLOCKING OF THE CATALYTIC INACTIVATION OF THE 60S
CC	RIBOSOMAL SUBUNIT RESULTS IN THE INHIBITION OF PROTEIN SYNTHESIS
CC	INTO THE CELL OF THE A CHAIN. B CHAINS ARE ALSO RESPONSIBLE FOR
CC	CELL AGGUTINATION (Endocytin Activity).
CC	-1- CATALYTIC ACTIVITY: Endocytolysis of the N-glycosidic bond at
CC	specific adenosine on the 28S rRNA.
CC	-1- SUBUNIT: disulfide-linked dimer of A and B chains.
CC	-1- PHARMACOKINetics: Due to its immunomodulatory effects it is being
CC	studied in clinical trials in cancer patients as it may slow the
CC	growth of cancer cells and be an effective treatment for solid
CC	-1- MISCELLANEOUS: TWO ISOMERS OF MIA EXIST: GLYCOSYLATED FORM MIAA
CC	AND NON-GLYCOSYLATED FORM MIB.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
CC	TYPE 2 RIP SUPERFAMILY.
CC	PIR: P00018; PD0018.
DR	HSSP; P1140; IABR.
DR	Interpro: IP0001574; RIP.
DR	Pfam: PF00061; RIP; 1.
DR	PRINTS: P000396; SHIGACIN.
DR	PROSITE: PS00025; SHIGA_RICIN; P000396; SHIGACIN.
KY	Plant dnf68002.5, Shiga, Ricin, P000396, SHIGACIN.
FT	ACT SITE 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 9

Query Match	95.7%	Score 1275; DB 1	Length 254;
Best Local Similarity	48.4%	Pred. No. 2,2e-94;	
Matches 250;	Conservative	1; Mismatches	3; Indels 0; Gaps 0;
QY	1	YKRLAVNTVKTQGEFFRFTLLADVNSSGSPNEIPLRGSTTPVSNQSPFLVLETN	60
DB	1	YKRLAVNTVKTQGEFFRFTLLADVNSSGSPNEIPLRGSTTPVSNQSPFLVLETN	60
QY	61	QGSDSLTAIVTNLVEVVAQGDQSYFLRDPGSGEHLFTGTSRSQSPVSGYDLER	120
DB	61	QGSDSLTAIVTNLVEVVAQGDQSYFLRDPGSGEHLFTGTSRSQSPVSGYDLER	120
QY	121	YKGRDQPLDGIDLQSVTALRPFQSGSTRVQASTLLIQMISEARFNPILRACYI	180
DB	121	YKGRDQPLDGIDLQSVTALRPFQSGSTRVQASTLLIQMISEARFNPILRACYI	180
QY	181	NSGASPLFPPVYMLRFTSMQSGTQVQSTGVNNPRLATPQNTLLNNRQVITSL	240
DB	181	NSGASPLFPPVYMLRFTSMQSGTQVQSTGVNNPRLATPQNTLLNNRQVITSL	240
QY	241	ATMLFVQGRSSSS 254	
DB	241	ATMLFVQGRSSSS 254	
RESULT 4			

ID	ABRA	ABRP	STANDARD;	PRT,	528 AA.	
AC	P11140;	P28589;				
DC	01-JUN-1989	(Rel. 11,	Created)			
DT	28-FEB-2003	(Rel. 29,	Last sequence update)			
DR	28-FEB-2003	(Rel. 41,	Last annotation update)			
DS	(RC 3.2.22);	Abria-a B chain)				
OC	Abria presacculus	(Indian bioscience)				
OC	Eukaryotes;	Viridiplantae,	Streptophyta;	Embryophyta;	Tracheophytes;	
OC	Spermatophyta;	Magnoliophyta;	Eudicotyledons;	Core eudicots;	Rosidae;	
OC	eucotids i;	Fabales;	Fabaceae;	Papilionoideae;	Abreae;	Abria.
NCBI_TaxId=3816;						
PN	SEQUENCE FROM N.A.					
PN	MEHLIN=91137296;	P0bwa6=421113;	Lin J.-Y.;			
PN	Primary structure of the catalytic domain of abria-a B chain determined by cDNA sequencing. Conservation and significance."					
PN	J. Mol. Biol.	229:263-267	(1993).			
PN	[2]					
PN	SEQUENCE OF 1-251.					
PN	Tissue=Seed.					
PN	Funatsu G., Taguchi Y., Kameosono M., Yanaka M.,					
PN	"The complete amino acid sequence of the A-chain of abria-a, a toxic protein from the seeds of Abria presacculus."					
PN	J. Biol. Chem.	261:1095-1097	(1986).			
PN	SEQUENCE OF 1-251 FROM N.A.					
PN	Tissue=Leaf.					
PN	MEHLIN=91201329;	P0bwa6=216300;				
PN	Brensen G., Nathiessen A., Sundan A.;					
PN	"Direct molecular cloning and expression of two distinct abria A-chains."					
PN	J. Biol. Chem.	266:6848-6852	(1991).			
PN	SEQUENCE OF 262-528.					
PN	MEHLIN=92372656;	P0bwa6=150574;				
PN	Chen Y.-Y., Chow L.-F., Tsengita A., Lin J.-Y.;					
PN	"The complete primary structure of abria-a B chain."					
PN	FEBS Lett.	309:115-118	(1992).			
PN	[5]					
PN	X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).					
PN	MEHLIN=95331188;	P0bwa6=7608950;				
PN	Tsaiiov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;					
PN	"Crystal structure of abria-a at 2.14 A."					
PN	J. Biol. Chem.	268:353-358	(1993).			
PN	"FUNCTION: THE CHAIN IS RESPONSIBLE FOR INITIATING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. ABRIA-A IS MORE TOXIC THAN RCIN."					
PN	"FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIA TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS."					
PN	"-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one					
PN	"-1- SUBUNIT: DISPERSED, TWO-DOMAIN PROTEIN. EACH DOMAIN					
PN	"-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN					
PN	"CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA)."					
PN	"-1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY."					
PN	"-1- SIMILARITY: Contains 2 rich B-type lectin domains."					
PN	"This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in Grenoble. Bioinformatics Institute. There are no restrictions on its use by anyone. The entry is in the public domain and is available for commercial and non-commercial use. The entry is not removed and for commercial use requires a license agreement. (See http://www.isb-sib.ch/announce/).					
PN	EMBL; M98344;	AAA2624.1;	ALT INT.			
PN	EMBL; X54872;	-;	NOT ANNOTATED. CDS.			

DB 187 PDAMSLNNMNDLSGVQSVQDFFPNO-----VTLLNINIEPVLVLSHPT 236
 QY 237 IASLAINPFCSSPSSSVRYWYVPIVADVTCAS-EPTVIVGNMVCVDRD 236
 DB 237 VAVLALMFLVNP-PNANS---PLILSIYKSKCSSEIPEVIGSDMVCVDYN 232
 QY 296 DFHDKQGLWPSKSNNDPNOLMTIRBGTIRNSGCTITGTAQYVWIPCKYRRE 355
 DB 293 GYHNGRIIMWCKDRLIEMQWLTLSKRTIRSNKCLTTGYAPGSYVWIDCTSNAB 352
 QY 356 XITWQWNGFTIINPRSNIVLAASGIGKTTVTVQVLDYLGQWLAGNDLPAREVTIG 415
 DB 353 ATWELWNGFTIINPRKALVLSASSNGGTLVTVQVEXYLRQWRTNTSPFVTSISG 412
 QY 416 FRLI CSNAGSGQWVETCVSSQGNMAYGSGIRPRKNDQCTCGRDSVTVINIVS 475
 DB 413 YSDLCMQAGSNVWADCDNKGQGMALITDSIHSYVWNNCLSHDKQGSTILLNG 472
 QY 476 CSNAGSGQWVETNEGALINLKNGLANMAYANPELRTIIRPKXKNGML 528
 DB 473 CSNAGSGQWVETNEGALISYLDVWVWVYGSFELQIILMPTGKNGIWL 525

RESULT 5

ABRCABRR STANDARD; FR; 562 AA.

AC P26530
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abirin-c precursor (Contains: Abirin-c A chain (rRNA N-glycosidase)
 DE (EC 3.2.2.22); Abirin-c B chain)
 DE Abirus pectatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eutrosid I; Papales; Fabaceae; Papilionoideae; Abiraceae; Abirus.
 OC NCBI TaxID=3816;
 DX SOURCE FROM N.A.
 RX MEDLINE=91266957; PubMed=2050149;
 RX TISSUE=Leaf;
 RT Wood K.A., Lord J.M., Nawrzymczak B.J., Platak M.,
 RT "Preproabirin: genomic cloning, characterization and the expression of
 RT the A-chain in Escherichia coli.";
 RT Eur. J. Biochem. 198;723-732(1991).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 CC BINDING OF ABIRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one
 CC specific adenosine.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ABPA, BETA, GAMMA).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC use by non-profit institutions, is retained. There are no restrictions on its
 CC modified and this statement is not altered as its content is in no way
 CC entitles requires a license agreement (See <http://www.isb-sib.ch/announcements/>
 CC or send an email to license@sib-sib.ch).

DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00275; SHIGA; RICIN; 1.
 KW plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.
 FT CHAIN 35
 FT REPEAT 35
 FT PREPIDE 286
 FT CHAIN 286
 FT DOMAIN 307
 FT DOMAIN 437
 FT DOMAIN 437
 FT REPEAT 317
 FT REPEAT 360
 FT REPEAT 403
 FT REPEAT 448
 FT REPEAT 487
 FT REPEAT 526
 FT ACETATE 529
 FT ACETATE 529
 FT ACETATE 529
 FT DISULFID 321
 FT DISULFID 321
 FT DISULFID 363
 FT DISULFID 451
 FT DISULFID 490
 FT MOD RES 35
 FT CARBOHYD 234
 FT CARBOHYD 395
 FT CARBOHYD 435
 SQ SEQUENCE 562 AA; 62817 NM; 1PQDA0C7D7BA6278 CRO64;
 Query Match 43.5%; Score 1214.5; DB 1; Length 562;
 Best local similarity 47.8%; Evid. No. 1e-62;
 Matches 250; Conservative 175; Indels 9; Gaps 7;
 QY 9 TQTTGGSEYPPFTLLRNPVYSSGNSSEIPLRQSTIPVSDAGPFLVETLNCQGSITR 68
 DB 43 TGAATSGYKQPIELRQRL-TGLIHIDPVLDPPT-TVEENRIVTELNSRESIEV 100
 QY 69 AIDVNLVYVQADQSYLSDAPRQAEHLFTGTTRSSLPFNGSPDLRYAAG-RDQ 127
 DB 101 GIDVNAVYVYVQASQSYLSDAPASATYLPFGTQVYSLRFDQSDGLRYAAGTKE 160
 QY 128 IRLGIDLOSATNALRFGQSTRTQASILLIQLTASARNPILMRQVINSQASFL 187
 DB 161 IRLGIDLOSATNALRFGQSTRTQASILLIQLTASARNPILMRQVINSQASFL 220
 QY 188 PPTVWLEETSGQSGTQVQSGTQVQV-NRPIALRPPQPTLNNRDVYASALMLFY 246
 DB 221 PPTVWLEETSGQSGTQVQSGTQVQV-NRPIALRPPQPTLNNRDVYASALMLFY 280
 QY 247 CSEPRSSDYVWYVPIVPIVADVTCAS-EPTVIVGNMVCVDRDFFDNGQICL 305
 DB 281 CVP-PNANS---PLILSIYKSKCSSEIPEVIGSDMVCVDYDNGKRLA 336
 QY 306 KRSKSNNDPNOLMTIRBGTIRNSGCTITGTAQYVWIPCKYRRE 365
 DB 337 WCKDRIENQWLTLSKRTIRSNKCLTTGYAPGSYVWIDCTSNAB 396
 QY 366 TTPNRNIVLAASGIGKTTVTVQVLDYLGQWLAGNDLPAREVTIG 425
 DB 397 TTPNRNIVLAASGIGKTTVTVQVLDYLGQWLAGNDLPAREVTIG 456
 QY 426 GSVWETCVSSQGNMAYGSGIRPRKNDQCTCGRDSVTVINIVS 485
 DB 457 SHVWADCDNKGQGMALITDSIHSYVWNNCLSHDKQGSTILLNG 516
 QY 486 VFTWELWNGFTIINPRKALVLSASSNGGTLVTVQVEXYLRQWRTNTSPFVTSISG 528
 DB 517 LFKDSDSYNLHDDVWVWVYGSFELQIILMPTGKNGIWL 559

RESULT 6
ABR1 ABR1R STANDARD; PRT; 527 AA.
ID ABR1 ABR1R STANDARD; PRT; 527 AA.
AC 006077; P81374; (Rel. 37, Created)
AD 006077; P81374; (Rel. 37, Last sequence update)
AE 006077; P81374; (Rel. 37, Last sequence update)
AF 15-DEC-1998 (Rel. 37, Last sequence update)
AG 28-FEB-2003 (Rel. 41, Last sequence update)
AH ABR1-b precursor [Contains: ABR1-b A chain (rRNA N-glycosidase)]
AI (EC 3.2.2.22) [ABR1-b B chain] (rRNA N-glycosidase)
AJ ABR1 precacortus (Indian licoice) (Crab's eye).
AK Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AL Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
AM eucoside 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
AN NCBI_TaxID=3816;
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Query Match 42.9% Score 1197.08 Length 527
Best local similarity 47.2% E-value 1.7e-168
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9 THGTGCEFRFTILRBYSSSSSEPLRQSTIVDAQRFVLEINQGGCSTIA 68
9 TEGATSSQKQFIALRQLTGLIHGIPVLPDTFLDERRTIVELSSSTESIA 66
69 AIDVNLVYVAYQAGDQSYLADARQATHLFVGTSSLPNGSPDLERYAGH-RDQ 127
67 GIDVNNVYVAYRAGRSYFLADATASRYLFTVQGYLAPNGSYTDLERLQRTQ 126
128 IFPGIDGLQSYTLAPFGSSTRTQASLITLIMSSAARPLTMRAYINSGASF 187
127 IFGLQLHNAHSLDQSGTDQDGIATLIVIGMSSAARVPSIRVGSINTVMAQ 185
188 PTVVLELSTWQGGQSTOVGSHSDVNNPRLAIPGNFVLTVL-RVVISALMTFV 246
186 PDAIIMLENNWDLSSGVQGSQDTFPAVATLSSNQGVYDLSLRQSVAVLMTFV 245
247 QGSRSSSVRYWELVIRPVADVTGNS-LPTVAVIRGNQGVYDDPDHGNQQL 305
246 GNP-FNNQSS--FLIRHSVSKSCSRIBPVLGIRGNQGVYDDGHNHNRITA 301
302 WKCKRLRNNQWTLKSKIRBNKCLTTRSVAPRNVVITGSAVAVLMTFV 361
366 TIINRANVLAASGIGITLVLTGAGQWLAGNDARREVTIVGPDICMESNG 455
362 TIINKALVLAASSWGGLTVVTEVIRQWNTNTSPFTISIGSYDLCMAQ 421
426 GSWVTCVSSQGNQALVGSIRFKNQDQCTTCRDSVTVINVSAGSSGGR 485
422 SNVLAACNNKGGQMLTIDSSKSHSVQNNRNLDSKRGQSSVLAACNNASQ 481
486 VFNKALINKNGLANDVQANPRTIIPVAGNOML 528
482 LFNQGSINLHDMVQVRSRPLKELIHPHKKKNQ 524

[illegible]

OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 NCBI_TaxId=4202;
 RA SEQUENCE FROM N.A.
 RC TISSUE=Barb.
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouse P., Van Leuven F., Pennaer K.J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
 from the bark of elderberry (Sambucus nigra).";
 RT Eur. J. Biochem. 237:505-513 (1996).
 RN
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Barb.
 RX MEDLINE=94003077; PubMed=8400135;
 RA Gidycz T., Clotier L., Ferreira J.M., Rojo M.A., Iglesias R.,
 RC "Isolation and characterization of a non-toxic
 RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
 nigra L."; Biol. 22:1181-1186 (1993).
 CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
 CC PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
 CC SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
 CC RIBOSOMES.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC or send a request to license@isb.slb.ch).
 CC -----
 DR EMBL: U01299; AB339475.1; -;
 DR F01; S37382; S37382.
 DR InterPro: IPR000772; Ricin_B_Lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PRO036; SHIGARICIN.
 DR PROSITE: PS0051; RICIN_2.
 DR PROSITE: PS0023; RICIN_1.
 DR PROSITE: PS0023; RICIN_2.
 KW Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 297 NIGRIN B A CHAIN.
 FT CHAIN 298 563 NIGRIN B B CHAIN.
 FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 434 559 RICIN B-TYPE LECTIN 2.
 FT REPEAT 316 356 1-ALPHA.
 FT REPEAT 357 397 1-BETA.
 FT REPEAT 400 432 1-GAMMA.
 FT REPEAT 433 465 2-BETA.
 FT REPEAT 466 524 2-GAMMA.
 FT REPEAT 527 554 2-ALPHA.
 FT ACT SITE 188 188 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 274 302 BY SIMILARITY.
 FT DISULFID 319 338 BY SIMILARITY.
 FT DISULFID 360 377 BY SIMILARITY.
 FT DISULFID 448 463 BY SIMILARITY.
 FT DISULFID 489 506 BY SIMILARITY.

FT CARBOHYD 221 221 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC...) (POTENTIAL).
 FT COMPLET 39 39 K -> V (IN REF. 2).
 SO SEQUENCE 563 AA; 62300 MW; F250C6E4621B8714 CRCS4;
 Query Match 32.1%; Score 895.5; DB 1; Length 563;
 Best Local Similarity 38.7%; Pred. No 1,1e-83;
 Matches 203; Conservative 95; Mismatches 205; Indels 21; Gaps 13;
 QY 17 YFFETLLADVYSSGSGFS-NRIFLRQSTIPYSDAQRFLVELTMOGDSITPAIDVTNL 75
 DB 43 YRDFPLSLKRTVANGTYEVMNLPVLRER-S-EVQKSRFLVPLTVANGNTVLAVDVNL 101
 QY 76 YVVAQAGQGSYFLRDPAGAEHLFTGTRRSIPFNGSYPOLRERVAG-HRDOIPLGIDQ 134
 DB 102 YVVAFSANASIFPKATEVQKSNLFVGRKQNTSTNTDNLTAANRRRSIELGSP 161
 QY 135 LIQSTLAPRGSTQTSGLIIILQMSSEARPLPRAQYINSASFLPYDYLME 194
 DB 162 LOCALITL-VHSDV--ASLIVQMSSEARPLYEGQVRRLQASSTPLNAMS 217
 QY 195 LETSGQGGQGYOYHSTGTV--FRRFIRLAIIPRQVPTLVNRPV--IASALMFQGR 280
 DB 218 MERNMSMELRTOAGNVSPFFGVOLANDHRLVDNFEELKITGIALIFRCSS- 276
 QY 251 PSSSDVYWFPLVR--PVADPYTCSASEPLVA-IVRNQKCVYVDQPFQDQOYLW 306
 DB 277 FSNDAIRNFDLADGDKRNDDECTLTSTFNTVARDLCLVYVNGYDSTPLQLM 336
 QY 307 PYSKNQPNQALMTYRQCTTRSGSCCTTGTACTGYMIFDQNTVRENTVQINGKT 366
 DB 337 FQSTGR-NQRTDSDDTLRSGKCTNANGNSNIVIFNSTRMNRNIMVYIDSS 394
 QY 367 INPSPSLVLAASGKGTITVQTLVTLGGKAGNDAPRSEITYGRRLCMNSG- 425
 DB 395 INPSPSLVLAASGKGTITVQTLVTLGGKAGNDAPRSEITYGRRLCMNSG- 454
 QY 426 -GSVAVETCVSSQONQRYALVPGSGIPKQNDQCLTCSDSVSTVINIVSCNAGSGQR 484
 DB 455 NNSVMEDECEMTSLQCGMALVGRITVNSVTRGLCVTNGYSKDLIIILKQ- 513
 QY 485 WYRTGRTATILNKGADVQAQNAKRLITLNGRPNQML 538
 DB 514 WPNSDDAIVNPKRHVYDPRASVNSLFEIILPAPGNQCMV 557
 RESULT 9
 ID RI22 BRVDI STANDARD; PRT; 282 AA.
 AC P98184; Q98810; 16-OCT-2001 (Rel. 40; Created).
 DT 16-OCT-2001 (Rel. 40; Last annotation update).
 DE R8-188-2003 (Rel. 41; Last annotation update).
 DE R8-188-2003 (Rel. 41; Last annotation update).
 DE Glycosidase (EC 3.2.2.22).
 OS Bryonia dioica (Red bryonia) (B2).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids I; Cucurbitales; Cucurbitaceae; Bryonia.
 OC NCBI_TaxId=3652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slegall C.B., Gawlak S.L., Margardt H.;
 RT Bryonia dioica 2, a ribosome-inactivating protein isolated from the plant
 RL Patient number UB5597569, 28-JAN-1997.
 RP SEQUENCE OF 22-42.
 RC TISSUE=Root;
 RX MEDLINE=951812; PubMed=7849072;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Nudicaulales; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBL_TaxID=50544;
 RN 111 Trichosanthes anguina.
 RP SEQUENCE FROM N.A. PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=cy. Anguina; TISSUE=seed.
 RX MEDLINE=99132006; PubMed=991318.
 RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
 Lin J.-Y.;
 RA "Purification, characterization and molecular cloning of trichosanthin,
 RT a novel type I ribosome-inactivating protein from the seeds of
 RT Trichosanthes anguina."
 RL Biochem. J. 338:211-219(1999).
 RN 120
 RP SOURCE OF 20-264.
 RC TISSUE=seed.
 RA Chow L.-P., Kano M., Lin J.-Y., Wang S.-H., Tang Y., Tang J.A.;
 RT "Amino acid sequence of trichosanthin, a ribosomal-inactivating
 RT protein from Trichosanthes anguina seeds."
 RL J. Biomed. Sci. 3:178-186(1996).
 CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN
 CC RIBOSOMES.
 CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC -1- TYPE 1 RIP SUBFAMILY.
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 CC EMBL; AF055086; AF026681; -.
 DR HSSP; F93185; 1SERV.
 DR PIRAT; P00156; RIF.
 DR PRINTS; P00156; RIF.
 DR PROSITE; P00025; SHIGA_RICIN.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 264
 FT PROPEP 265 294
 FT ACT_SITE 177 177
 FT ACT_SITE 180 180
 FT CARBOHYD 220 220
 FT CONFLICT 51 51
 FT CONFLICT 65 65
 FT CONFLICT 84 84
 FT CONFLICT 152 152
 FT CONFLICT 174 174
 FT CONFLICT 245 245
 SQ SEQUENCE 294 AA; 32234 MW; DA4F8B7CE3290994 CRC64;
 Query Match 11.7%; Score 327.5; DB 1; Length 234;
 Blast local 34.0%; Freq. No. 8e-19;
 Matches 85; Conservative 47; Mismatches 105; Indels 13; Gaps 6;
 Oy 13 TGEYFRITLADYVSGSSNDEIPILQSTIPVAGQRYVLEHMGQSGSTLADIV 72
 Db 29 TKKSYSTIOLRDALDTGIVGCIPLPST--ASQSQWRPFPNLTIVYDSTITVAVAV 85
 Oy 73 TMLVYVAYAGDQSYFLNDAPRGATHLFTGTTSSSLPENGQVYDLEKRYG-HEDQIPLG 131
 Db 86 TMYIVAFRADAVSYFEDFTAFKFLFAGRTKTKLPFSQNDYKLSQVVGQSRMIEIG 145
 Oy 132 IDQLQSYVTLAPRGSTTQANSILLIOMISAKARFPIIWRNQTINSQASFLPDVY 191
 Db 146 IPLASSLITNNVY--YDQSTALALLVLQCTAARAKRYIEQVSSHLSS--NFPVQA 201
 Oy 192 MLELTSGQSQSTQVQ--HSTQGVFNRPRIAPGQVFTLVNVD--VIASLAIMLFV 246
 Db 202 VISLNNWALSKQIDIMNRTHQGFENHVELNFDGFRSTVNTSAGVYKNTKILLIV 261
 Oy 247 CGERSSSPY 256
 Db 262 KASVGSFYDI 271
 RESULT 12
 RIPT_TRIXI STANDARD; PRT; 289 AA.
 AC P09589;
 DT 01-MAR-1989 (rel. 10; Created)
 DI 12-SEP-1990 (rel. 16; Last sequence update)
 DE 12-SEP-2003 (rel. 42; Last annotation update)
 DE R1387-2003 (rel. 14; Last annotation update)
 DE (rRNA N-glycosylase) EC 3.2.2.22 (Alpha-D-glucosylase)
 DE Trichosanthes kirilowii (Mongolian snake-gourd).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBL_TaxID=5677;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RX MEDLINE=91153657; PubMed=1899291;
 RA Shaw P.C., Hung R.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RT "Cloning of trichosanthin cDNA and its expression in Escherichia
 RT coli."
 RL Gene 97:267-272(1992).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RX MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Pataek M.;
 RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RT type I ribosome-inactivating protein."
 RL J. Biol. Chem. 265:8670-8674(1990).
 RN 122
 RP SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz; TISSUE=Rubrous root;
 RX MEDLINE=90256789; PubMed=2341399;
 RA Collins R.D., Robertus J.D., Iopresti M., Stone K.L., Williams K.R.,
 Wu P., Huang K., Pataek M.;
 RT "Primary amino acid sequence of alpha-trichosanthin and molecular
 RT models for abrin A-chain and alpha-trichosanthin."
 RL J. Biol. Chem. 265:8665-8669(1990).
 RN 144
 RP SEQUENCE OF 24-270.
 RC STRAIN=Rubrous root;
 RX MEDLINE=9334383; PubMed=13070.
 RA Tian G.Y., Ni C.Z., Gu Z.M., Jin S.W., Zhang L.Q., Xia Z.X.,
 RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
 RT application."
 RL Pure Appl. Chem. 58:789-798(1996).
 RN 151
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen W., Lin Y., Pan K.;
 RT "Structure of trichosanthin at 1.88-A resolution."
 RL Proteins 19:4-15(1994).
 RN 152
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=9534383;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RT deactivating mechanism of two ribosome-inactivating proteins."
 RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS

CC	CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
CC	INACTIVATES ENKAYOTIC 60S RIBOSOMAL SUBUNITN.
CC	-1. CATALYTIC ACTIVITY: Phosphorylase of the N-glycosidic bond at one
CC	specific adenosine on the 28S rRNA.
CC	-1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC	-1. RIB. SUBFAMILY.
CC	
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CC	between the Swiss Institute of Bioinformatics and the EMBL consortium
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by aid for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcements
CC	or send an email to license@isb-sib.ch).
DR	BEMBL; M34895; KABA3207.1; -
DR	BEMBL; M34895; KABA3206.1; -
DR	PDB; 1MRJ; 07-FEB-95.
DR	PDB; 1MRX; 07-FEB-95.
DR	PDB; 1YCS; 10-JUL-95.
DR	PDB; 1I4G; 28-JAN-03.
DR	PDB; 1MLI; 21-JAN-03.
DR	PDB; 1OD2; 24-APR-00.
DR	InterPro; IPR001574; R.PP.
DR	Fam: PF00161; RLP.1.
DR	PROSITE; PR00025; SHAGRICIN_1.
DR	PROSITE; PR00025; SHAGRICIN_1.
KW	Plant defense; Antiviral; protein synthesis inhibitor; Hydrolase;
KW	Toxin; Signal; 3D-structure.
FT	SIGNAL 1 23
FT	CHAIN 24 270
FT	PT
FT	PROPER 271 289
FT	ACT SITE 183 183
FT	CONFLECT 57 60
FT	CONFLECT 87 87
FT	CONFLECT 92 92
FT	CONFLECT 143 144
FT	CONFLECT 136 136
FT	CONFLECT 215 216
FT	CONFLECT 231 231
FT	CONFLECT 234 234
FT	CONFLECT 246 266
FT	CONFLECT 247 247
FT	STRAND 25 28
FT	HELIK 34 46
FT	TURND 47 47
FT	STRAND 50 53
FT	TURND 55 56
FT	STRAND 57 60
FT	HELIK 66 69
FT	TURND 70 76
FT	STRAND 78 79
FT	HELIK 82 88
FT	TURND 92 93
FT	STRAND 100 101
FT	TURND 102 105
FT	HELIK 109 114
FT	TURND 115 117
FT	TURND 120 121
FT	STRAND 124 127
FT	HELIK 134 141
FT	TURND 142 142
FT	HELIK 142 142
FT	STRAND 150 150
FT	HELIK 152 153
FT	TURND 164 165
FT	HELIK 167 180
FT	TURND 181 181
FT	TURND
FT	RIBOSOME-INACTIVATING PROTEIN ALPHA-RICHOSANTHIN. MISSING IN MATURE PROTEIN. BY SIMILARITY. LEU1->DELT (IN REF. 4). MISSING (IN REF. 4). V->YUNGPENNAV (IN REF. 4). KI->GL (IN REF. 4). K->S (IN REF. 4). WS->LML (IN REF. 4). Q->T (IN REF. 4). S->T (IN REF. 2). MISSING (IN REF. 4). T->M (IN REF. 2).

	FT	HELIX	182	187	186
	FT	STRAND	187	187	
	FT	HELIX	188	195	
	FT	TURN	196	196	
	FT	STRAND	202	202	
	FT	HELIX	206	226	
	FT	TURN	227	230	
	FT	STRAND	231	243	
	FT	TURN	241	243	
	FT	STRAND	245	250	
	FT	TURN	251	252	
	FT	HELIX	254	258	
	FT	TURN	259	259	
	FT	STRAND	260	260	
	FT	STRAND	263	263	
	FT	TURN	268	268	
SC	SEQUENCE	289 AA; 31676 MW; 5CE03B5630575B93 C6C64;			
Query Match	Similarity	11.7%; Score 326; DB.1: Length 289;			
Matches	86; Conservative	36.0%; Pct. Matches 8; 85; Indels 14; Gaps 9;			
QY	13	TGEYRPFITLLRQVYSSGSFSENEPIPLTOSTIPVSDXQKFFVLVETLNGGDSSTFALDV 72			
Db	33	TSSSYGVFTSLRKLAPRERKDYDPLR-SGLPGS-QGVALHILTYAERITSVAILDV 85			
QY	73	TNDVYVQADQDSYFLSDA-PRQATHLRFGTTRS-SLEFNGSYDLSRYAHG-RDQIP 129			
Db	90	KNVITLQSGVATGSRITPRHSAIKATKAYVEFGMAKQVTLFISQNIETDQYKNSHLP 149			
QY	130	LIGDPLDQSGVATLPRFGDSRFRQASLILLCWISPAFAENILMLRQVYNSGASFLPD 189			
Db	150	LIGPLDLSATLITFLFY--VYNAASAPALMWLIGSTSSAPAKYKEQIGKRVDK--TFIIS 205			
QY	150	VYVMEELTNSQSGSTVQ--HSTGVQNNPRLALPQNSVTLNVRD--VISALAIWL 244			
Db	206	LALISLWSNALSRLQIDSLTNSQSFSEVVLINAOHETVTLNDAQVTSNIALLL 264			
RESULT 13					
RIPS	TRIXI	STANDARD; PRT; 289 AA.			
ID	RIPS	TRIXI			
AC	P24478;				
DT	01-MAR-1992 (Rel. 21, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Ribosome-inactivating protein Katsururin precursor (cRNA				
DE	N-glycosylase) (EC 3.2.2.22)				
DE	Trichosanthes kirilowii (Mongolian snake-gourd)				
CC	Trichosanthes kirilowii (Mongolian snake-gourd); Trichocarpus				
CC	Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots; Rosidae;				
CC	eucnids I; Cucurbitales; Cucurbitaceae; Trichosanthes.				
OX	NCBI Taxid:3677;				
NP	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Root tuber;				
RC	MEDLINE=97356562; PubMed=9212998;				
RA	Miyakami H., Iida K., Kondo T., Ogihara Y.;				
RA	Cloning and bacterial expression of a gene encoding ribosome-				
RA	inactivating protein Katsururin-R and Katsururin-C, from Trichosanthes				
PT	kitilowii.				
PT	Biol. Pharm. Bull. 20:711-713(1997).				
RN	[2]				
RN	SEQUENCE OF 24-270.				
RA	MEDLINE=92005921; PubMed=1514009;				
RA	Toyokawa S., Takeeda T., Kato Y., Wakabayashi K., Ogihara Y.;				
RT	The complete amino acid sequence of an abortifacient protein,				
RT	Katsururin." Bull. 39:1244-1249(1991)				
NC	Chem. Pharm. Bull. 39:1244-1249(1991)				
NC	-1- O-GLYCOSYLATION-INDUCING PROTEIN, IT INACTIVATES EUKARYOTIC				
NC	80S RIBOSOMES BY HYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE				
NC	-1- CATALYTIC ACTIVE SITE.				
NC	specific adenosine on the 28S rRNA				

```
CC ----- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: AB000666; BAA1786.1;
CC PIR: JCS606; JCS606.
CC PIR: J00393; J00393.
CC HSP: P09989; 1MRJ.
CC InterPro: IP001574; RIP.
CC Pfam: PF00161; RIP; 1.
CC PRINTS: PR00366; SHIGARICIN.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC Toxin; Signal.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 270 KARASORIN-C.
CC PROPEP 271 289 REMOVED IN MATURE FORM.
CC ACT SITE 183 BY SIMILARITY.
CC SEQUENCE 289 AA; 31704 MW; 88303E324287B26 CRC64;
SQ
Query Match 11.6%; Score 325; DB 1; Length 289;
Best Local Similarity 36.8%; Pred. No. 1.2e-18;
Matches 88; Conservative 50; Mismatches 87; Indels 14; Gaps 9;
QY 13 TGEYFRTLLRDYSSGSFNEIFLRSGTIVSDQRFVYELTNGGDSITAAIDYV 72
Db 33 TSSGVFISNKKALPKRKMDIFLR-STLPS-QRYLTHIMVDETSVAVIV 89
QY 73 TELYVAYQAGDSYFLDA-PRGAEYHLPFGTTRS-SLPFGSYDLEARYAH-RQIP 129
Db 90 TNYVYGRADGTYFNEKSTAKVYFDKAKRYLPGSGYERQIADAKRENIIP 149
QY 130 LGIDQLGSVTLRPPGSTRQARISILLIQISEARNEFLIMARQYNSGSELPD 189
Db 150 LQPLADSNITLIF--YNNANASALMAYLQSTSEAKRTKIQSGSRVDA--TFLS 205
QY 190 VYMLLETSMGQGSTVQ--HSTDGVPNNRILAPPCNPFVLTNVDVATSLATMEV 244
Db 206 LAISLENSWALSNOQIATNGQETVVLINQSGVITINVDAGVTSNTALL 264
RESULT 14
ID RIP_CUCFI STANDARD; PRT; 286 AA.
AC Q9FEK4; 2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Cucumis figareli.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=131071;
RN 11
RS SEQUENCE FROM N.A.
RA Noland P.A., Garrison D.A., Beller M.;
RT Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareli."
RL Plant Biotechnol. 17:337-340(2000)
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
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CC ----- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch)
CC
CC EMBL: AB045560; BAB19677.1;
CC HSP: P16094; 1AHG.
CC InterPro: IP001574; RIP.
CC Pfam: PF00161; RIP; 1.
CC PRINTS: PR00366; SHIGARICIN.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC Toxin; Signal.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
CC ACT SITE 185 185 BY SIMILARITY.
CC CARBOHYD 183 183 N-LINKED (GLYCAN. . .) (POTENTIAL).
CC CARBOHYD 252 252 N-LINKED (GLYCAN. . .) (POTENTIAL).
CC SEQUENCE 286 AA; 31771 MW; 4ERD966E804DA1 CRC64;
SQ
Query Match 11.1%; Score 310.5; DB 1; Length 286;
Best Local Similarity 32.8%; Pred. No. 1.7e-17;
Matches 78; Conservative 53; Mismatches 93; Indels 13; Gaps 7;
QY 15 EYEFRTLLRDYSSGSFNEIFLRSGTIVSDQRFVYELTNGGDSITAAIDYV 74
Db 38 KSYKFRITKRNALPAGDITNIPILVPS--ISGSRITLMQLSNYSNTYAAVDVN 94
QY 75 LLYVYAYQAGDSYFLDA-PRGAEYHLPFGTTRS-PLPGSYDLEARYA-GRQIPICAI 132
Db 99 VYIMGVYNGTSTYFNEFDQALSKTFVQGTSTLTPVSGNQCKQSYAKRKRISIPICF 154
QY 133 LGIDQLGSVTLRPPGSTRQARISILLIQISEARNEFLIMARQYNSGSELPD 191
Db 155 MALDASISITLYY--YNSRANAFIVLQYTFEAKRXYI---EKQIIDISGVSDIA 209
QY 192 MLELETSMGQGSTVQ--HSTDGVPNNRILAPPCNPFVLTNVDVATSLATMEV 246
Db 210 ALSELENSWALSNOQIATNGQETVVLINQSGVITINVDAGVTSNTALL 266
RESULT 15
ID RIP_GELMU STANDARD; PRT; 316 AA.
AC P33186;
DT 01-OCT-1993 (Rel. 27, Created)
DR 01-NOV-1995 (Rel. 32, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gelatinase-inactivating protein gelonin precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Gel.
OS Gelidium multiseptum (Euphorbiaceae himalayae)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Gelonium.
OX NCBI_TaxID=3979;
RN 11
RS SEQUENCE FROM N.A.
RA Noland P.A., Garrison D.A., Beller M.;
RA Noland P.A., Garrison D.A., Beller M.;
RT Cloning and expression of a gene encoding gelonin, a ribosome-
RT inactivating protein from Gelonium multiseptum."
RL Gene 134:223-227(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC Montecuch P.C., Lazzerini A.M., Barbieri L., Stripe F., Sorla M.,
```

Rt	Lapdi D.
Ft	"N-terminal sequence of some ribosome-inactivating proteins."
Db	Int. J. Pept. Protein Res. 33:263-267(1989).
Nl	[3]
Rn	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
Rx	MEDLINE=95331189; PUBMED=7608981;
Rk	Hosur M.V., Nair B., Sankaranarayanan P., Misrauth S., Surolia A.,
Rt	"X-ray structure of gelatin at 1.8-A resolution."
Rf	J. Mol. Biol. 250:166-180(1995).
Rc	-1. CARBOLYTIC ACTIVITY: Endoglycosylase of the N-glycosidic bond at one specific adenine on the 28S rRNA.
Cc	-1. SUBUNIT: Homodimer.
Cc	-1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
Cc	TYPE I RIP SUBFAMILY.
Cc	-----
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Cc	cc send an email to licenses@sib-sb.ch)
Dr	PHE1, L12243; AAA6332.1; "
Dr	EPR; J07053; J07053.
Dr	HSPD; P09989; IMRI.
Dr	InterPro; IPRO01574; RIP.
Dr	Ffam; PF00161; RIP_1.
Dr	PRINTS; PR003366; SHGACITCN.
Dr	PROSITE; PS00275; SHIG_RICIN; FALSE NEG.
Km	plant defense, protein synthesis inhibitor, Hydrolase; Toxin; Signal;
Km	Signal peptide, Protein
Ft	STRIP
Ft	PROPEP 1 27 46 POTENTIAL.
Ft	CHAIN 27 46
Ft	PROPEP 47 297
Ft	PROPEP 298 316
Ft	DISULFID 90 96
Ft	CARBOHYD 235 235
Ft	ACT SITE 212 212
Ft	COMFLICT 90 90 C -> K (IN REF. 2).
Ft	COMFLICT 93 93 P -> D (IN REF. 2).
SQ	SEQUENCE 316 AA; 1252367BT0901885 CRC64;
Query Match	
Best Local	Similarity 10.2%; Score 305.5; DB 1; Length 316;
Matches	89; Conservative 37; Mismatches 109; Indels 21; Gaps 5;
Qy	9 THQTGGEEFFRTLLRLPYVSGSSGSNE-----IFLRQSTIRPSDAKREVL 55
Db	42 TSKTGIDGVTSFKATGYIYVLENRKYALKPGNSHGPIFLRKCC--DPGRKCVL 99
Qy	56 VELTKVGCGSIATIAIVTNLYVAQAQGQSFTAFARAGAEHFLFGTTASISLPENASY 115
Db	100 VALSDNDGQLAETADIVSYVYGQVQRNRSFPFKAADAAVEGSLFNKIKTRLFQGSY 159
Qy	116 POLERVAGHRDQPLAQIDCL---IQSVTLAPPGSSTFOARSJILLIOMISRAEAFNY 172
Db	150 FLSBHQKAKRTDLDEIEAIGDKLDKNDAIYNCFETIASLVLTQWSEKAAPFI 219
Qy	173 LWRAEQVINGSAKTDIVYLMEFSNGSCDYCHS--TGGPRNNPKRALPGNTVLT 231
Db	220 ENQIIRN--NFQGRLEPAWNITSLENKGKGLSFQIFRASNQMFSEVATELBABKKTYVI 277
Qy	232 NWVDVYSIALINEPV 246
Db	278 ADVQVKETALKKEV 292

Matches 522; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 60
1 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 60

Db 61 QGGDSITAIADIVTNLYVAOAGDSYFLRDAPEGATHLFTCTRSSLPENSGYDPLER 120
61 QGGDSITAIADIVTNLYVAOAGDSYFLRDAPEGATHLFTCTRSSLPENSGYDPLER 120

QY 121 YAGRDQIPLEGIDQLQSVTALRFGSGTRTQASILLIQMISEARPNPILRARQYI 180
121 YAGRDQIPLEGIDQLQSVTALRFGSGTRTQASILLIQMISEARPNPILRARQYI 180

QY 181 NSGASFLPDVYMLETSWGQOSTVQASHSDGVNNPRLAIPGNFVTLTNRVIASL 240
181 NSGASFLPDVYMLETSWGQOSTVQASHSDGVNNPRLAIPGNFVTLTNRVIASL 240

QY 241 AMLFVCGERSSSDVRYMPLVRADVTCASSEPVRVLRKQKQCVADVDHFG 300
241 AMLFVCGERSSSDVRYMPLVRADVTCASSEPVRVLRKQKQCVADVDHFG 300

QY 301 NQIQAPSKSNNDPQATLTKEGDTIRNSGCLTGYGTAGYVMIPOCNAREATNG 360
301 NQIQAPSKSNNDPQATLTKEGDTIRNSGCLTGYGTAGYVMIPOCNAREATNG 360

QY 361 IWNGTIIIPRSNLVLAASGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFPLC 420
361 IWNGTIIIPRSNLVLAASGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFPLC 420

QY 421 MESNGSVWVETCSGQONRVALYGDGSIHPQKQNDQCLTGGDSVSTVINIVSGNS 480
421 MESNGSVWVETCSGQONRVALYGDGSIHPQKQNDQCLTGGDSVSTVINIVSGNS 480

QY 481 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531
481 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531

Db 531 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531

RESULT 2

Q8W243 PRELIMINARY; PRT; 565 AA.

ID Q8W243
AC 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=15976;
RN [1]
RP SEQUENCE FROM N.A.
RA Fark N.-B., Liu S.;
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe).";
RT B. (2002) Cloning of Viscum album subsp. coloratum (Korean mistletoe).
CC -1- CATALYTIC ACTIVITY: ENDOPOLYASIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF69961; ALA0417.1; -
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00161; RLP; 1.
DR PROSITE; PS50331; RICHIN_B_LECTIN; 2.
DR PROSITE; PS50331; RICHIN_B_LECTIN; 2.
FT CHAIN 23 273 POTENTIAL.
FT CHAIN 309 565 VCA ALPHA CHAIN.
SQ SEQUENCE 565 AA; 62401 MW; 991E3994DA005F11 CRC64;

Query Match 85.7%; Score 2392.5; DB 10; Length 565;
Rest Local Similarity 85.6%; Pred. No. 9.3e-190;
Matches 459; Conservative 27; Mismatches 41; Indels 9; Gaps 2;

QY 1 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 60
1 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 60

Db 34 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 93
34 YERLRLATVHTQTGEYFRFTLLADYVSAGSFENRIPILROSTIPVSDAORFVLVELTN 93

QY 61 QGGDSITAIADIVTNLYVAOAGDSYFLRDAPEGATHLFTCTRSSLPENSGYDPLER 120
61 QGGDSITAIADIVTNLYVAOAGDSYFLRDAPEGATHLFTCTRSSLPENSGYDPLER 120

QY 121 YAGRDQIPLEGIDQLQSVTALRFGSGTRTQASILLIQMISEARPNPILRARQYI 180
121 YAGRDQIPLEGIDQLQSVTALRFGSGTRTQASILLIQMISEARPNPILRARQYI 180

QY 181 NSGASFLPDVYMLETSWGQOSTVQASHSDGVNNPRLAIPGNFVTLTNRVIASL 240
181 NSGASFLPDVYMLETSWGQOSTVQASHSDGVNNPRLAIPGNFVTLTNRVIASL 240

QY 241 AMLFVCGERSSSDVRYMPLVRADVTCASSEPVRVLRKQKQCVADVDHFG 300
241 AMLFVCGERSSSDVRYMPLVRADVTCASSEPVRVLRKQKQCVADVDHFG 300

QY 301 NQIQAPSKSNNDPQATLTKEGDTIRNSGCLTGYGTAGYVMIPOCNAREATNG 360
301 NQIQAPSKSNNDPQATLTKEGDTIRNSGCLTGYGTAGYVMIPOCNAREATNG 360

QY 361 IWNGTIIIPRSNLVLAASGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFPLC 420
361 IWNGTIIIPRSNLVLAASGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFPLC 420

QY 421 MESNGSVWVETCSGQONRVALYGDGSIHPQKQNDQCLTGGDSVSTVINIVSGNS 480
421 MESNGSVWVETCSGQONRVALYGDGSIHPQKQNDQCLTGGDSVSTVINIVSGNS 480

QY 481 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531
481 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531

Db 531 SCGRVYVTEGATILNKGADVYKSNRKLRIIIPATGKPNQMLFVP 531

RESULT 3

Q8W243 PRELIMINARY; PRT; 560 AA.

ID Q8W243
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Type 2 ribosome-inactivating protein cinnamomin III precursor
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Cinnamomum camphora (Camphor tree).
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Q., Gong Z.Z., Liu X.Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns.";
CC Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOPOLYASIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF039803; AA82460.1; -
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00161; RLP; 1.
DR PROSITE; PS50331; RICHIN_B_LECTIN; 2.
DR PROSITE; PS50331; RICHIN_B_LECTIN; 2.

KW Hydrolase; Signal; Toxin. POTENTIAL.
 FT SIGNAL 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CHAIN 33 580 CINNAMOMIN II
 SQ SEQUENCE 580 AA; 64421 MW; 940010P01E7P558 CRG64;
 Query Match 48.8%; Score 1361; DB 10; Length 580;
 Best Local Similarity 53.0%; Pred No. 3.5e-104;
 Matches 287; Conservative 76; Mismatches 157; Indels 22; Gaps 11;

QY 9 TQCTGEYPRFTLLADYVSSGSFNEIPLAQ-STIPVSDAQRVAVELTNGQGS-I 66
 DB 40 TKNATKSTYOTFIALRQALASGEHPGIPVMEKSTVP--DSKRTIVELSNMADSPV 97
 QY 67 TAAIDVTMLVYVAYQAGDSYFLR-DAFQAGATHLFTGTSSSLPTNGSYPLERYAG-H 124
 DB 98 TLAVDVYNAIVAYVAYRGSSEFLRQEDNDPDALENLPDTRKATFFPSGSYTLDERVAGER 157
 QY 125 RDOIPLGIDLOISYVTLARFG-GSTRTOAKSLILLOISSEARFPLMAQYING 183
 DB 158 REEILGNDPLENRLISLMTSNLQOALASLIYQWAAVAFRFPIRYVESITRA 217
 QY 184 ASFLPDVYMLETSMQGSQTOVQSTG-DVFNPPRLALPFGNFTLVNPD-VIASLA 241
 DB 218 EMRFPDPAMLSENNKMSALSNVQGSQGVSSPEVLESLNRPVYGSVSRVIGSLA 277
 QY 242 IMLFVC--GEPSSSDVRYWPLVIRPYLD-----DYTCSASEPTVIRVGNKC 289
 DB 278 IMLFICGSTDSQOFTDLMLRPLLDVADVATDMDTCADEPTVIRISGNGLC 337
 QY 290 VDVEDDHDQNOIQLPKSNNDPNQALMTIKXGTHRSNGSCLTYGTAGYVMAIFPC 349
 DB 338 VDVEDKKNKGNPQLMPCKQNSDVQWLTRPDGTHRSNGCLTNGYSAGDYVWIDC 397
 QY 350 NTAVREKTIQWIMNGTINPRSNVLAASGIGKTLTVQTLDTLQCGMLANDPAP 409
 DB 398 RPYVTASIMQFWANGTINPOSALVLSBESGPRITTVQADLYASRQMLAGNTEFP 457
 QY 410 EYTVGFRLCMESNGSVWETCVSSQGNQALYGDGSIPEKQNDQCLT-CGRDSVS 468
 DB 458 VTSIVGFNOLCMQAGNDMMVVESSKRAKAGALPFGSIRPHQDDKCLSTDNHSG 517
 QY 469 TVINIVSGAGSSGQGRVTFNEGAILNKGALANDPACNRLRIITVANCXKQML 528
 DB 518 SIIILSSCSFGSSQGRVTFNDGILNKGALANDVAGNSLSLQIIMVANCXKQML 577
 QY 529 PV 530
 DB 578 PL 579

RESULT 4
 Q918W4 PRELIMINARY; ERT; 580 AA.
 AC 094BW4
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamonin II precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinamomum.
 RX NCBI_TaxId=3429;
 RP SEQUENCE FROM N.A.
 RA Yang O., Gong Z.Z., Liu W.Y.
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamonin proteins and study of their expression
 RT patterns.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDORIBOZYCLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; A039602; AK82459.1; "-
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Interpro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR ProDom; PD00316; SHIGABICIN.
 DR PRF03; PRF0316; SHIGABICIN.
 DR SMART; SM00458; RICIN_2.
 DR ProSITE; PS00231; Ricin B_lectin; 2.
 KW Hydrolase; Signal; Toxin; POTENTIAL.
 FT SIGNAL 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CHAIN 33 580 CINNAMOMIN II.
 SQ SEQUENCE 580 AA; 64265 MW; 3784289SCC0CBPF CRG64;
 Query Match 48.8%; Score 1357; DB 10; Length 580;
 Best Local Similarity 52.8%; Pred No. 5e-104;
 Matches 286; Conservative 74; Mismatches 180; Indels 22; Gaps 11;

QY 9 TQCTGEYPRFTLLADYVSSGSFNEIPLAQ-STIPVSDAQRVAVELTNGQGS-I 66
 DB 40 TKNATKSTYOTFIALRQALASGEHPGIPVMEKSTVP--DSKRTIVELSNMADSPV 97
 QY 67 TAAIDVTMLVYVAYQAGDSYFLR-DAFQAGATHLFTGTSSSLPTNGSYPLERYAG-H 124
 DB 98 TLAVDVYNAIVAYVAYRGSSEFLRQEDNDPDALENLPDTRKATFFPSGSYTLDERVAGER 157
 QY 125 RDOIPLGIDLOISYVTLARFG-GSTRTOAKSLILLOISSEARFPLMAQYING 183
 DB 158 REEILGNDPLENRLISLMTSNLQOALASLIYQWAAVAFRFPIRYVESITRA 217
 QY 184 ASFLPDVYMLETSMQGSQTOVQSTG-DVFNPPRLALPFGNFTLVNPD-VIASLA 241
 DB 218 EMRFPDPAMLSENNKMSALSNVQGSQGVSSPEVLESLNRPVYGSVSRVIGSLA 277
 QY 242 IMLFVC--GEPSSSDVRYWPLVIRPYLD-----DYTCSASEPTVIRVGNKC 289
 DB 278 IMLFICGSTDSQOFTDLMLRPLLDVADVATDMDTCADEPTVIRISGNGLC 337
 QY 290 VDVEDDHDQNOIQLPKSNNDPNQALMTIKXGTHRSNGSCLTYGTAGYVMAIFPC 349
 DB 338 VDVEDKKNKGNPQLMPCKQNSDVQWLTRPDGTHRSNGCLTNGYSAGDYVWIDC 397
 QY 350 NTAVREKTIQWIMNGTINPRSNVLAASGIGKTLTVQTLDTLQCGMLANDPAP 409
 DB 398 RPYVTASIMQFWANGTINPOSALVLSBESGPRITTVQADLYASRQMLAGNTEFP 457
 QY 410 EYTVGFRLCMESNGSVWETCVSSQGNQALYGDGSIPEKQNDQCLT-CGRDSVS 468
 DB 458 VTSIVGFNOLCMQAGNDMMVVESSKRAKAGALPFGSIRPHQDDKCLSTDNHSG 517
 QY 469 TVINIVSGAGSSGQGRVTFNEGAILNKGALANDPACNRLRIITVANCXKQML 528
 DB 518 SIIILSSCSFGSSQGRVTFNDGILNKGALANDVAGNSLSLQIIMVANCXKQML 577
 QY 529 PV 530
 DB 578 PL 579

RESULT 5
 Q918W4 PRELIMINARY; ERT; 549 AA.
 AC 094W42
 DT 01-DEC-2001 (Tremblrel. 15, Created)
 DT 01-MAR-2003 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinnamonin (EC 3.2.2.22) (rRNA
 DE N-glycosidase) (Fragment).
 OS Cinamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinamomum.
 RX NCBI_TaxId=3429;

[1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RT "Molecular cloning of cinnamomyl A-, B-chain and the expression,
 RT purification, characterization and mutagenesis of the A-chain";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOPHYTOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL: AF039601; GenBank: AF039601; DDBJ: AF039601.
 DR HSRP: P02879; 2A1.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_lectin; 5.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 DR HydroLase; Toxin.
 KM NON_TSR
 FT SEQUENCE 549 AA; 60648 MW; 02607BE6C7CA430 CRC64;
 SQ
 Query Match 47.2%; Score 1316.5; DB 10; Length 549;
 Best Local Similarity 51.4%; Pred. No. 1.6e-100;
 Matches 279; Conservative 76; Mismatches 165; Indels 23; Gaps 11;

QY 9 THQTGEYRFFITLLRDYSSSSGFSNEIPLRQ-STIPVSDAQRFVAVELTNGQSDS-I 66
 DB 8 TKAYVTSYTFETALRQALSGEPHGPVMEKSTVP--DSKRFILVLSNMAADSV 65
 QY 67 TLAIDVNLVYVAYQAGDSYFLR-DAPRQATFLFTGTSSLPFNSGYPDLERYAG-H 124
 DB 66 TLADVYNAIVAYAKRISQSEFLKEDNDPAILNLPDKTKITTFSSSYDLEGVAGER 125
 QY 125 RDQIPFGIDQLQSVTLAPFG-GSTRTQASGILILQWISLAAEPNFIIMFAQYINGG 183
 DB 126 REELTGMPLDLENALISLMTSNLQOQALASLIVIQWVAEVRERFIEYRSGISRA 185
 QY 184 ASFLPDVYMLETSMQSGSTVQVSHTD-GVFNKSRILAPPGNYFTLNTNR-VTASLA 241
 DB 186 EWERPDPAWLSLNNKMSALSNVQSGVSSPVALSISNRPYVASVSRVTSGLA 245
 QY 242 IMLFVNC--GERSSSDYRWATLTPVAD-----DYCSASPEYRIVGRKNC 289
 DB 246 IMLFETGSDIASDQPIIDMLMIRPLVDVAVATDANDDTCADPEPTVIRSGMGIC 305
 QY 290 VYVDDDDPDGNOQLQWPKSGNDPQWLTKKDGITISNGSCITTYGTAGYVWIFDC 349
 DB 306 VYVDDKKNNGNPQLQWPKQNSDVQQLMTLRDQALISNGKCLTNGYSADGYVWIFDC 365
 QY 350 NTVAREATTQWINGNTIINPSNLVLAASSGIKGTLTVQGLDYLQGGWLAANDPAG 409
 DB 366 RPYVTAASIWQFANGLTINPSALVLAASGKGRFTLVQANTYASRGGLANNTEFP 427
 QY 410 EYTVGFRLCMENSGSTWETCVSSQONRMLYGDGSTRPKQND--QCLTQGRDSV 467
 DB 426 VTSIVGFNDLQVANGDPAWVEECSSKQKQKALYPPDSIIPQDQDPAACPLDNRHQ 485
 QY 468 STVINIVSCAGSGSQRWFTNEGAILNKNGLANDVQANPKRLIITYPANGKQWMA 527
 DB 486 GSIIIISSCSPGSEGRWFTNMDGVNLKNGLVWDYKSNPSLHIIIMPRGKRNHEW 545
 QY 528 LPV 530
 DB 546 LPV 548

RESULT 6
 ID Q94BWS PRELIMINARY; PRT; 561 AA.
 AC Q94BWS;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DB Type 2 ribosome-inactivating protein cinnamomyl 1 precursor
 DB (EC 3.2.2.22) (RNA N-glycosidase).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Rosidiales; Laurales; Lauraceae; Cinnamomum.
 DX NCBI_taxonomy:15125;
 RN
 RA SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomyl proteins and study of their expression
 RT patterns";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOPHYTOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL: AF039601; GenBank: AF039601; DDBJ: AF039601.
 DR HSRP: P02879; 2A1.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_lectin; 5.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 DR HydroLase; Signal; Toxin.
 KM SIGNAL
 FT CHAIN 33 581
 FT SEQUENCE 581 AA; 64215 MW; 026F3B8FAD3D96 CRC64;
 SQ
 Query Match 47.1%; Score 1315.5; DB 10; Length 581;
 Best Local Similarity 51.4%; Pred. No. 2.1e-100;
 Matches 279; Conservative 75; Mismatches 166; Indels 23; Gaps 11;

QY 9 THQTGEYRFFITLLRDYSSSSGFSNEIPLRQ-STIPVSDAQRFVAVELTNGQSDS-I 66
 DB 40 TKARKTSYTFETALRQALSGEPHGPVMEKSTVP--DSKRFILVLSNMAADSV 97
 QY 67 TLAIDVNLVYVAYQAGDSYFLR-DAPRQATFLFTGTSSLPFNSGYPDLERYAG-H 124
 DB 98 TLADVYNAIVAYAKRISQSEFLKEDNDPAILNLPDKTKITTFSSSYDLEGVAGER 157
 QY 125 RDQIPFGIDQLQSVTLAPFG-GSTRTQASGILILQWISLAAEPNFIIMFAQYINGG 183
 DB 156 REELTGMPLDLENALISLMTSNLQOQALASLIVIQWVAEVRERFIEYRSGISRA 217
 QY 184 ASFLPDVYMLETSMQSGSTVQVSHTD-GVFNKSRILAPPGNYFTLNTNR-VTASLA 241
 DB 218 EWERPDPAWLSLNNKMSALSNVQSGVSSPVALSISNRPYVASVSRVTSGLA 277
 QY 242 IMLFVNC--GERSSSDYRWATLTPVAD-----DYCSASPEYRIVGRKNC 289
 DB 276 IMLFETGSDIASDQPIIDMLMIRPLVDVAVATDANDDTCADPEPTVIRSGMGIC 337
 QY 290 VYVDDDDPDGNOQLQWPKSGNDPQWLTKKDGITISNGSCITTYGTAGYVWIFDC 349
 DB 338 VYVDDKKNNGNPQLQWPKQNSDVQQLMTLRDQALISNGKCLTNGYSADGYVWIFDC 397
 QY 350 NTVAREATTQWINGNTIINPSNLVLAASSGIKGTLTVQGLDYLQGGWLAANDPAG 409
 DB 398 RPYVTAASIWQFANGLTINPSALVLAASGKGRFTLVQANTYASRGGLANNTEFP 457
 QY 410 EYTVGFRLCMENSGSTWETCVSSQONRMLYGDGSTRPKQND--QCLTQGRDSV 467
 DB 458 VTSIVGFNDLQVANGDPAWVEECSSKQKQKALYPPDSIIPQDQDPAACPLDNRHQ 517
 QY 528 LPV 530
 DB 518 LPV 517

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Db          578 IPI 580

RESULT 7
Qd          041174
AD          PREIMINARY;          PRT          541 AA.
Qd          041174
AD          01-NOV-1996 (ZEMRETEL) 01. Created)
DT          01-NOV-1996 (ZEMRETEL) 01. Last sequence update)
DT          01-MAR-2003 (ZEMRETEL) 2.3. Last annotation update)
DE          D1 Proicin A chain (EC 3.2.2.22) (rSN N-glycosidase)
DS          (Fragment).
OS          Rictus communis (Castor bean).
OC          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophytes;
OC          Spermatophyta, Magnoliophyta, eudicotyledons, core eudots; Rosidae;
OC          eurosids I; Malpighiales; Euphorbiaceae; Rictus.
CN          [1] "rctd-3988";
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=92338377; PubMed=1633311;
RA          Roberts L.M., Tregear J.W., Lord J.M.;
RT          "Molecular cloning of rictin."
RL          Tagged Disign. Ther. 7:81-97(1992).
CC          -1 CATALYTIC ACTIVITY: ENDODIOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC          SPECIFIC ADONOSINE ON THE 28S RRNA.
CC          -1 EMBL=U00001 ON THE 28S RRNA -INACTIVATING PROTEIN FAMILY.
DR          HSRP. P02879; 1866.
DR          InterPro: IPRO00772; Rictin_B_lectin.
DR          InterPro: IPRO01574; RIF.
DR          InterPro: IPRO01400; Somatotropin.
DR          Pfam: P000652; Rictin_B_lectin; 6.
DR          Pfam: P00161; RIF; 1.
DR          PRINTS: PR00396; SHIBABICIN.
DR          SMART: SM00458; RICTIN; 2.
DR          PROSITE: PS00331; RICTIN_3_ELECTIN; 2.
DR          PROSITE: PS00338; SHIBABICIN.
DR          PROSITE: PS00338; SOMATOTROPIN_2; 1.
KY          Hs01aase; Toxicin.
FT          NON TER          1
SQ          SEQUENCE          541 AA; 60281 MW; 2B7B2CDEF1FE29D9 CRC64;

Query Match          46.7%; Score 1303; DB 10; Length 541;
Best Local Similarity 50.8%; Pred. No. 26-99;
Matches 272; Conservative 83; Mismatches 160; Indels 20; Gaps 11

OY          9 TDTGCEGEEPRITLLLEDTYSQGS -RSMERPLI-RSGTTPSSQDPRVMEVETGCGGSI 66
DB          13 TPAATVQSYTNHIAKVRKSLTADPDIPLPRKGLPIN -GRPLVHSHSLAEIV 70

OY          67 TAAIDVTLVVAQAQDQSFYR-DABRQAE -THLFTGR-TRSSLPFGSYEDLERIA 122
DB          71 TLALDVTAAYVGRASNAAFHPDNDQDAEATLHFLDVQKRYTPAFQGYRIEOLA 130

OY          123 GH-RQDIFPDIGDILQSGTALRP--PGSRTQASILLIDNIGSEAAENFLIMRABQ 178
DB          131 GANRHEIDANQGEAEKALALITSTGQTLPLASSFLICLQWISNANRQYIEGEMT 190

OY          179 YINSAGSLPDTMYMLELETSNGGQSTQVCHSTGDPNPNISALIPGSAFLTLNMPRIVA 238
DB          191 RIRNRRAEDSVITLLENSGRSLTAQSSNGAFASPDICLRNKGKSYVDSIILP 250

OY          235 SLATMLFYQCEPSSSSVYVYVPLVPIVAD--DYVCASBPETPAIVYSGNACVYRD 295
DB          236 DHDNGQLQCAKPPSSQ--FSLIRPVREREMAD-CADDEPFAIVGSGVADVRGG 305

OY          296 IETPAGNQLCAKPPSSQ--FSLIRPVREREMAD-CADDEPFAIVGSGVADVRGG 355
DB          306 RFRNNGALQMPCKSTNDQNLTLKEDNTHISNKCLITTYGYSPOYVWIDCNIAAD 365

OY          356 ATTMQWQNGTILINRSNIVLAASQIGKTLTLVQTLVDVLTGQGMALNQAFAEVIYIG 415
DB          366 ATRMQWQNGTILINRSNIVLAASQNGKTLTLVQTLVVAASQGMALNQAFAEVIYIG 425

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[illegible]

Db 303 WKCKRLRBNQTLTKNSKLTTEGTAAGVYVYIDCTSAVAEATWEIDNG 362
Qy 366 TTPRSNVLAAASGKIGTTLTVOITLDTLGGGRLAGNDTAPAEVITYGRDLQMSNG 425
Db 363 TTPRSKALVLAASSSSWGGLTVOITNEIMRQGRGNNTSPVVISISGIDLOMOAG 422
Qy 426 GSWVETVSSQGRKALYGRSIFPKQNDQCTTCGDSVSTVINITVSCASGQRM 485
Db 423 SNVWADQNRKQGRNLTDSISVQTNCLIKKHQKSPVYLAHNSWASQGN 482
Qy 486 VPTNBAIILNKGLANDVAQNPRLRIITYPACGKQNMWL 528
Db 483 LPKNDGISLYDDMWVDVGSQSPSKOITIMPYGKQNMWL 525

RESULT 9

08LKQ2 PRELIMINARY; PRT; 263 AA.

AC 08LKQ2:2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lactin chain B isoform 2 (fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE:20102702; PubMed:1170524;
RA Lactin B isoform 2, Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.,
RT "CDNA cloning and sequence analysis of the lactin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN [2]
RS SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF505918; AM446936.1; B. Jectin.
DR Genbank: AF505918; B. Jectin.
DR PIR: P00652; Ricin B_lectin, 5.
DR SMART: SMO0458; Ricin B_lectin, 2.
DR PROSITE: PS00231; Ricin B_lectin, 2.
FT NON TER 1
FT 263
SQ SEQUENCE 263 AA; 29150 MW; B685CB7C49C8DIF CRC64;

Query Match 42.6%; Score 1189; DB 10; Length 263;
Best Local Similarity 82.5%; Pred. No. 2e-90; Indels 0; Gaps 0;
Matches 217; Conservative 20; Mismatches 26;

Qy 269 DPTGASAPPTRIYGRGKQVDVDDPHQNGIQGRKNDPQGLTKIKGCTIR 328
Db 1 DQGTASAPPTRIYGLNGCTDVYNGKTHGNFIQTPCKNDPQGLTKIKGCTIR 60
Qy 329 NSCLITGATAGVYVITFCQNTAREATITQWNGGIIINPSSVLAAASGKIGTTL 368
Db 61 NSKCLITGATAGVYVITFCQNTAREATITQWNGGIIINPSSVLAAASGKIGTTL 120
Qy 389 VQITLDTLGGGRLAGNDTAPAEVITYGRDLQMSNGSWVETVSSQGRKALY 448
Db 121 VQITLDTLGGGRLAGNDTAPAEVITYGRDLQMSNGSWVETVSSQGRKALY 485
Qy 449 STPKQNDQCTTCGDSVSTVINITVSCASGQRMVPTNBAIILNKGLANDVA 508
Db 181 STPKQNDQCTTCGDSVSTVINITVSCASGQRMVPTNBAIILNKGLANDVA 525
Qy 509 PKLRRIITYPACGKQNMWL 528
Db 509 PKLRRIITYPACGKQNMWL 528

Db 241 PSIRRIITYPACGKQNMWL 528

RESULT 10

Qy 09M69 PRELIMINARY; PRT; 547 AA.

AC 09M69:2002 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproagglutinin (BC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosides I; Fabales; Fabaceae; Papilionoideae; Abreace; Abrus.
OX NCBI_TaxID=3816;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE:20102702; PubMed:10616890;
RA Liu C.Y., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
RA "Primary Structure and Function Analysis of the Abrus precatorius
RT agglutinin A chain by site-directed mutagenesis: Protein of Amphiphilic
RT alpha-helix H impairs protein synthesis inhibitory activity";
RL J. Biol. Chem. 275:1897-1901(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AF190173; AF28309.1; -;
CC Genbank: AF190173; AF28309.1; -;
DR EMBL: AF190173; AF28309.1; B. Jectin.
DR Genbank: AF190173; AF28309.1; B. Jectin.
DR PIR: P00157; Ricin B_lectin, 6.
DR SMART: SMO0458; Ricin B_lectin, 2.
DR PROSITE: PS00231; Ricin B_lectin, 2.
DR PROSITE: PS00231; Ricin B_lectin, 2.
DR PROSITE: PS00231; Ricin B_lectin, 2.
SQ SEQUENCE 547 AA; 61248 MW; 355A3252354A1BD CRC64;

Query Match 41.7%; Score 1164.5; DB 10; Length 547;
Best Local Similarity 45.5%; Pred. No. 6.4e-88;
Matches 242; Conservative 87; Mismatches 174; Indels 29; Gaps 8;

Qy 9 THQTEYEYRFTLLADVSSGSPENRIPLRQSTPVSQARFVLVELTQGGDIT 68
Db 28 TGSATYVQFIDALBERLGLIYQ-IVLRDPS-TEPKQNYVTELSQDVIDL 85
Qy 69 AIDVNLVYVQAGDSSFTLADPAGETLFTCTTNGSSIFPNSSPDLERYACH 127
Db 86 GIDVNLVYVQAGDSSFTLADPAGETLFTCTTNGSSIFPNSSPDLERYACH 145
Qy 128 FGLDNLVYVQAGDSSFTLADPAGETLFTCTTNGSSIFPNSSPDLERYACH 187
Db 146 FGLDNLVYVQAGDSSFTLADPAGETLFTCTTNGSSIFPNSSPDLERYACH 205
Qy 188 PPTVMELETSWQGSYQVQSTGVFNNRIRLAPRGVFTLVNVRD- 236
Db 206 PPTVMELETSWQGSYQVQSTGVFNNRIRLAPRGVFTLVNVRD- 255
Qy 237 TASIALMVFQGRSSSVRRVYLVRVYADVTGSAS-EPVTVYGRNQCIVRQD 295
Db 256 TASIALMVFQGRSSSVRRVYLVRVYADVTGSAS-EPVTVYGRNQCIVRQD 311
Qy 296 DPTGASAPPTRIYGRGKQVDVDDPHQNGIQGRKNDPQGLTKIKGCTIR 328
Db 312 DPTGASAPPTRIYGRGKQVDVDDPHQNGIQGRKNDPQGLTKIKGCTIR 368
Qy 356 ATIQWNGGIIINPSSVLAAASGKIGTTLTVOITLDTLGGGRLAGNDTAPAE 415
Db 372 ATIQWNGGIIINPSSVLAAASGKIGTTLTVOITLDTLGGGRLAGNDTAPAE 485

QY 416 FRLDCEANGSGSWWETCVSSQONMALXGDSIRPKONODQLTCGRDSVSTVNIIVS 475
 DB 432 FFKLCMEHNSMMLDVCITREKQAMVYPPDSIRPVQNTNMCCEHKOQATVWNG 491
 QY 476 CSAGSSGQRTFNEGAILNKGLANDYQANETFRITIIYPATCKENQNM 527
 DB 492 CSNMAQSNVPSDGTIYIXDMVMDVSSDPSRLQIIMFYIKNQNM 543

RESULT 11

Q8RXH7 PRELIMINARY; PRT; 249 AA.
 AC Q8RXH7; 01-JUN-2002 (TRENBERL 21, Created)
 DT 01-JUN-2002 (TRENBERL 21, Last sequence update)
 DT 01-MAR-2003 (TRENBERL 23, Last annotation update)
 DE Lectin chain A isoform 2 (EC 3.2.2.22) (RNA N-glycosidase)
 DF Lectin chain A isoform 2 (EC 3.2.2.22) (RNA N-glycosidase)
 DR Viscum album (European mistletoe)
 CS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=3972;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Leaf;
 RC Paramasiavam M., Sriinivasan A., Singh T.P.;
 RT Viscum Album (Indian) mRNA for Mistletoe Lectin Chain A, isoform 2.*;
 RL Submitted (2002) to EMBL/GenBank/DBS databases.
 RT Submitted (2002) to EMBL/GenBank/DBS databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AY081148; ALA87005.1; -
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.1.
 DR Hydrolase; Toxin.
 FT NON_TER 1
 FT NON_TER 249
 FT SEQUENCE 249 AA; 27944 MW; 89FARF78309A83B3 CRC64;
 SQ

Query Match 41.5%; Score 1159; DB 10; Length 249;
 Best Local Similarity 91.2%; Pseq No 5.7e-88;
 Matches 227; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 YERLRVHTQGTGEYFRITLLRDYVSSGSPSNEIFLLRQSTIPVSDAQRPVLYELIN 60
 DB 1 YERLRVHTQGTGEYFRITLLRDYVSSGSPSNEIFLLRQSTIPVSDAQRPVLYELIN 60
 QY 61 QGGDSITNADIVTNLYVAYAGQDSYFRADAPGAEHTLFTGTRSSLPENSGYDLER 120
 DB 61 QGGDSITNADIVTNLYVAYAGQDSYFRADAPGAEHTLFTGTRSSLPENSGYDLER 120
 QY 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 DB 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 QY 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 DB 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 QY 181 NSGASFLPDVYMLETSNGQOSTQVGHSTGVFNPRILALPFGVFTLNNRVIASI 240
 DB 181 NSGASFLPDVYMLETSNGQOSTQVGHSTGVFNPRILALPFGVFTLNNRVIASI 240
 QY 241 AMLFVCGE 249
 DB 241 AMLFVCGE 249

RESULT 12

Q8LXQ6 PRELIMINARY; PRT; 254 AA.
 AC Q8LXQ6; 01-OCT-2002 (TRENBERL 22, Created)
 DT 01-OCT-2002 (TRENBERL 22, Last sequence update)
 DT 01-MAR-2003 (TRENBERL 23, Last annotation update)

DE Lectin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)
 DE (Fragment).
 OS Viscum album subsp. coloratum.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2156752; PubMed=1170524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum)."
 RL Mol. Cells 12:215-220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT Submitted (May-2002) to the EMBL/GenBank/DBS databases.
 RL Submitted (May-2002) to the EMBL/GenBank/DBS databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AF508914; AA046932.1; -
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.1.
 DR PRINTS: PR00356; SHIGARICIN.
 DR Hydrolase; Toxin.
 FT NON_TER 1
 FT NON_TER 254
 FT SEQUENCE 254 AA; 28446 MW; 6DB5C3B18F4AF8E0 CRC64;
 SQ

Query Match 41.5%; Score 1159; DB 10; Length 254;
 Best Local Similarity 89.4%; Pseq No. 5.9e-88;
 Matches 227; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 YERLRVHTQGTGEYFRITLLRDYVSSGSPSNEIFLLRQSTIPVSDAQRPVLYELIN 60
 DB 1 YERLRVHTQGTGEYFRITLLRDYVSSGSPSNEIFLLRQSTIPVSDAQRPVLYELIN 60
 QY 61 QGGDSITNADIVTNLYVAYAGQDSYFRADAPGAEHTLFTGTRSSLPENSGYDLER 120
 DB 61 QGGDSITNADIVTNLYVAYAGQDSYFRADAPGAEHTLFTGTRSSLPENSGYDLER 120
 QY 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 DB 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 QY 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 DB 121 YAGHDDQPIGIDQLQSVTLAFPGQSTRTQASILLIOMISAPAFNPLTKARQYI 180
 QY 181 NSGASFLPDVYMLETSNGQOSTQVGHSTGVFNPRILALPFGVFTLNNRVIASI 240
 DB 181 NSGASFLPDVYMLETSNGQOSTQVGHSTGVFNPRILALPFGVFTLNNRVIASI 240
 QY 241 AMLFVCGE 254
 DB 241 AMLFVCGE 254

RESULT 13

Q8LXQ1 PRELIMINARY; PRT; 263 AA.
 AC Q8LXQ1; 01-OCT-2002 (TRENBERL 22, Created)
 DT 01-OCT-2002 (TRENBERL 22, Last sequence update)
 DT 01-MAR-2003 (TRENBERL 23, Last annotation update)
 DE Lectin chain A isoform 3 (Fragment).
 DF Viscum album subsp. coloratum.
 DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2156752; PubMed=1170524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF508919; AM46931.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1 1
FT NON_TER 263 263
SQ SEQUENCE 263 AA; 29071 MW; 389CADAB60F061D CRC64;

Query Match 41.4%; Score 1155; DB 10; Length 263;
Best Local Similarity 80.6%; Pred. No. 1,3e-87;

Matches 212; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 269 DDTYCSASPTPTVIGENGVGVDPDDPHDQGLMPGSKNNDDNGLTTRRGTIS 328
DB 1 DDGCTPSEPTVWVGLNGLVDVPRGKFDNDPGLMPCKANTDNQWLTIRRGTIS 60

QY 329 NGSCLTGYAGVYVIMFPDNTVREATVQWINGCTINPRANVYLAASSGIGCTIT 388
DB 61 NSKCLTGYAGVYVIMFPDNTVREATVQWINGCTINPRANVYLAASSGIGCTIT 120

QY 389 VQTLDTTLCGGLTANDTAPREVTITGFRLCENSGSWVETCVSSQONKALIGG 448
DB 121 VQTAHSLQGLTASHDAPREVTITGFRLCENSGSWVETCVSSQONKALIGG 180

QY 449 SRRPNQDGLTGGDSVTVINVSAGSSGGWPTNKGALINLKGALMDVQAN 508
DB 181 SRRPNQDGLTGGDSVTVINVSAGSSGGWPTNKGALINLKGALMDVQAN 240

QY 509 PGLRRITTPATGKPNQWLPVP 531
DB 241 PGLRRITTPATGKPNQWLPVP 263

RESULT 14
ID O8LK03 PRELIMINARY; PRT; 249 AA.
AC O8LK03;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Lectin chain A isoform 2 (IPC 3.2.2.22) (rRNA N-glycosidase)
OS (Fragment).
DS Viscum album subsp. coloratum.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Euphorbiales; Vitaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]_TaxID=159976;
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508919; AM46931.1; -
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00366; SHIGARICIN.
DR HYDROLase; Toxin.
FT NON_TER 1 1
FT NON_TER 249 249
SQ SEQUENCE 249 AA; 27821 MW; 3C5870E833EDAB5 CRC64;

Query Match 40.8%; Score 1140; DB 10; Length 249;
Best Local Similarity 89.1%; Pred. No. 2.2e-86;

Matches 220; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 1 YERLRVTHQTEGEYFRITLLDQVSSGSPNEIPLRQSTIPVSDAOPVYELTN 60
DB 1 YERLRVTHQTEGEYFRITLLDQVSSGSPNEIPLRQSTIPVSDAOPVYELTN 60

QY 61 QGGGRTNALDPTWVYVNOAGDSYFPRDAPRGAETLFGCTTRASLPYSGYDGLR 120
DB 61 QGGGRTNALDPTWVYVNOAGDSYFPRDAPRGAETLFGCTTRASLPYSGYDGLR 120

QY 121 YAGHDQIPGHDLIQSYTLRFPGSPRTQASILLIQWISAPARNPILRRQYI 180
DB 121 YAGHDQIPGHDLIQSYTLRFPGSPRTQASILLIQWISAPARNPILRRQYI 180

QY 181 NSGASFLPDVYMLELFTSQGQSTGVGSHSDGVNPNRLAIPGNPVTYVWDVYASL 240
DB 181 NSGASFLPDVYMLELFTSQGQSTGVGSHSDGVNPNRLAIPGNPVTYVWDVYASL 240

QY 241 AMLRPG 247
DB 241 AMLRPG 247

RESULT 15
ID O8LK03 PRELIMINARY; PRT; 266 AA.
AC O8LK03;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Lectin chain B isoform 1 (Fragment).
OS Viscum album subsp. coloratum.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Vitaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]_TaxID=159976;
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF508917; AM46931.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1 1
FT NON_TER 266 266
SQ SEQUENCE 266 AA; 29537 MW; 4A51473C7B94C73 CRC64;

Query Match 38.0%; Score 1060.5; DB 10; Length 266;
Best Local Similarity 72.6%; Pred. No. 9.4e-80;

Matches 193; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

Qy 269 DDVTCASEPTVAIVGNMVCVDRDDPHDGNQIOLMPSKANDPNQWTIKRDGITS 328
 Db 1 DDVTCASEPTVAIVGNMVCVDRDDPHDGNQIOLMPSKANDPNQWTIKRDGITS 60
 Qy 329 NSGCTTYGTAQYVWIFPCYVREATWQIMQNTIINRGNL--AASGIXGT 385
 Db 61 NGRCLTTYGTAQYVWIFPCYVREATWQIMQNTIINRGNL--AASGIXGT 120
 Qy 386 TLVQTLDTYTGQGWLAGNDTAPREVTIYGFRLCNSNGSWEVETCSQONQWALY 445
 Db 121 TPLQTLDTYTGQGWLAGNDTAPREVTIYGFRLCNSNGSWEVETCSQONQWALY 180
 Qy 446 GPGSIRPKONDOCLTGNDSTVTINIVCSQSSQWVETNEGALINXGLAMDYA 505
 Db 181 GPGSIRPKONDOCLTGNDSTVTINIVCSQSSQWVETNEGALINXGLAMDYA 240
 Qy 506 GANPKRRIIIPATKKNOMLPP 531
 Db 241 RNDPSLRRIIIPATKKNOMLPP 266

Search completed: December 11, 2003, 14:01:00
 Job time : 41.9287 secs

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	279.1	100.0	53	1	AA25875	Msi1eclo lectin I
2	279.1	100.0	53	20	AA25876	Msi1eclo lectin I
3	277.0	99.2	56	18	AAW10021	Pedro msi1eclo I
4	277.0	99.2	56	4	AAW90127	Msi1eclo lectin P
5	277.0	99.2	56	20	AA25870	Msi1eclo lectin P
6	251.9	90.3	53	3	AA25876	Msi1eclo lectin P
7	251.9	90.3	53	30	AA25876	Msi1eclo lectin P
8	252.5	84.3	55	23	ABR9150	Msi1eclo-lectin B
9	140.0	50.9	26	3	AA25885	Msi1eclo lectin B

ALIGNMENTS

RESIST I	
AAZ5979	AAZ5979 standard; Protein, 551 AA.
XX	
XX	AAZ5979;
XX	
DT	18-OCT-1999 (first entry)
XX	
D2	Mistletoe lectin I protein fragment.
XX	
KM	Mistletoe lectin; antitumor; immunostimulant; A-chain; MZA; immunity;
KM	ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KM	cancer; cytotoxicity; antigen; isoform; lectin I.
XX	
XX	Viscum album.
OS	
FN	DE19804210-AL.
XX	
PD	12-AUG-1999.
XX	
XX	03-FEB-1998; 98DE-1004210.
XX	
PR	03-FEB-1998; 98DE-1004210.
XX	
PA	(BIOSYN ARZNEIMITTEL GMBH.
XX	
PI	Morris P, Stiefel T, Voelter W, Welters P;
XX	
DR	WPI; 1999-44535/38.
DR	N-PSDB; AA209103.
XX	

PT Preparation of mistletoe lectins in heterologous systems.
PT particularly for use as anticancer agents and immunostimulants
XX
XX
XX Claim 7, Fig 1b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a mistletoe lectin I protein fragment.
XX
SQ Sequence 531 AA:
Query Match 100.0%; Score 2791; DB 20; Length 531;
Best Local Similarity 100.0%; Pred. No. 2, 8e-244;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRATVHTQGTGEYFRFTLLRDVYSSGSFSENEIPILRSGTIPVGDARFVLVELIN 60
DB 1 YERLRATVHTQGTGEYFRFTLLRDVYSSGSFSENEIPILRSGTIPVGDARFVLVELIN 60
QY 61 QGSDITPAIDVTNLVYVAOAGDSYFLRPAAGATLFTGTSSLPFGSYDLE 120
DB 61 QGSDITPAIDVTNLVYVAOAGDSYFLRPAAGATLFTGTSSLPFGSYDLE 120
QY 121 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
DB 121 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
QY 122 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
DB 122 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
QY 181 NSGASFLPDVYMLELTSWGQSTOVQASTGVFNRIELALPPGAPVTLNVRDVIASL 240
DB 181 NSGASFLPDVYMLELTSWGQSTOVQASTGVFNRIELALPPGAPVTLNVRDVIASL 240
QY 241 AMLFVCGERSSSDVRYVPLVIRPVADVTGASBPVTRIVGRNMCVTRDDPHDG 300
DB 241 AMLFVCGERSSSDVRYVPLVIRPVADVTGASBPVTRIVGRNMCVTRDDPHDG 300
QY 301 NOIQMPKSNNDPQGLMTIRKDTIRNSGCLITTYGTVNRYVNLFCNTNVRALNTQ 360
DB 301 NOIQMPKSNNDPQGLMTIRKDTIRNSGCLITTYGTVNRYVNLFCNTNVRALNTQ 360
QY 361 INWGNTIINPNSVLTAASSGIGKGTLLVQGLDVTLGQMLAGNDAPREVITYGFDLC 420
DB 361 INWGNTIINPNSVLTAASSGIGKGTLLVQGLDVTLGQMLAGNDAPREVITYGFDLC 420
QY 421 MESNGSYWVETVCSQONKALYDGSIRPKONQDCLTQONDSVTVINVSAGS 480
DB 421 MESNGSYWVETVCSQONKALYDGSIRPKONQDCLTQONDSVTVINVSAGS 480
QY 481 SCORVYFNEGAILNLKGLANDVQAAMPKRIIITYPANGRPKMTLPPV 531
DB 481 SCORVYFNEGAILNLKGLANDVQAAMPKRIIITYPANGRPKMTLPPV 531
RESULT 2
AAZ5982
AAZ5982 standard; Protein; 532 AA.
AAZ5982;
18-OCT-1999 (first entry)
Mistletoe lectin I (variant) protein fragment.
Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;

KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW particularly for use as anticancer agents and immunostimulants
KW cancer; cytotoxicity; antigen; isoform; lectin I.
XX
XX Viscum album.
XX
XX DEL9804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (Bios) BROSVA ARZEMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Welters P;
XX
XX WPI: 1999-445335/38.
XX
XX N-PSDB: AA209106.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 4b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin I protein variant.
XX
SQ Sequence 532 AA:
Query Match 100.0%; Score 2791; DB 20; Length 532;
Best Local Similarity 100.0%; Pred. No. 2, 8e-244;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRATVHTQGTGEYFRFTLLRDVYSSGSFSENEIPILRSGTIPVGDARFVLVELIN 60
DB 1 YERLRATVHTQGTGEYFRFTLLRDVYSSGSFSENEIPILRSGTIPVGDARFVLVELIN 60
QY 61 QGSDITPAIDVTNLVYVAOAGDSYFLRPAAGATLFTGTSSLPFGSYDLE 120
DB 61 QGSDITPAIDVTNLVYVAOAGDSYFLRPAAGATLFTGTSSLPFGSYDLE 120
QY 121 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
DB 121 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
QY 122 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
DB 122 YAGHDDIPLGIDQLIGSTALRPGASTTQASITLLTOMISPAARNPILMARQYT 180
QY 181 NSGASFLPDVYMLELTSWGQSTOVQASTGVFNRIELALPPGAPVTLNVRDVIASL 240
DB 181 NSGASFLPDVYMLELTSWGQSTOVQASTGVFNRIELALPPGAPVTLNVRDVIASL 240
QY 241 AMLFVCGERSSSDVRYVPLVIRPVADVTGASBPVTRIVGRNMCVTRDDPHDG 300
DB 241 AMLFVCGERSSSDVRYVPLVIRPVADVTGASBPVTRIVGRNMCVTRDDPHDG 300
QY 301 NOIQMPKSNNDPQGLMTIRKDTIRNSGCLITTYGTVNRYVNLFCNTNVRALNTQ 360
DB 301 NOIQMPKSNNDPQGLMTIRKDTIRNSGCLITTYGTVNRYVNLFCNTNVRALNTQ 360
QY 361 INWGNTIINPNSVLTAASSGIGKGTLLVQGLDVTLGQMLAGNDAPREVITYGFDLC 420
DB 361 INWGNTIINPNSVLTAASSGIGKGTLLVQGLDVTLGQMLAGNDAPREVITYGFDLC 420

QY 421 MESNGSVWVETCVSSQONQSMALYDGSIRPKONODCLTCGRDSVSVIVIVCSAGS 480
DB 421 MESNGSVWVETCVSSQONQSMALYDGSIRPKONODCLTCGRDSVSVIVIVCSAGS 480
QY 481 SGGKWTFTNEGAILNFKGLMDVYQANPFLKRIITITATGKPNQMLPVP 531
DB 481 SGGKWTFTNEGAILNFKGLMDVYQANPFLKRIITITATGKPNQMLPVP 531

RESULT 3
AA10021
ID AA10021 standard; Protein; 564 AA.

AA10021;
18-DEC-1997 (first entry)
Prepro mistletoe lectin.

Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.

Viscum album.

BE751221-A1.

02-JAN-1997.

26-JUN-1995; 95EP-0109949.

26-JUN-1995; 95EP-0109949.

(MADU) MADUS KOEHLN AG.

Baur A, Sock J, Lentzen H, Zinke H;

WEI; 1997-054678/06.

N-PDB; AA70473.

Nucleic acid encoding prepro form of mistletoe lectin - for
therapeutic or diagnostic use

Claim 12; Fig 4c; 30pp; German.

Mistletoe lectin is a cytotoxic agent that has been used for tumour
therapy. It can be used in immunotoxic and medicaments. Nucleic
acid fragments can be used in diagnostic methods. Mistletoe lectin (
AA70473) comprises an A chain (AA70473) and a B chain (AA70475).

Sequence 564 AA;

Query Match 99.2%; Score 2770; DB 18; Length 564;

Best Local Similarity 99.1%; Pred. No. 2.4e-242;

Matches 526; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YERLRATVHTGTEGEEYRRTLRADYSSGSNSRITPLRGSTIPYDAGQRYVLYEYLN 60
DB 34 YERLRATVHTGTEGEEYRRTLRADYSSGSNSRITPLRGSTIPYDAGQRYVLYEYLN 93
QY 61 OGGDSITAIIDVNLVVAAYAGQSYFLRARGAEHLFTGTRESIPNSGYDLEK 120
DB 94 OGGDSITAIIDVNLVVAAYAGQSYFLRARGAEHLFTGTRESIPNSGYDLEK 153
QY 121 YAGRDITFLGIDILGISTVTLRPPGSGTRQASITLILQMSBARFNLIMARQYT 180
DB 154 YAGRDITFLGIDILGISTVTLRPPGSGTRQASITLILQMSBARFNLIMARQYT 213
QY 181 NSGASFLPDVYNLELETSWQGSQYVGHSTGTFNNPRLAIPGNFTLITNRYVLSL 240
DB 214 NSGASFLPDVYNLELETSWQGSQYVGHSTGTFNNPRLAIPGNFTLITNRYVLSL 273
QY 241 AITLFCGEPSSSDVRYWPLVIRPVADVTCSASEPTVRLVSGNMCVVDDEDFDQ 300

DB 274 AITLFCGEPSSSDVRYWPLVIRPVADVTCSASEPTVRLVSGNMCVVDDEDFDQ 333
QY 301 NOTLAPSSKANDPNQLTIRKDGITISNSCLTYTGTAQYVNLTCNTAVKATLWQ 360
DB 334 NOTLAPSSKANDPNQLTIRKDGITISNSCLTYTGTAQYVNLTCNTAVKATLWQ 393
QY 361 IKNQGTILNPRSLVLAASGIGKTLTYQLDYTLGGMLAGNDAPREVTIYGRDLC 420
DB 394 IKNQGTILNPRSLVLAASGIGKTLTYQLDYTLGGMLAGNDAPREVTIYGRDLC 453
QY 421 MESNGSVWVETCVSSQONQSMALYDGSIRPKONODCLTCGRDSVSVIVIVCSAGS 480
DB 454 MESNGSVWVETCVSSQONQSMALYDGSIRPKONODCLTCGRDSVSVIVIVCSAGS 513
QY 481 SGGKWTFTNEGAILNFKGLMDVYQANPFLKRIITITATGKPNQMLPVP 531
DB 514 SGGKWTFTNEGAILNFKGLMDVYQANPFLKRIITITATGKPNQMLPVP 564

RESULT 4

AAW90127
ID AAW90127 standard; Protein; 564 AA.

AAW90127;

20-MAR-2003 (updated)

30-APR-1995 (first entry)

Mistletoe lectin prepro-protein.

Mt; mistletoe; lectin; Mt; transgenic plant; glycosylation;
dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
cancer.

Viscum album.

EP84388-A1.

16-DEC-1998.

26-JUN-1995; 95EP-0105660.

26-JUN-1995; 95EP-0109949.

26-JUN-1995; 95EP-0105660.

(MADU) MADUS KOEHLN AG.

Baur A, Eck J, Lentzen H, Zinke H;

WEI; 1999-026592/03.

N-PDB; AA74182.

New transgenic plant expressing mistletoe lectin - useful for
producing recombinant lectin in e.g. cancer diagnosis and therapy

Claim 1a; Fig 4c; 30pp; German.

This invention describes a novel transgenic plant transformed with a
vector capable of encoding a mistletoe (Viscum album) lectin

preproprotein or a biologically active fragment. The specific lectin
CC also describes a polypeptide produced by a plant where the polypeptide
CC exhibits at least one enzymatic modification other than the glycosylation
CC that occurs in Viscum album or the polypeptide is a fusion protein, a
CC mistletoe lectin polypeptide dimer and an immunotoxin used for large-scale
CC polypeptide of mistletoe lectin for diagnostic or therapeutic purposes
CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
CC used in the method of the invention.

(Updated on 20-MAR-2003 to correct pf field.)

Sequence 564 AA;

Query Match 99.2%; Score 2770; DB 20; Length 564;

```
Best Local Similarity 99.1%; Pred. No. 2,48-242;
Matches 526; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YERLRATVQTGEYFRFTLLRDYVSSGSFSNEIFLLRQSTIPVSDAQRFVLVLIN 60
DB 34 YERLRATVQTGEYFRFTLLRDYVSSGSFSNEIFLLRQSTIPVSDAQRFVLVLIN 93
QY 61 QGSGTAAIDVNLVYVAHQDGYTLADAPRATMLPTGTFSSLPKNSYPLER 120
DB 94 QGSGTAAIDVNLVYVAHQDGYTLADAPRATMLPTGTFSSLPKNSYPLER 153
QY 121 YAGRPDIPLGIDPLQIOSVTAAPFGASTTQASIIILQIMSEAPRPILMARQYI 180
DB 154 YAGRPDIPLGIDPLQIOSVTAAPFGASTTQASIIILQIMSEAPRPILMARQYI 213
QY 181 NSGASFLPDVYMLELTSWQOOSTOVQSHDGVFNNTIILAIPGNVTLTNRDVIASL 240
DB 214 NSGASFLPDVYMLELTSWQOOSTOVQSHDGVFNNTIILAIPGNVTLTNRDVIASL 273
QY 241 AALPFCGERPSSDGYWYMLYIEPVLAADVYCSASEPTVRIVGRNQCVDVDDDFDG 300
DB 274 AALPFCGERPSSDGYWYMLYIEPVLAADVYCSASEPTVRIVGRNQCVDVDDDFDG 333
QY 301 NCGLMPKSNNDPQGLATIKRIGDTIRNSCLTTGRTAGVYVMPDCTATREACTIQ 360
DB 334 NCGLMPKSNNDPQGLATIKRIGDTIRNSCLTTGRTAGVYVMPDCTATREACTIQ 393
QY 361 IWNGCTIIPRSLVLAASGIKGTLVQTLDTYLLQGMLAGNDVAPREVITYGFDDLC 420
DB 394 IWNGCTIIPRSLVLAASGIKGTLVQTLDTYLLQGMLAGNDVAPREVITYGFDDLC 453
QY 421 MESNGSVVETVCSQONRMALKQDSIRPNQVQCLTCGSDVSTVYINVSQAS 480
DB 454 MESNGSVVETVCSQONRMALKQDSIRPNQVQCLTCGSDVSTVYINVSQAS 513
QY 481 SGQRWFTNEGAILNLKNGJAMVDVQAPKLEPIITYPATGPKQWMLPVP 531
DB 514 SGQRWFTNEGAILNLKNGJAMVDVQAPKLEPIITYPATGPKQWMLPVP 564

RESULT 5
AAV25970
ID AAV25970 standard; protein; 533 AA.
XX
XX AAV25970;
XX
DT 18-OCT-1999 (first entry)
XX
XX
DE Mistletoe lectin protein consensus sequence 1.
XX
XX
KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
KW ribozyme 26S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform.
XX
XX
OS Viscum album.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /label= Asp, Glu
FT Misc-difference 63 /label= Gly, Gln
FT Misc-difference 66 /label= Ile, Val
FT Misc-difference 107 /label= Leu, Ala
FT Misc-difference 113 /label= Asp, Arg or none
FT Misc-difference 117 /label= Asn, Thr
FT Misc-difference 134 /label= Pro, Thr

FT FT /label= Asp, Glu
FT FT Misc-difference 141 /label= Ser, Thr
FT FT Misc-difference 145 /label= Phe, Tyr
FT FT Misc-difference 152 /label= Thr, Ala
FT FT Misc-difference 177 /label= Ala, Tyr
FT FT Misc-difference 185 /label= Tyr, Asp
FT FT Misc-difference 191 /label= Ala, Glu
FT FT Misc-difference 191 /label= Val, Met
FT FT Misc-difference 219 /label= Ile, Phe
FT FT Misc-difference 224 /label= Pro, Ser
FT FT Misc-difference 225 /label= Pro, Thr
FT FT Misc-difference 236 /label= Thr, Ser
FT FT Misc-difference 267 /label= Asp, Ser
FT FT Misc-difference 290 /label= Asn, Ser
FT FT Misc-difference 325 /label= Cys, Arg
FT FT Misc-difference 365 /label= Gly, Asn
FT FT Misc-difference 420 /label= Gly, Gln
FT FT Misc-difference 435 /label= Val, Asp
FT FT Misc-difference 439 /label= Gln, Lys
FT FT Misc-difference 442 /label= Gly or none
FT FT Misc-difference 443 /label= Arg, Lys
FT FT Misc-difference 460 /label= Cys, Ser, Val
FT FT Misc-difference 481 /label= Ala, Gly
FT FT Misc-difference 483 /label= Gly, Ala
FT FT Misc-difference 483 /label= Ser, Gly
FT FT Misc-difference 494 /label= Gly, Ser
FT FT Misc-difference 493 /label= Gly, Tyr
FT FT Misc-difference 500 /label= Asn, Ser, Thr, Lys
FT FT Misc-difference 501 /label= Ser, Gly
FT FT Misc-difference 502 /label= Leu, Pro
FT FT Misc-difference 503 /label= Ala, Met
FT FT Misc-difference 504 /label= Met, Val
FT FT Misc-difference 533 /label= Pro, Phe
FT FT
PX DEJ9804210-A1.
PO 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX
XX
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XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX MPI; 1999-44535/38.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 1; Page 25-26; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, to stimulate immunity. (I) and its
XX fragments are used as immunostimulants. The A-chain (MLA) is
XX obtained by cleaving the whole lectin with a specific protease. The
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin described in the
XX specification.
XX
XX Sequence 533 AA;
XX
XX Query Match 90.3%; Score 2519; DB 20; Length 533;
XX Best Local Similarity 92.5%; Pred. No. 1,4e-219;
XX Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
XX
XX 1 YERLRKRVHQTGGEYFRFILLRDYSSGSFSNEIPLRSGTITVSDAQRVFLVLEIN 60
XX 1 YERLRKRVHQTGGEYFRFILLRDYSSGSFSNEIPLRSGTITVSDAQRVFLVLEIN 60
XX 61 QGSDSTIALDVTNLVYVAYQAGQSYPLRPARAGAEHLFGTTR-SGLPFGNSYDULE 119
XX 61 QGSDSTIALDVTNLVYVAYQAGQSYPLRPARAGAEHLFGTTR-SGLPFGNSYDULE 119
XX 120 RYAGHROIPIGIDLIQSVYALAFPGSGTQASIIILILQMSRAAPPIILWRAQY 179
XX 120 RYAGHROIPIGIDLIQSVYALAFPGSGTQASIIILILQMSRAAPPIILWRAQY 179
XX 121 RYAGHROIPIGIDLIQSVYALAFPGSGTQASIIILILQMSRAAPPIILWRAQY 180
XX 121 RYAGHROIPIGIDLIQSVYALAFPGSGTQASIIILILQMSRAAPPIILWRAQY 180
XX 180 INSGASTLEDVYALELETSWQGSSTVOGSDTGVFNNEILALIPGNGFVTLVWVDYAS 239
XX 180 INSGASTLEDVYALELETSWQGSSTVOGSDTGVFNNEILALIPGNGFVTLVWVDYAS 239
XX 181 INSGASTLEDVYALELETSWQGSSTVOGSDTGVFNNEILALIPGNGFVTLVWVDYAS 240
XX 181 INSGASTLEDVYALELETSWQGSSTVOGSDTGVFNNEILALIPGNGFVTLVWVDYAS 240
XX 240 LAIKFPGSGSSSVYRVEYPLRPIADDTGASAPRTVIGRNGCKTVDRDDFD 299
XX 240 LAIKFPGSGSSSVYRVEYPLRPIADDTGASAPRTVIGRNGCKTVDRDDFD 299
XX 241 LAIKFPGSGSSSVYRVEYPLRPIADDTGASAPRTVIGRNGCKTVDRDDFD 300
XX 241 LAIKFPGSGSSSVYRVEYPLRPIADDTGASAPRTVIGRNGCKTVDRDDFD 300
XX 300 GNOIOLMPKSNNDPVOLATIRKDTIRNSGCLITVYAGVYVIMPCDTAVEAIV 360
XX 300 GNOIOLMPKSNNDPVOLATIRKDTIRNSGCLITVYAGVYVIMPCDTAVEAIV 360
XX 360 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 419
XX 360 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 419
XX 361 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 420
XX 361 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 420
XX 420 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 478
XX 420 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 478
XX 421 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 480
XX 421 QIMNGTIIINRSNTVLAASGGIKATTLVOTLDVTLLQGMALNDPAREVITVGFAD 480
XX 479 GSSGQWVFTNEGAILNKGLADVYQANPKERIIYPAIGKGNOMFLPV 530
XX 479 GSSGQWVFTNEGAILNKGLADVYQANPKERIIYPAIGKGNOMFLPV 530
XX 481 KSKXQWVFTNEKAILNKXXXXVQANPKERIIYPAIGKGNOMFLPV 532
XX 481 KSKXQWVFTNEKAILNKXXXXVQANPKERIIYPAIGKGNOMFLPV 532

AAZ5973
ID AAZ5973 standard; protein: 533 AA.
XX
XX AAZ5973;
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin protein consensus sequence 2.
XX
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform.
XX
XX Viscum album.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 15 /label= Asp, Glu
XX Misc-difference 51 /label= Gly, Glu
XX Misc-difference 56 /label= Ile, Val
XX Misc-difference 75 /label= Leu, Ala
XX Misc-difference 107 /label= Asp, Arg, none
XX Misc-difference 113 /label= Asn, Thr
XX Misc-difference 118 /label= Pro, Thr
XX Misc-difference 134 /label= Asp, Glu
XX Misc-difference 141 /label= Ser, Thr
XX Misc-difference 145 /label= Phe, Tyr
XX Misc-difference 152 /label= Thr, Ala
XX Misc-difference 177 /label= Ala, Tyr
XX Misc-difference 186 /label= Tyr, Asp
XX Misc-difference 188 /label= Ala, Glu
XX Misc-difference 191 /label= Val, Met
XX Misc-difference 219 /label= Ile, Phe
XX Misc-difference 224 /label= Phe, Ser
XX Misc-difference 229 /label= Pro, Thr
XX Misc-difference 233 /label= Thr, Ser
XX Misc-difference 236 /label= Asp, Ser
XX Misc-difference 287 /label= Asn, Ser
XX Misc-difference 290 /label= Cys, Arg
XX Misc-difference 325 /label= Gly, Asn
XX Misc-difference 422 /label= Gly, Asp
XX Misc-difference 435 /label= Gly, Glu
XX Misc-difference 439 /label= Val, Asp
XX Misc-difference 442 /label= Glu, Lys
XX Misc-difference 442 /label= Gly, none

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Page 6

QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	5
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D6		6.	QKSDSKTALIDVYNNVAHQAGDGSFFELADPEGAETHLFTGTTRKASSIPFASXYCLE	120
OY		120	RVGAGNRQTPTGLDIOLISGVTALRPFGGSTFRONRSIIILLIOWISEAARPNILMEAPROY	179
D6		121	RVAGRGTPPTFGJIOIGSYALKRFPGSSIRKQNSIIILLQWISDAERENILIMARKX	180
OY		160	INSGASTPYMTFLFIQSOMQSCVOHSDGVNNEFLRIALPSPGFLLTNRPVLVS	239
D6		161	INSGASTPDYMLFEIISMGQDSQQVGHSTDGVPANRLAIIXGAFVTLNREAXIAS	240
OY		240	IATMIFPCRSESSSVRYPMFLVTFPIVALDVTCASSEPFWARVERNGKVDVEDDFHD	259
D6		241	IATMIFPCRSESSSVRYPMFLVTFPIVALDVTCASSEPFWARVERNGKVDVEDDFHD	300
OY		300	GNOCLMPKSNNDPROGANTVDOGTIRNSGCLTYGTGTGYVMFLPDONTAVAREATIM	359
D6		301	GNCLMPKSNNDPROGMTIKDDITIRNSGCLTYGTGTGYVMFLPDONTAVAREATIM	360
OY		360	QIMGKGTINPPSHVLVAASGGIKETLTIVOTLDVYLGGQWLAKGDPAEPETVYGFDL	419
D6		361	QIMGKGTINPPSHVLVAASGGIKETLTIVOTLDVYLGGQWLAKGDPAEPETVYGFDL	420
OY		420	CMSNGSWMZTCVCSQOND-SMALVYGDGSIIRPXONDCTICGRDSVTVINIVCSA	478
D6		421	CMSNXKSQWTNPENGGAILNLSMDLMDVQAMPLEARIITPATCKPKOMKLFV	530
OY		479	GSGCGRWTFNPNKGAILNLSMDLMDVQAMPLEARIITPATCKPKOMKLFV	530
D6		481	KSXQRWFETNEKAILNLKXXXXXXDVDAQPRPLRIIITPATCKPKOMKLPV	532
RESULT		7		
AAY25976		ID	AAY25976 standard; protein; 533 Aa.	
AA25976:				
18-OCT-1999			(first entry)	
DB			Mistletoe lectin protein consensus sequence 3.	
XX		XX		
KM		XX	Mistletoe; lectin; antitumour; immunostimulant; A-chain; MUA; immunity;	
KM		KW	tibiozyme 285 subunit; non-cytotoxic; T-cell activation, immune response;	
KW		KW	lymphokine-producing macrophage; uncontrolled cell growth; treatment;	
XX		XX	cancer; cytotoxicity; antigen; isoform.	
XX		XX	Viscum album.	
XX		XX		
FH		Key	Location/Qualifiers	
FN		Misc-difference 15	/label= Asp, Glu	
FN		Misc-difference 63	/label= Gly, Gln	
FN		Misc-difference 66	/label= Ile, Val	
FN		Misc-difference 75	/label= Leu, Ala	
FN		Misc-difference 107	/label= Asp, none	
FN		Misc-difference 113	/label= Asn, Thr	
FN		Misc-difference 117	/label= Pro, Thr	
FN		Misc-difference 134	/label= Ser, Glu	
FN		Misc-difference 143	/label= Asp, Thr	
FN		Misc-difference 145	/label= Phe, Tyr	
FN		Misc-difference 152	/label= Thr, Ala	
FN		Misc-difference 177	/label= Ala, Tyr	

Dy 479 GSGGCRWVFTEGGAILNLKGLAMDVAQNPCLRRIITYPATCKPNOMLPEV 530
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 481 KSKXQRWFETEXAILNLKKXXXXDVAQNPKLRRIITYPATGKNOMMLPV 532

RESULT 7	
AAV25976	
ID	AAV25976 standard; protein; 533 AA
XX	
AC	AAV25976;
NC	

DT	18-OCT-1999 (first entry)
XX	
DE	Mistletoe lectin protein consensus sequence 3.

AA Mistletoe; lectin; antitumour; immunostimulant; A-chain; MDA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform.

OS Viscum album.

Alt FH	Key	Location/Qualifiers

```

FT      MISC-difference is
FT      /label= Asp, Glu

```

```

FT      Misc-difference 63
FT      /label= Gly, Gln
FT

```

Misc-difference 66

Misc-difference 75

FT Misc-difference 107

```
ET / label=asp, none
ET Misc-difference 113
```

```

ET      /Label= Asn, Jnr
ET      Misc-difference 117

```

```

ET 134 /label= Pro, Thr
DE 134

```

FT	/label= Asp, Glu
FT	

```

FT      /label= Ser, Thr
FT

```

FT	Misc-difference	Label=	Phe, Tyr
FT	145		

FT Misc-difference 152 /1961 = Thr 21a

FT Misc-difference 177

[illegible]

FT Misc-difference 180 /label= Tyr, Asp
 FT Misc-difference 183 /label= Ala, Glu
 FT Misc-difference 191 /label= Val, Met
 FT Misc-difference 219 /label= Ile, Phe
 FT Misc-difference 224 /label= Pro, Ser
 FT Misc-difference 225 /label= Thr, Thr
 FT Misc-difference 232 /label= Thr, Ser
 FT Misc-difference 236 /label= Asp, Ser
 FT Misc-difference 287 /label= Asn, Ser
 FT Misc-difference 290 /label= Cys, Arg
 FT Misc-difference 325 /label= Gly, Asn
 FT Misc-difference 364 /label= Gly, Asp
 FT Misc-difference 426 /label= Gly, Glu
 FT Misc-difference 435 /label= Val, Asp
 FT Misc-difference 438 /label= Glu, Lys
 FT Misc-difference 442 /label= Gly, none
 FT Misc-difference 443 /label= Arg, Lys
 FT Misc-difference 464 /label= Cys, Ser, Val
 FT Misc-difference 480 /label= Ala, Gly
 FT Misc-difference 481 /label= Ser, Gly
 FT Misc-difference 483 /label= Ser, Gly
 FT Misc-difference 484 /label= Gly, Ser
 FT Misc-difference 493 /label= Gly, Tyr
 FT Misc-difference 500 /label= Asn, Ser, Thr, Lys
 FT Misc-difference 501 /label= Ser, Gly
 FT Misc-difference 503 /label= Leu, Pro
 FT Misc-difference 504 /label= Ala, Met
 FT Misc-difference 533 /label= Met, Val
 FT Misc-difference 533 /label= Pro, Phe
 XX DE19804210-AL.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL, GMBH.
 XX Morris F, Stiefel T, Voelter W, Welters P;
 XX WPI, 1999-44535/38.
 XX

FT Preparation of mistletoe lectins in heterologous systems,
 FT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 40; Page 37-38; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have anticancer and immunostimulatory activity. The A-chain (MA)
 CC of mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Not only does (I) inactivate itself and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX
 SQ Sequence 533 AA;
 Query Match 90.3%; Score 2519; DB 20; Length 533;
 Best Local Similarity 92.5%; Pred. No. 1,4e-219;
 Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
 QY 1 YERLRLVHQTGEYFRFTLLADYSSGSFSENEPLRSGSTPVSADAPFVLELTN 60
 1 YERLRLVHQTGEYFRFTLLADYSSGSFSENEPLRSGSTPVSADAPFVLELTN 60
 DB 61 QGDSITAIADYTNLYVAVTQGDSTFRLAPRGAEHLFTGTR-SGLPNSGPDLR 119
 61 QGDSITAIADYTNLYVAVTQGDSTFRLAPRGAEHLFTGTR-SGLPNSGPDLR 119
 QY 120 RYVGRROQPGIDOLIOGYVLAEPGSGSTGTOARSHIILITWISSEAPPIIMAPAOY 179
 120 RYVGRROQPGIDOLIOGYVLAEPGSGSTGTOARSHIILITWISSEAPPIIMAPAOY 179
 DB 121 RYVGRROQPGIDOLIOGYVLAEPGSGSTGTOARSHIILITWISSEAPPIIMAPAOY 180
 121 RYVGRROQPGIDOLIOGYVLAEPGSGSTGTOARSHIILITWISSEAPPIIMAPAOY 180
 QY 180 INSGASLPDYVMELETSGQOSTVOCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 239
 180 INSGASLPDYVMELETSGQOSTVOCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 239
 DB 181 INSGASLPDYVMELETSGQOSTVOCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 240
 181 INSGASLPDYVMELETSGQOSTVOCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 240
 QY 240 LAIMEFCGERSSGSPVWFLIRPVADVYTCASLSEPTVIRGNKQCVADDDPHD 299
 240 LAIMEFCGERSSGSPVWFLIRPVADVYTCASLSEPTVIRGNKQCVADDDPHD 299
 DB 241 LAIMEFCGERSSGSPVWFLIRPVADVYTCASLSEPTVIRGNKQCVADDDPHD 300
 241 LAIMEFCGERSSGSPVWFLIRPVADVYTCASLSEPTVIRGNKQCVADDDPHD 300
 QY 300 GNOICLWPKSNNDPQWLITKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 359
 300 GNOICLWPKSNNDPQWLITKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 359
 DB 301 GNOICLWPKSNNDPQWLITKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 301 GNOICLWPKSNNDPQWLITKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 QY 360 QITMGNTIINRSNVLAASSGSKOTLLVOTLDYTLQCGMLAGNDTAREYTYFFDL 419
 360 QITMGNTIINRSNVLAASSGSKOTLLVOTLDYTLQCGMLAGNDTAREYTYFFDL 419
 DB 361 QITMGNTIINRSNVLAASSGSKOTLLVOTLDYTLQCGMLAGNDTAREYTYFFDL 420
 361 QITMGNTIINRSNVLAASSGSKOTLLVOTLDYTLQCGMLAGNDTAREYTYFFDL 420
 QY 420 QESNGSGWETCTGSGQONQ-RNALYGDGSIIPKQNDQCLTCGRDSYVINIVCSA 478
 420 QESNGSGWETCTGSGQONQ-RNALYGDGSIIPKQNDQCLTCGRDSYVINIVCSA 478
 DB 421 QESNGSGWETCTGSGQONQ-RNALYGDGSIIPKQNDQCLTCGRDSYVINIVCSA 480
 421 QESNGSGWETCTGSGQONQ-RNALYGDGSIIPKQNDQCLTCGRDSYVINIVCSA 480
 QY 479 GSSQGRVFTTEGALINIXXGMLAMDVAVQANPKLRITITYPATGKNQMWLEPV 530
 479 GSSQGRVFTTEGALINIXXGMLAMDVAVQANPKLRITITYPATGKNQMWLEPV 530
 DB 481 KXKXQWVFTTEGALINIXXGMLAMDVAVQANPKLRITITYPATGKNQMWLEPV 532
 481 KXKXQWVFTTEGALINIXXGMLAMDVAVQANPKLRITITYPATGKNQMWLEPV 532
 XX
 RESULT 8
 AB079450 standard; Protein, 551 AA.
 XX
 AC AB079450;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Galactose-recognising mistletoe lectin.
 XX

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.rag

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XV	Mistlec; galactose-recognising mistlelec lectin; MIII.
XX	Viscum album.
OS	Key Location/Qualifiers
FH	Misc-difference 223 /note= "Encoded by ATG"
FT	Misc-difference 251 /note= "Encoded by TTT"
FT	Misc-difference 344 /note= "Encoded by TCG"
FT	Misc-difference 380 /note= "Encoded by GCC"
FT	Misc-difference 448 /note= "Encoded by GTC"
FN	D8I00944027-A1.
PN	14-MAR-2002.
XX	06-SEP-2000; 2000DBE-1044027.
PF	06-SEP-2000; 2000DBE-1044027.
PR	06-SEP-2000; 2000DBE-1044027.
PA	(VISC-) VISCUM AG.
XX	Kieff S;
PI	WFI; 2002-316737/36.
NX	N-BSDH; ABLS6947.
PT	New nucleic acid encoding preprolactin of mistlelec lectin, useful as diagnostic and therapeutic agents, also encodes polypeptide -
PS	Claim 1; Fig 1; 6pp; German.
XX	The invention relates to a nucleic acid molecule (ABLS6947) that encodes a preprolactin (AB793450) which, after maturation, has the biological activity of the galactose-recognising mistlelec lectin (MIII). The MIII encoding nucleic acid molecule, primers specific to it or complements of it, and encoded (oligonucleic) polypeptides are useful as diagnostic and therapeutic agents.
CC	Sequence 551 AA;
SQ	Query Match 84.3%; Score 2352.5; DA 23; Length 551; Best Local Similarity 88.0%; Pred. 1.9e-204 Matches 449; Conservative 21; Mismatches 35; Indels 5; Gaps 1
OY	1 YEBLAEVHTQFTESEFFPITLLADYSSGSFSNEIPILROSTIPVSDAORFVLVELTN 60
Db	34 YEHLAEVHTQFTEDEFPITLLADYSSGSFSNBIPLKOSTIPVSDAORFVLVELTN 93
OY	61 QGGDSITAIPIITLVIAVAAGDGSFLFDAPGAETHLPFGTTRSLSPNGSITDLER 120
Db	94 QGGDSITAIPIIVLVIAVAGDGSFLFDAPGARHLTGITRSSLPNGSIDLER 153
OY	121 YAAHDQDPISIDLOISTVLAEPGSGPTPARSGILTIOMISEANRPILPARAOYT 180
Db	214 NSSGFPLDTVLELETSGQSSTVOQGSDGVENRPIRLISTNPVLISWDVYASL 273
OY	154 YAAHDQDPISIGIELIOSVALYSALYGSSTPAQASIIILIOISSEANRPILFRWRQDI 213
Db	181 NSGAFPLEDVVLELETSGQSSTVOHSTGDVTNNPKILAIPGNPVTLINWEDVIASL 240
OY	241 AATLTNGCGRSSSDVFVWPIETRT-----ADDTCSAEPFTRIYGSKCTVDIRD 295
Db	274 AATLTNGCGRSSSDVFVWPIETRT-----ADDTCSAEPFTRIYGSKCTVDIRG 333
OY	296 DPEDDNQIQAWSSANNPDNLMTKRKGRISSNGSLTYGYGTAGYVWIPDCNAVE 355
Db	334 KEFANSPQLWCCEFNPDNPWTIRRGFISNSGRCLTYGYGTAGYVWIPDCNAVE 353

Oy		356	AATHTQWIKNGKGIINPNSULVLAASGIGKOTLLTVORTLDYTLQQOMLANSNDAPREVIYVG	415
Dd		394	ATLMWDINKGIIINPNSULVLGAAGSGSTLVLTVOGVYSLSQGMLANGDIPAREVIYVG	453
Oy		416	FEDLCMESGSJWVEVCVSQQONRMALYKDSSIRPKXODPOLCTCGSDSVSTVINIVS	475
Dd		454	FEDLCMEANGLASVWEVTCCSGSNRMAALYKDGSIIRFKNOPOCLCTCGSDSVSTVINIVS	513
Oy		476	CNAGSGSCGWFFINBGTAILMTEKRLAADVIA	505
Dd		514	CNAGSGSCGWFFINBGTILLNLNGIADVIA	543
		RESULT 9		
Xx		AAKZ5985		
Xx		AAI25985 standard; Protein: 263 AA.		
Xx		AAI25985;		
Dt		18-OCT-1999	(first entry)	
Dt		Mistletoe lectin B protein fragment.		
Xx		Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;		
Kw		Ilyosoyne 288 subunit; non-cytotoxic; T-cell activation; immune response;		
Kw		lymphokine-producing macrophages; uncontrolled cell growth; treatment;		
Xx		cancer; cytotoxicity; antigen; isoform; lectin B.		
Xx		Viscum album.		
Cs		DELJ9804210-A1.		
Fm		12-AUG-1999.		
Pd		03-FEB-1998; 98DE-1004210.		
Xx		03-FEB-1998; 98DS-1004210.		
Xx		(EIOS-) BIOSYN ARNEIMITTEL GMBH.		
Pa		Morris P, Stiefel T, Voelter W, Welters P;		
Fi		WPI: 1999-445335/38.		
Dr		N-PDB: AA209109.		
Xx		Preparation of mistletoe lectins in heterologous systems,		
Pf		particularly for use as anticancer agents and immunostimulants		
Xx		Claim 9; Fig 7B; 78pp.; German.		
Bz		This invention describes a novel mistletoe lectin (I) and its fragments		
Cc		CC which have antitumor and immunostimulatory activity. The A-chain (MAA)		
Cc		of the mistletoe lectin binds to, and inactivates, the 28S subunit of		
Cc		ribosomes. Non-cytotoxic forms of (I) activate T-cell and CC		
Cc		lymphokine-producing macrophages, so stimulate immunity. (I) and its		
Cc		fragments are used to treat uncontrolled cell growth, particularly of the		
Cc		cancers, and also they induce cytotoxic, humoral and cellular length of the		
Cc		antigen and are thus ideal for use as adjuvanted antigen		
Cc		CC (tumour-associated, bacterial or viral). "The method allows production of		
Cc		mistletoe lectin, and its individual chains, in many different isoforms		
Cc		and on a large scale, at any time of the year. Recombinant products are		
Cc		free from toxins present in natural mistletoe extracts. This sequence		
Cc		represents a fragment of a mistletoe lectin B protein.		
Xx				
Sq		Sequence 263 AA:		
		Query Match: 50.9%; Score 1420; DB 20; Length 263;		
		Percent Similarity: 100.0%; Pseq No 0/2, 6e-120;		
		Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
Dd		265	DVDTCSASEPTFARVRKMKGVAVDDPDHDGNOLWMPSPKSNNPNQWLTKDKGGTIS	328
Dd		1	DVDTCSASEPTFARVRKMGKVAVDDPDHDGNOLWMPSPKSNNPNQWLTKDKGGTIS	60

QY 329 NSGCLTYGTAGYVWIFDCNTAVRENTIWOIMNGTIIINPSNVLAAASGKGTTLT 388
DB 61 NSGCLTYGTAGYVWIFDCNTAVRENTIWOIMNGTIIINPSNVLAAASGKGTTLT 120
QY 389 VOTLDITLGGSLAGNDTAPREVITIGFRDLCSNCSGSWVETCVSSQONQRMALYDGG 448
DB 121 VOTLDITLGGSLAGNDTAPREVITIGFRDLCSNCSGSWVETCVSSQONQRMALYDGG 180
QY 449 SIRPKONODQCLTCGRDSVSTVINIVSCNASSGQRMWFTNSGAILNLKNGLAMPVQAN 508
DB 181 SIRPKONODQCLTCGRDSVSTVINIVSCNASSGQRMWFTNSGAILNLKNGLAMPVQAN 240
QY 509 PKLRRIIIVPATGKPNQMWLPVP 531
DB 241 PKLRRIIIVPATGKPNQMWLPVP 263

RESULT 10

AAV25991
ID AAV25991 standard; Protein: 264 AA.

AC AAV25991;

DT 18-OCT-1999 (first entry)

DE Mistletoe lectin B variant protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;

KW 288 amino acid; non-cytotoxic; T-cell activation; immune response;

KM lymphoma; cancer; antitumor; antitumor; antitumor; antitumor;

XX cancer; cytotoxicity; antigen; isoflavon; lectin B.

OS Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelter W, Welters P;

DR WPT; 1999-445335/38.

DR N-PSDB; AA209115.

PT Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 138; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumor and immunostimulatory activity. The A-chain (MIA)

XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and

XX lymphokine-producing macrophages, so stimulate immunity. (I) and its

XX fragments are used to treat uncontrolled cell growth (particularly

XX (tumour-associated) particularly to a co-administered antigen

XX and on a large scale, at any time of the year. In many different isoforms

XX free from toxins present in natural mistletoe extracts this sequence

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 269 DDTVCASAPRVIITIGRCKCTDRDDPHHNCQQLMBSKNDPQMLTIRGOTTIR 328
DB 1 DDTVCASAPRVIITIGRCKCTDRDDPHHNCQQLMBSKNDPQMLTIRGOTTIR 60
QY 329 NSGCLTYGTAGYVWIFDCNTAVRENTIWOIMNGTIIINPSNVLAAASGKGTTLT 388
DB 61 NSGCLTYGTAGYVWIFDCNTAVRENTIWOIMNGTIIINPSNVLAAASGKGTTLT 120
QY 389 VOTLDITLGGSLAGNDTAPREVITIGFRDLCSNCSGSWVETCVSSQONQRMALYDGG 448
DB 121 VOTLDITLGGSLAGNDTAPREVITIGFRDLCSNCSGSWVETCVSSQONQRMALYDGG 180
QY 449 SIRPKONODQCLTCGRDSVSTVINIVSCNASSGQRMWFTNSGAILNLKNGLAMPVQAN 508
DB 181 SIRPKONODQCLTCGRDSVSTVINIVSCNASSGQRMWFTNSGAILNLKNGLAMPVQAN 240
QY 509 PKLRRIIIVPATGKPNQMWLPVP 531
DB 241 PKLRRIIIVPATGKPNQMWLPVP 263

RESULT 11

AAW6462
ID AAW6462 standard; Protein: 263 AA.

AC AAW6462;

DT 23-OCT-1998 (first entry)

DE Mistletoe TMB variant protein.

XX Mistletoe TMB variant protein; effect; cytotoxic;

KW 288 amino acid; non-cytotoxic; T-cell activation; immune response;

KM lymphoma; cancer; antitumor; antitumor; antitumor; antitumor;

XX cancer; cytotoxicity; antigen; isoflavon; lectin B.

OS Viscum album.

XX W09829540-A2.

XX 09-JUL-1998.

XX 02-JAN-1998; 98WO-EP00009.

XX 02-JAN-1997; 97EP-010012.

PA (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.

PI Beck J, Schmidt A, Zinke H;

DR WPT; 1998-38122/33.

DR N-PSDB; AAV51344.

PT Disclosure; Fig 11b; 115pp; German.

XX This sequence represents a variant mistletoe lectin B-chain, TMB. This

XX sequence can be used in the construction of a fusion protein which

XX comprises an effector module that is cytotoxic intracellularly, a

XX processing module covalently bonded to the effector module and

XX covalently bonded to the processing module, able to bind specifically to

XX the surface of a cell, so as to facilitate the internalisation of the fusion

Query Match	50.4%	Score 1406;	DB 19;	Length 263;
Best Local Similarity	98.9%;	Pred. No. 4.9e-119;		
Matches 260;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0

269 D V T C S A S E P T R I V R K N C M C V D A R D D F H D G N O I O L M B S K S N N D P N O L M T I R K D G T I R S 328

329 NGSGLTITTYGTAGVYVMI^{PD}ONTAVREATI^{WQ}I^WNGNGTITNPRSNLVLAASSGIKGT^{LT} 388

Db 61 NSCLTYYGAYGVYMFDCNTAVBATHWQJWNGTIIINPRNVLVAASSGIGKLT 120

Dp 121 VQITDYLTGGGVLGNDTAPREVLTIGFRDLQIESNGGSWAVETCVSSQKNGKRALYGDG 180

449 SIREKONODCTTCGRDSTVINITVYSCAGSSGQRWPFNEGAILNLKNGLANDVAQAN 508

QY 509 PKLRRIIYPATSKPNQWLLPVP 531

Db 241 PKLRRIIYPATGKKNQMMPLVP 263

RESULT 12
AAW10023

XX
AC
AAW10023;

DT 18-DEC-1997 (first entry)
XX
XX

XX Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.
KW
XX

OS Viscum album.
XX
XX
PV FFF71333 11

XX 02-JAN-1997.
PD
YY

PF 26-JUN-1995; 95EP-0109949.
XX
PR 26-JUN-1995; 95EP-0109949

XX
PA (MADU) MADATUS KOELN AG.
XX

PI Baur A, Eck J, Ientzen H, Zinke H;
XX
DR WPI: 1997-054678/06

DR	N-PSDB, AAT70475.
XX	
PT	Nucleic acid encoding neuro form of mistletoe lectin - for

PT
XX therapeutic or diagnostic use

Mistletoe lectin is a cytotoxic agent that has been used for tumour therapy. It can be used in immunotoxins and medicaments. Nucleic acid fragments can be used in diagnostic methods. Mistletoe lectin (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).

Sequence 264 AA;

Best Local Similarity	Best Match	Best Match	Best Match
98.9%	98.9%	98.9%	98.9%
2; Mismatches	2; Mismatches	2; Mismatches	2; Mismatches
1; Indels	1; Indels	1; Indels	1; Indels
0; Gaps	0; Gaps	0; Gaps	0; Gaps

QY 269 DDVTCASBPYRIVSGNMCVDVRDDDFHGNQIQIWPESKSNNDPNQIWTIKRDCITRS 328

329 NGSCLTYGVAVGVYWI FDCNDAVRBAATIMQIMNGTIIINPRSNIVLAASSGIGKGYLT 388

62 NGSCLTITGYTAGVYVMI FDCNPAVREKLTLMQJWNGNTI INPRSNLVLAASSGKIGTITLT 121

Db 122 VCTLDYTLGQGLAGNDTAPRETTIYGRFDLCMBENGGSVWVETCVSSQKNQRMALYGDG 181

QY 449 SIREKONDOCLTCGRDSVSTVINIVSCSAGSSGGRWVFTEGAILNLKXGLAMDYAOAN 508

QY 509 PKLRRIITYPATGKPNQMMLPV 531

Db 242 PXLRIIIYPATGKNQMMIPV 264

RESULT 13
AAW90126

XX
AC AAW90126;
AC

DT	20-MAR-2003	(updated)
DT	30-APR-1999	(first entry)

DE Mistletoe ML B-chain protein.
XX

KW dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
KW cancer.

OS Viscum album.
XX
XX

XX
PD 16-DEC-1998.
XX

PF 26-JUN-1995; 98EP-0105660.
XX
00 JUN 1995 0000 0100010

PR 26-JUN-1995; 98EP-0105660.
XX
BT (MORT) MARIUS KOVY NC

XX Baur A, Eck J, Lentzen H, Zinke H;
PI
XX

```
DR WPI; 1999-026582/03.
DR N-PSDB; AAV74181.
XX
```

PT New transgenic plant expressing mistletoe lectin - useful for
PT producing recombinant lectin in e.g. cancer diagnosis and therapy
XY

PS Disclosure; Fig 4b; 30pp; German.
XX
CC This invention describes a novel transgenic plant transformed with a

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Page 12

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XX 03-FEB-1998; 98DE-1004210.
PF
XX 03-FEB-1998; 98DE-1004210.
PR
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Welters P;
XX MPI: 1999-44535/38.
XX N-PSDB; AA209110.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 8b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (WLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different
XX organisms, and on a large scale, at any time of the year. The products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B1 protein.
XX
XX Sequence 264 AA:
SQ
Query Match 48.0%; Score 1339.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 5.4e-113;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 269 DVTCSASEPTVIVGNMNCYDPRDDPDRDPSQIQMPKSNDRPDLTIKEDTIR 328
DB 1 DVTCSASEPTVIVGNMNCYDPRDDPDRDPSQIQMPKSNDRPDLTIKEDTIR 60
QY 329 NSGCTVGTAGVYWMIFPCNTAVREATIMQIMKNTINPESNVLAAAGIKGTLT 388
DB 61 NSGCTVGTAGVYWMIFPCNTAVREATIMQIMKNTINPESNVLAAAGIKGTLT 120
QY 389 VQTLDTYLGQGNLANDTAPREVTIVGFADLCMESNGSVMWETCVSSQONO-RNALYED 447
DB 121 VQTLDTYLGQGNLANDTAPREVTIVGFADLCMESNGSVMWETCVSSQONALYED 180
QY 448 GSIRKONODCLTQERDSYVTINIVYSCAGSSQKRVFTNEGATINRGLACVPAQA 507
DB 181 GSIRKONODCLTQERDSYVTINIVYSCAGSSQKRVFTNEGATINRGLACVPAQA 240
QY 508 NPKLRRIIIVPATCKKQNMWLPV 530
DB 241 NPKLRRIIIVPATCKKQNMWLPV 263
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Search completed: December 11, 2003, 14:07:42
Job time : 53.4693 secs

Thu Dec 11 16:09:54 2003

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Page 1

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 34.2191 Seconds

2886.029 Million cell updates/sec

Title: US-09-601-667C-4

Perfect score: 2791

Sequence: 1 YERLRKLVHTQTGEYFRF.....REIITYPATCKNQMWLPVP 531

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 18593659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.*

- 1: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 3: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
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- 5: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 6: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 7: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 8: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 9: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 10: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 11: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 12: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 13: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 14: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 15: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 16: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 17: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*
- 18: /cgm2_6/p/rodetea/1/pubpa/US07_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1406	50.4	263	9	US-09-347-064-10
2	1406	50.4	267	9	US-09-347-064-4
3	1304	46.7	576	12	US-10-083-356A-1
4	1285	46.0	252	9	US-09-347-064-8
5	1281	45.9	252	9	US-09-347-064-2
6	1271	45.9	252	9	US-09-347-064-2
7	387	13.9	257	12	US-10-127-890-3
8	387	13.9	257	12	US-10-127-890-4
9	344.5	12.3	253	12	US-10-127-890-4
10	326	11.7	247	10	US-09-792-793A-39
11	326	11.7	247	12	US-10-375-209A-19
12	324	11.6	247	12	US-10-127-890-6
13	319	11.4	289	12	US-10-280-679B-4
14	317.5	11.4	251	12	US-10-127-890-111
15	313.5	11.2	251	12	US-10-127-890-102

16	308.5	11.1	251	12	US-10-127-890-101	Sequence 101, App
17	308.5	11.1	251	12	US-10-127-890-110	Sequence 110, App
18	308	11.0	332	9	US-09-765-527-251	Sequence 251, App
19	307.5	10.9	251	12	US-10-127-890-99	Sequence 99, App
20	307.5	10.9	251	12	US-10-127-890-100	Sequence 100, App
21	303.5	10.9	251	12	US-10-127-890-105	Sequence 105, App
22	303.5	10.9	251	12	US-10-127-890-107	Sequence 107, App
23	302.5	10.9	251	12	US-09-765-527-247	Sequence 247, App
24	304.5	10.9	251	12	US-10-127-890-2	Sequence 2, App
25	304.5	10.9	251	12	US-10-127-890-103	Sequence 103, App
26	304.5	10.9	251	12	US-10-127-890-106	Sequence 106, App
27	304.5	10.9	251	12	US-10-127-890-108	Sequence 108, App
28	304.5	10.9	251	12	US-10-127-890-109	Sequence 109, App
29	304.5	10.9	507	12	US-10-174-586-11	Sequence 11, App
30	303.5	10.9	251	12	US-10-127-890-104	Sequence 104, App
31	301.5	10.8	251	12	US-10-127-890-107	Sequence 107, App
32	301.5	10.8	303	9	US-09-765-527-253	Sequence 253, App
33	291.5	10.6	247	10	US-09-792-793A-34	Sequence 34, App
34	294.5	10.6	247	12	US-10-375-209A-34	Sequence 34, App
35	284.5	10.2	263	12	US-10-127-890-7	Sequence 7, App
36	276	9.9	198	12	US-10-083-356A-3	Sequence 3, App
37	276	9.9	198	12	US-10-083-356A-7	Sequence 7, App
38	276	9.9	199	12	US-10-083-356A-5	Sequence 5, App
39	276	9.9	200	12	US-10-083-356A-10	Sequence 10, App
40	276	9.9	200	12	US-10-083-356A-9	Sequence 9, App
41	262.5	9.4	185	12	US-10-127-890-5	Sequence 5, App
42	260	9.3	248	12	US-10-083-356A-4	Sequence 4, App
43	254	9.1	188	12	US-10-083-356A-8	Sequence 8, App
44	254	9.1	189	12	US-10-083-356A-6	Sequence 6, App
45	254	9.1	189	12	US-10-083-356A-6	Sequence 6, App

ALIGNMENTS

RESULT 1
US-09-347-064-10
Sequence 10, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Bcr, Jungsen
APPLICANT: Schmidt, Arno
APPLICANT: Schmidt, Arno
TITLE OF INVENTION: Ribosome Inactivating Proteins Based on
TITLE OF INVENTION: Ribosome Inactivating Proteins of the mistlecote Viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347_064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/E99/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
SEQUENCE NO. 10 NOS: 38
SEQUENCE NO. 10 NOS: 38
SEQUENCE NO. 10 NOS: 38
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
Query Match: 50.4%; Score 1406; DB 9; Length 263;
Best Local Similarity: 98.9%; Pred. No. 3.6e-128;
Matches: 260; Conservative: 1; Indels: 0; Gaps: 0;
DB 1 DDVTGASABPTFRAVGNMCKVVDVDDFDGNDQQLMFSSKNNDDPDLTIRKGTIRIS 328
329 NSGCLTYGYTAGYVWIPDGNFAVRENTWQIMGNQTIIPRSNVLVAASGICGTTLT 386
61 NSGCLTYGYTAGYVWIPDGNFAVRENTWQIMGNQTIIPRSNVLVAASGICGTTLT 120

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Page 2

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Qy 389 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 448
Db 121 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 180
Qy 449 SIRPKONODCLTCGRDSVSTVIVIVSCAGSSGQGVFTMEGALINIKKGLANDVAQAN 508
Db 181 SIRPKONODCLTCGRDSVSTVIVIVSCAGSSGQGVFTMEGALINIKKGLANDVAQAN 240
Qy 509 PCLRRITITPATKPKQMWLPVP 531
Db 241 PCLRRITITPATKPKQMWLPVP 263

RESULT 2
US-09-347-064-4
/ Sequence 4, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Eck, Jurgen
/ APPLICANT: Schmidt, Arno
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on
/ TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
/ TITLE OF INVENTION: album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347, 064A
/ EARLIER FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 38
/ TYPE: PRT
/ ORGANISM: Viscum Album
US-09-347-064-4

Query Match 50.4%; Score 1406; DB 9; Length 267;
Best Local Similarity 98.9%; Pred. No. 3,6e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 269 DDTYCSASEPTTIVARNKCYVDREDDFHDGNOICLMPKSNNDNQWLTIKGTITG 328
Db 1 DDTYCSASEPTTIVARNKCYVDREDDFHDGNOICLMPKSNNDNQWLTIKGTITG 60
Qy 329 NSGCLTYGTAGVYVMIFPCCTAVREATIMQWNGIINPRNLTVAASGIGKTTT 388
Db 61 NSGCLTYGTAGVYVMIFPCCTAVREATIMQWNGIINPRNLTVAASGIGKTTT 120
Qy 389 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 448
Db 121 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 180
Qy 449 SIRPKONODCLTCGRDSVSTVIVIVSCAGSSGQGVFTMEGALINIKKGLANDVAQAN 508
Db 181 SIRPKONODCLTCGRDSVSTVIVIVSCAGSSGQGVFTMEGALINIKKGLANDVAQAN 240
Qy 509 PCLRRITITPATKPKQMWLPVP 531
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RESULT 3
US-10-083-336A-1
/ Sequence 1, Application US/10083336A
/ Publication No. US2003018165A1
/ GENERAL INFORMATION:
/ APPLICANT: Zinke, Holger
/ APPLICANT: Willard, Charles B
/ APPLICANT: Byrne, Michael P
/ APPLICANT: Wannenmacher, Robert W

Qy 389 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 448
Db 121 VQTLDTLGGGMLAGNDTAPREVTYGRFLCMESNGSVWETCVSSQGNQANALYGG 180
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Db 181 SIRPKONODCLTCGRDSVSTVIVIVSCAGSSGQGVFTMEGALINIKKGLANDVAQAN 240
Qy 509 PCLRRITITPATKPKQMWLPVP 531
Db 241 PCLRRITITPATKPKQMWLPVP 263

RESULT 4
US-09-347-064-8
/ Sequence 8, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Eck, Jurgen
/ APPLICANT: Schmidt, Arno
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on
/ TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
/ TITLE OF INVENTION: album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347, 064A
/ EARLIER FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 38
/ TYPE: PRT
/ ORGANISM: Viscum Album
US-09-347-064-8

Query Match 46.7%; Score 1304; DB 12; Length 576;
Best Local Similarity 51.0%; Pred. No. 9,8e-118;
Matches 273; Conservative 81; Mismatches 161; Indels 20; Gaps 11;

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Db 106 TLADLVNNAVGVYKAGSAIFPHDQEDBAITLFTDVQWRYTATGQVYDRELA 165
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Db 166 GNRANIELANGPLEASALVYSTGQVLPETLARSFICQMSDAPAFQYIEBWT 225
Qy 179 YINSGAFPLPDVMLELTSWQOSTVQSHTDGVNPNRILAIIPGNVLTINVDVYA 238
Db 226 RIKRIRKSAADPSVITLNSKSLTALQSNQARASIQLOQRNKSASFVIVSLIP 285
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Qy 356 ATTWQWNGTINPESNLVLAASGIGKTTITVQTLDTLGGGMLAGNDTAPREVTY 415
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Qy 416 FRLCMESNGSVWETCVSSQGNQANALYGGIRPKONODCLTCGRDSVSTVIVIV 475
Db 461 ATRWQWNGTINPESNLVLAASGIGKTTITVQTLDTLGGGMLAGNDTAPREVTY 460
Qy 461 LYLCLQNGQGVIEDCSKREQVNAIYALGSIIPQONDDCLTSISIREVYVITIS 520
Db 476 CSAGSSQGVFTMEGALINIKKGLANDVAQANXKRLRIITPATKPKQMWLPVP 530
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/ Sequence 1, Application US/10083336A
/ Publication No. US2003018165A1
/ GENERAL INFORMATION:
/ APPLICANT: Zinke, Holger
/ APPLICANT: Willard, Charles B
/ APPLICANT: Byrne, Michael P
/ APPLICANT: Wannenmacher, Robert W
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SRQ ID NO 8
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-8

Query Match 46.0%; Score 1285; DB 9; Length 252;
Best Local Similarity 99.6%; Pred No. 1, 9e-116;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRVTHQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELIN 60
DB 1 YERLRVTHQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELIN 60
QY 61 QGDSITAIADVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLER 120
DB 61 QGDSITAIADVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLER 120
QY 121 VAGHRQIFLIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYI 180
DB 121 VAGHRQIFLIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYI 180
QY 181 NSGASFEPDVMLETSWGQOSTOVQSHTDGVFNPRILAIPEGVYTLNVRVIA 240
DB 181 NSGASFEPDVMLETSWGQOSTOVQSHTDGVFNPRILAIPEGVYTLNVRVIA 240
QY 241 AMLFVCGERP 252
DB 241 AMLFVCGERP 252

RESULT 5
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
FILE REFERENCE: US20020045208A1
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-2

Query Match 45.9%; Score 1281; DB 9; Length 252;
Best Local Similarity 99.6%; Pred. No. 4, 9e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YERLRVTHQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELIN 60
DB 1 YERLRVTHQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELIN 61
QY 61 QGDSITAIADVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLER 120
DB 61 QGDSITAIADVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLER 121
QY 121 VAGHRQIFLIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYI 180
DB 121 VAGHRQIFLIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYI 181

QY 181 NSGASFEPDVMLETSWGQOSTOVQSHTDGVFNPRILAIPEGVYTLNVRVIA 240
DB 182 NSGASFEPDVMLETSWGQOSTOVQSHTDGVFNPRILAIPEGVYTLNVRVIA 241
QY 241 AMLFVCGERP 251
DB 242 AMLFVCGERP 252

RESULT 6
US-10-282-935-3
Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: RIBOSOMAL INHIBITORS
FILE REFERENCE: US20020045208A1
CURRENT APPLICATION NUMBER: US/10/282,935
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abusus precatorius
US-10-282-935-3

Query Match 17.0%; Score 474; DB 12; Length 251;
Best Local Similarity 42.6%; Pred. No. 1, 4e-37;
Matches 107; Conservative 37; Mismatches 83; Indels 24; Gaps 5;
QY 9 THQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELINQGSISITA 68
DB 9 THQGTGEYFRITLLADYSSGSFSNNEIFLLRQSTIPVSDAQRFVLYELINQGSISITA 66
QY 69 AIDVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLERVAGH-EPQ 127
DB 69 AIDVTNLVYVAYAGQSYFLRDAFGAETHLFTGTRSSILPPNGSYPLERVAGH-EPQ 126
QY 126 IEGIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYINSGASPL 187
DB 126 IEGIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYINSGASPL 186
QY 187 IEGIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYINSGASPL 240
DB 187 IEGIDQLQSVYALRFGSGSTRQARSLILQWISBAARFVILMARQYINSGASPL 236
QY 237 VAVIALMLFVC 247
DB 237 VAVIALMLFVC 247

RESULT 7
US-10-282-935-1
Sequence 1, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: RIBOSOMAL INHIBITORS
FILE REFERENCE: US20020045208A1
CURRENT APPLICATION NUMBER: US/10/282,935

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Page 4

CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 267
ORIGIN: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-282-935-1

Query Match 13.9%; Score 387; DB 12; Length 267;
Best Local Similarity 40.0%; Pred. No. 4,5e-29;
Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGHERFETTLRDVSSGS-FSNEIPL-RGSTIPVSADQRFVLYELTNGGDSI 66
13 TGAIVQSYTHFAVGRGRTGADYRHEIFVLRKVGALIN-QRIIVELSKHAEISV 70
QY 67 TAAIDVTNLYVAQAGDSYFLR-DAPRGAR--THLFTGT-TRSSLPNGSYDLEERYA 122
DB 71 TAAIDVTNLYVAQAGDSYFLR-DAPRGAR--THLFTGT-TRSSLPNGSYDLEERYA 130
QY 123 GH-RDQIPGIDQIGSVYALR--PGSGTQASIIILQWISPAFNPILMARQ 178
DB 131 GNLRENIHNGPLEAIALSYVSTGQPLTARSPICQWISPAFNPILMARQ 190
QY 179 YINSASFLPDYVMELEFSGQSTQVSGTGFNNPILALFPQNFVLTINRDYA 238
DB 191 RIRYRKADPSVYILHNSGALSTALDSNQAFAPIQLGRNSKRSYVDVSLIP 250
QY 239 SLATMLFVCGERPSS 253
DB 251 IIALMYRCAPPPSS 265

RESULT 8
US-10-127-890-1
Sequence 4, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/127,890
FILING DATE: 23-NOV-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
FIRM: McAndrews, Held & Malloy, Ltd.
ADDRESS: 500 West Madison Street, 34th floor
CITY: Chicago, IL 60661
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 13.9%; Score 387; DB 12; Length 267;
Best Local Similarity 40.0%; Pred. No. 4,5e-29;
Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGHERFETTLRDVSSGS-FSNEIPL-RGSTIPVSADQRFVLYELTNGGDSI 66
13 TGAIVQSYTHFAVGRGRTGADYRHEIFVLRKVGALIN-QRIIVELSKHAEISV 70
QY 67 TAAIDVTNLYVAQAGDSYFLR-DAPRGAR--THLFTGT-TRSSLPNGSYDLEERYA 122
DB 71 TAAIDVTNLYVAQAGDSYFLR-DAPRGAR--THLFTGT-TRSSLPNGSYDLEERYA 130
QY 123 GH-RDQIPGIDQIGSVYALR--PGSGTQASIIILQWISPAFNPILMARQ 178
DB 131 GNLRENIHNGPLEAIALSYVSTGQPLTARSPICQWISPAFNPILMARQ 190
QY 179 YINSASFLPDYVMELEFSGQSTQVSGTGFNNPILALFPQNFVLTINRDYA 238
DB 191 RIRYRKADPSVYILHNSGALSTALDSNQAFAPIQLGRNSKRSYVDVSLIP 250
QY 239 SLATMLFVCGERPSS 253
DB 251 IIALMYRCAPPPSS 265

RESULT 9
US-10-127-890-4
Sequence 4, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/127,890
  FILING DATE: 23-Apr-2002
  INVENTOR: <INVENTOR>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/646,360
    FILING DATE: 13-MAY-1996
    APPLICATION NUMBER: PCT/US94/05348
    FILING DATE: 12-MAY-1994
    APPLICATION NUMBER: US 08/064,691
    FILING DATE: 12-MAY-1993
    APPLICATION NUMBER: US 07/988,430
    FILING DATE: 09-DEC-1992
    APPLICATION NUMBER: US 97/901,707
    FILING DATE: 08-NOV-1992
    APPLICATION NUMBER: US 07/787,567
    FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Mcnicholas, Janet M.
  REGISTRATION NUMBER: 32,918
  REFERENCE/POCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312/707-8899
  TELEFAX: 312/707-9155
  TELER: 650 388-1248
  INFORMATION: 352 170-1150
SEQUENCE CHARACTERISTICS:
  LENGTH: 263 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

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Query Match 12.3%; Score 344.5; DN 12; Length 263;
Best Local Similarity 14.8%; Pct. No. 6e-25;
Matches 89; Conservative 54; Mismatches 92; Indels 19; Gaps 9;

13 TGEYPRFETLLADYVSSGSPSN--ELPLRGSTIPVSDAPFVAVETMGQSDSTTA 69
10 LKNTIKET--EDRPALPFSKHYDPLDLNST--LSSRPRLMLDSTAIETISVA 63
QY IYVNVAVVAYAGQAGQSPFLPAPRGAEHLFGCTSTSLPFGNSPPEATVAG--PQ 127
70 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 127
Db IYVNVVAVVAYRRDVSYPFKSPSPKAVMLFGTRKITPLPTONYENLQT-AAHKIR 122
QY IPIGIDILQSVTAAPPGGSGRTQANSTILLQMSAPRANMLIMAAQYNSAGSE 187
123 IDLGIPALSSAITFLFYNNQASGSA--LVLQRTTEAAKXIKIRVAKVY--ANRK 178
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 178
QY 188 PDVYMELETSGQSGSTV--GUSTGVFANPILPILAPGAVFTLNNRPVNASIAIMF 245
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 238
QY 246 VCGEPSSDVRV 258
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 250
239 L-NSRASTDENP 250

RESULT 10
US-09-792-793A-39
Sequence 39, Application US/09792793A
GenPat. No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: MCGILL JOHN R.
TITLE OF INVENTION: PHILLS
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0

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? SEQ ID NO 39
?
? LENGTH: 247
?
? ORIGIN: Trichostema hillebrandii
US-09-792-793A-39

Query Match      11.7%; SCORE 326; DB 10; Length 247:
Best Local Similarity 36.0%; Pred. NO. 3.4e-23;
Matches      86; Conservative 54; Mismatches 85; Indels 14; Gaps 9

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[illegible]

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RESULT 11
US-10-375-209A-39
; Sequence 39, Application US/10375209A
; Publication No. US2003021542A1
GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogswine, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
; TITLE OF INVENTION: 5020 OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; CURRENT PRIORITY NUMBER: US/10/375, 209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ. ID NOS.: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO. 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosantheus killowii
US-10-375-209A-39

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	Query Match Similarity	11.7%	Score 326,	DB 12	Length 247
	Best Local Similarity	35.0%	Pred. No. 3.4e-23		
	Matches	85	Conservative	54	Mismatches 85, Indels 14
					Gaps 9
QY	13	TGEEYFRFTILRDYVSSGSSSEIPELIRGOSTIFVSDAGRFVLVBELNÖGSGSTITAIIDV	72		
Db	10	TSSSGYFISINRFLAKRNLRTDIPLLR-SLEGGSS--GRKALPHETNLTDSVAILDV	66		
QY	73	66			
Db	67	126			
QY	130	189			
Db	127	182			
QY	190	244			
Db	183	241			

RESULT 12

US-10-127-890-6

; Sequence 6, Application US/10127890

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Page 6

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: Proteins

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrew, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1993
APPLICATION NUMBER: US 07/801,567
PUBLICATION NO.: EP 048XV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR OTHER INTERESTS:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

Query Match: 11.6%, Score 324, DB 12, Length 247;
Best Local Similarity 12.6%, 172, S, 4e-22
Matches 95, Conserving 54, Mismatches 86, Indels 14, Gaps 9

OY 13 TGEYRPTITLADVSQSSFSNRKILIRSGTIPVSDAQRVELIINQSGSITAIV 72
DB 10 TSSEGVGINSRKALNERNRLVDIFLR-SLPDS--GRVALIHITNYADETSVAIV 139
OY 73 TNLYVAAGAGDSYFLRA--PRGATHTPLTGTRS-SUPNSGYDLERYGH-RDQIP 139
DB 67 TNVYLIGRGADGTSPFNRSALKDAKTIVEGMKATVPILSNTERLOTAKGISNP 126
OY 130 IGDIDTGLTPASPGSTRQASILLICOMSPAAPPILMAAQINSASLTMD 169
DB 127 LGFPAIDAEATTFEY--YNASSAASMLWVLIGSTETSAKYKFTBOIQIKVRK--FTLS 182
OY 190 VYMIELEINSGQSIVQC--ASTDGFVNPIRLALPCGAFVTLNNRD--VIASLATM 244
DB 183 LAISLEINSSALSACQITASLNNGQPSPVLIIMDNQCVATITINDAGVVNSALL 241

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RESULT 13
US-10-280-679B-4
Sequence 4, Application US/10280679B
Publication No. US20030150019A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc. Biologics Corporation
TITLE OF INVENTION: Monoclonal RNA Virus Transformation Elements
FILE REFERENCE: LSBC-0109-US93
CURRENT FILING DATE: US/10/280, 679B
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 09/557,941
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 08/484,341
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1993-08-23
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
PRIOR APPLICATION NUMBER: 07/739,143
PRIOR FILING DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/710,881
PRIOR FILING DATE: 1991-07-26
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1.
SEQ ID NO 4
LSNR: 389
US-10-280-679B-4
ORGANISM: Chinese cucumber protein alpha-1,2-mannosidase
US-10-280-679B-4

Query Match 11.4%; Score 319; DB 12; Length 289;
Best Local Similarity 35.6%; Pseq. No. 2,16-22;
Matches 85; Conservativity 53; Mismatches 87; Indels 14; Gaps 9

QY 13 TGEERFRFLTRDLYVSSGSSNEMRLRGTGTPNDQRPVLYEKLQMGQSTDAITY 72
DB 33 TSSGVGFINKKALPMKRYDIFLFR SGLGSS -GVVALIHFNVDVDSVALIV 89
QY 73 TNYVVAQAGQGGYEFARLA-FGAEHLFTVGTTRS-SLPNSQSPDLEEVAGH-RDQIF 129
DB 90 TNYVIMGRKQGTGYEFMAELAEAKAYKKNARKYLPYSGNVEKRLDPAAGKRIEPT 149
QY 130 IGIDQILQSVYALSPGCGSTFGQASIIILHOMISEAFNFIEMARQIUNSGASTFD 189
DB 150 LQALPADAQSLTPPLP-TPANSAKSLNKLWQISSEBAKAKETIQOKYKVR--TLGS 205
QY 190 VYALPELDAQSGQYQVQ--ASTGYFNFNFIPLAPGAPFTLVNQRQ--VINSIALM 244
DB 206 LALISLEMSKSLASQVQIOLASTNNGQGFETVYALINAGQRVMIINVDAGVTSINALL 264

RESULT 14
US-10-127-890-111
Sequence 111, Application US/10127890
Publication No. US20030166196A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc. Biologics Corporation
TITLE OF INVENTION: Immature Toxins Comprising Ribosome-Inactivating Proteins
APPLICANT: Carroll, Stephen F.
Stunkka, Gary M.
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Heald & Malloy, Ltd.

```

Thu Dec 11 16:09:54 2003

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Page 7

1 STREET: 500 West Madison Street, 34th floor
2 CITY: Chicago
3 STATE: Illinois
4 COUNTRY: USA
5 ZIP: 60661
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent In Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/10/127,890
14 FILING DATE: 23-Apr-2002
15 CLASSIFICATION: <unknown>
16 PRIORITY:
17 APPLICATION NUMBER: US/08/646,360
18 FILING DATE: 13-May-1996
19 APPLICATION NUMBER: PCT/US94/05348
20 FILING DATE: 12-May-1994
21 APPLICATION NUMBER: US 07/988,430
22 FILING DATE: 09-Dec-1992
23 APPLICATION NUMBER: US 07/901,707
24 FILING DATE: 19-Jun-1992
25 APPLICATION NUMBER: US 07/787,567
26 FILING DATE: 04-Nov-1991
27 ATTORNEY/AGENT INFORMATION:
28 NAME: McNicholas, Janet M.
29 REGISTRATION NUMBER: 32,918
30 REFERENCE/DOCKET NUMBER: 200-70,64
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 312/707-8889
33 TELEFAX: 312/707-9155
34
35 INFORMATION FOR SEQ ID NO: 111:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 251 amino acids
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 SEQUENCE DESCRIPTION: SEQ ID NO: 111:
41
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1 GENERAL INFORMATION:
2 APPLICANT: Better, Marc D.
3 Carroll, Stephen F.
4 Studnicka, Gary M.
5 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
6 Proteins
7 NUMBER OF SEQUENCES: 173
8 CROSS-REFERENCE TO RELATED APPLICATIONS:
9 ADDRESS: Better, Marc D., Heald & Malloy, Ltd.
10 STREET: 500 West Madison Street, 34th floor
11 CITY: Chicago
12 STATE: Illinois
13 COUNTRY: USA
14 ZIP: 60661
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: floppy disk
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/10/127,890
22 FILING DATE: 23-Apr-2002
23 CLASSIFICATION: <unknown>
24 PRIORITY:
25 APPLICATION NUMBER: US/08/646,360
26 FILING DATE: 13-May-1996
27 APPLICATION NUMBER: PCT/US94/05348
28 FILING DATE: 12-May-1994
29 APPLICATION NUMBER: US 08/064,691
30 FILING DATE: 09-Dec-1992
31 APPLICATION NUMBER: US 07/988,430
32 FILING DATE: 19-Jun-1992
33 APPLICATION NUMBER: US 07/901,707
34 FILING DATE: 04-Nov-1991
35 ATTORNEY/AGENT INFORMATION:
36 NAME: McNicholas, Janet M.
37 REGISTRATION NUMBER: 32,918
38 REFERENCE/DOCKET NUMBER: 200-70,64
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 312/707-8889
41 TELEFAX: 312/707-9155
42
43 INFORMATION FOR SEQ ID NO: 102:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 251 amino acids
46 MOLECULE TYPE: protein
47 SEQUENCE DESCRIPTION: SEQ ID NO: 102:
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QY 241 ALMEFVC 247
DB 241 ALMEFVC 247

Search completed: December 11, 2003, 14:48:47
OOD time : 35.2191 secs

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Page 2

Db 334 NOTCLMPKSNNDPQWLTIKEDGTHIRNSGCLTITGAGVYVHEDCNVAREATLMO 393
QY 361 IMNGTIINPRSNVLAASGIGKTLTVOITDVTLAGQMLAGNDTAREVTIYGRDLC 420
Db 394 IMNGTIINPRSNVLAASGIGKTLTVOITDVTLAGQMLAGNDTAREVTIYGRDLC 453
QY 421 MESNGSVWETCVSSQONQOMALYGDGSTRPKONQDCLTCGRDSVTVINIYCSAGS 480
Db 454 MESNGSVWETCVSSQONQOMALYGDGSTRPKONQDCLTCGRDSVTVINIYCSAGS 513
QY 481 SCORWFTNEGAILNNGNLANDVQANPDLRIIIPATCKPQMWLPVP 531
Db 514 SCORWFTNEGAILNNGNLANDVQANPDLRIIIPATCKPQMWLPVP 564

RESULT 2
US-08-776-059-43
Sequence 43, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: ZINKE, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
CURRENT APPLICATION NUMBER: US/08/776, 059B
FILE REFERENCE: 674503-2003
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-43

Query Match 50.4%; Score 1406; DB 3; Length 263;
Best Local Similarity 98.9%; Pred. No. 6,1e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 269 DDTVCASSEPTVRIYGRNQCVDVDDPDRQVQIOLWPKSNNDPQWLTIKEDGTHIR 328
Db 1 DDTVCASSEPTVRIYGRNQCVDVDDPDRQVQIOLWPKSNNDPQWLTIKEDGTHIR 60
QY 329 NSCLTITGAGVYVHEDCNVAREATLMOINNGTIINPRSNVLAASGIGKTLT 388
Db 61 NSCLTITGAGVYVHEDCNVAREATLMOINNGTIINPRSNVLAASGIGKTLT 120
QY 389 VQITDVTLAGQMLAGNDTAREVTIYGRDLCMESNGSVWETCVSSQONQOMALYGDG 448
Db 121 VQITDVTLAGQMLAGNDTAREVTIYGRDLCMESNGSVWETCVSSQONQOMALYGDG 180
QY 449 SIREPKONQDCLTCGRDSVTVINIYCSAGSQQRWFTNEGAILNNGNLANDVQAN 508
Db 181 SIREPKONQDCLTCGRDSVTVINIYCSAGSQQRWFTNEGAILNNGNLANDVQAN 240
QY 509 PDLRIIIPATCKPQMWLPVP 531
Db 241 PDLRIIIPATCKPQMWLPVP 263

RESULT 3
US-08-776-059-33
Sequence 33, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen

APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 264
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-33

Query Match 50.4%; Score 1406; DB 3; Length 264;
Best Local Similarity 98.9%; Pred. No. 6,1e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 269 DDTVCASSEPTVRIYGRNQCVDVDDPDRQVQIOLWPKSNNDPQWLTIKEDGTHIR 328
Db 2 DDTVCASSEPTVRIYGRNQCVDVDDPDRQVQIOLWPKSNNDPQWLTIKEDGTHIR 61
QY 329 NSCLTITGAGVYVHEDCNVAREATLMOINNGTIINPRSNVLAASGIGKTLT 388
Db 62 NSCLTITGAGVYVHEDCNVAREATLMOINNGTIINPRSNVLAASGIGKTLT 121
QY 389 VQITDVTLAGQMLAGNDTAREVTIYGRDLCMESNGSVWETCVSSQONQOMALYGDG 448
Db 122 VQITDVTLAGQMLAGNDTAREVTIYGRDLCMESNGSVWETCVSSQONQOMALYGDG 181
QY 449 SIREPKONQDCLTCGRDSVTVINIYCSAGSQQRWFTNEGAILNNGNLANDVQAN 508
Db 182 SIREPKONQDCLTCGRDSVTVINIYCSAGSQQRWFTNEGAILNNGNLANDVQAN 241
QY 509 PDLRIIIPATCKPQMWLPVP 531
Db 242 PDLRIIIPATCKPQMWLPVP 264

RESULT 4
US-08-776-059-31
Sequence 31, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: ZINKE, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-31

Query Match 46.0%; Score 1285; DB 3; Length 253;
Best Local Similarity 99.6%; Pred. No. 3e-116;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YERLALNVTQTEGEYFRFTILADYVSSGSFNEIFLMQSTIPVSDQSFVLELTIN 60

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.rai

Page 3

D2	2	YAKHILNKHQCTGEEFFPTLLADHYVSSGSFNNELPLMGSTIVSDAKRPVLYELTN	61
QY	61	QGGSDSTRAIDVTLNLYVYAQDQSYFPLDAPAGHITLFTGCTRSGLPNSGTPLEER	120
D2	62	QGGSDSTRAIDVTLNLYVYAQDQSYFPLDAPAGHITLFTGCTRSGLPNSGTPLEER	121
QY	121	YAAHSDIDPLIGDILQSYVTLNLPFGSGSTTQASGIIILCOMSEAAFPFLIMAAQYI	180
D2	122	YAAHSDIDPLIGDILQSYVTLNLPFGSGSTTQASGIIILCOMSEAAFPFLIMAAQYI	181
QY	181	NSGASFPDIPVYELTSLTSMGQSTQVHSSTQANPILALPCHVTLTINRDTIAGL	240
D2	182	NSGASFPDIPVYELTSLTSMGQSTQVHSSTQANPILALPCHVTLTINRDTIAGL	241
QY	241	AIIMLVFGGRPS	252
D2	242	AIIMLVFGGRPS	253

US-08-776-059-39
Sequence 39, Application US/087760593
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
INVENTOR: LENTZEN, Hans
APPLICANT: BUCH, Siegen
APPLICANT: BUCH, Siegen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN [PMTL]
PUBLICATION NO.: 6271368
CURRENT APPLICATION NUMBER: 674503-2003
PRIORITY DATE: 1996-06-27, EP96/02273
EARLIER APPLICATION NUMBER: 674503-2003
EARLIER PILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SEQUENCE ID NOS: 1-56
SEQ ID NOS: 38
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-39

	Query Match	Best Local Similarity	100.0%;	Score 1197;	DB 3;	Length 235;
	Matches 235;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	18	FERTILLARYSSGSSNEIPILAROSTTVPVSDAGREYVLEINVOGGSITTAIDVINYV	77			
DB	1	FERTILLARYSSGSSNEIPILAROSTTVPVSDAGREYVLEINVOGGSITTAIDVINYV	60			
QY	78	VAYOGQSGYVILAPARATETPTGTSSILPNSGSPVPLBVRVGRQDPLACIDLIQ	137			
DB	61	VAYOGQSGYVILAPARATETPTGTSSILPNSGSPVPLBVRVGRQDPLACIDLIQ	130			
QY	138	SYTLARPPGQSTGRQAFSIIILQNISSAARPNILMAAQQYNSGASGLPPVYMELET	197			
DB	121	SYTLARPPGQSTGRQAFSIIILQNISSAARPNILMAAQQYNSGASGLPPVYMELET	180			
QY	198	SWGQGSSTVQGSSTDYGFNNFIRILAPGQFVTLINNEGVYASIASIAIMLFPVCGERS	252			
DB	181	SWGQGSSTVQGSSTDYGFNNFIRILAPGQFVTLINNEGVYASIASIAIMLFPVCGERS	235			

US-08-378-761A-77
 RESULT 6
 ; Sequence 77, Application US/08378761A
 ; Patent No. 5653384
 ; GENERAL INFORMATION:
 ; APPLICANT: WALSH, TERENCE A
 ; APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEIN, INACTIVE
 TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 TITLE OF INVENTION: USING
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS: 81
 CORRESPONDENT: ANDREA T. BORUCKI
 STREET: 3330 KENYARD ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION NUMBER: 33651
 CURRENT APPLICATION DATE: 10/2/87, Version #1.25
 APPLICATION NUMBER: US/08/378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BORUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 382728
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 337-4946
 IMPROVED NUMBER: 382728
 SEQUENCE CHARACTERISTICS: 77:
 LENGTH: 540 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IS-08-378-761A-77

	Query Match	42.7%	Score 139.15	DS: 1	Length 540;
	Best Local Similarity	47.6%	Pred. No. 1.2e-106;		
	Matches 254;	Conservative 84;	Mismatches 177;	Indels 19;	Gaps 10;
QY	THQTGTGGEAPFILLADPYVSSGS-FGNEIFLL-RGSTFVPVSAARFVVEKLVNQDQSI	66			
Db	13 TADATVASYTFIRARSHITGADVHRIFVLPNNVLEPIS--ORILVELSHNAESTV	70			
QY	TAIDVTNLVYVAQVQSGSYFLR-DAPRGAE--TLTSTQTRRS-SLPNQSYPDLERYA	122			
Db	71 TTAIDVTNNVYVGRGKSNKSYFFHDPQDEAELTTLTQVQNSTPAGQNDVRELDQ	110			
QY	123 GRHQDIFGLDILQISVYALRF--PGSSTFTRQARSILIDQNISEKAPFPIIMARQY	179			
Db	131 GRIHEIETQSTPEQDIALYLYVSTCTQITPLARSFVQICQISEAPRYEGEMKTR	139			
QY	186 INHSGASTLDVYMLHLETSVQSGDSTVOGSHSTDEGVPMNDIFLAPGAPVLTINRVDTAS	230			
Db	151 AKRNEASSTVETLHNSGKSTPILAD--QSGGAPSTQIQRNRSKKNVYDLSITPI	250			
QY	240 LAMTEPFCGERSSSSWYKPLRYTPRSD--DVTSASEPFTVYGNKSCMKCYRQDD	296			
Db	251 ILMATVCKAPRSSQ----ISLIRIPVYENMAD-CMDEPFIYALVGNKSLCYDVTSE	305			
QY	297 FHDNGIOLAMSGSKNNDDQGLTIKREDGTINSGSLTQVGYTAQVYVTEPCKTAYEA	356			
Db	306 FPDGNPIQWCKSTNDWQGLTKRDTISNKGKLTIKSKSPQGVYIVNGSTATGCA	365			
QY	357 TTIQMQMONTITINRSNLYVLAASGIKATLTLYQVLDLTLYGQMLAANDPAREVYTGAF	416			
Db	366 TTMQMQMONTITINRSGLVLAATSANSYTKLTQVQIPIYVASQGLPNTNTOFPVTTIYGL	425			
QY	417 RDLQENSGSVVVEFYVSSQONRMALYGGSIIRKXNDQDCLTCGRQSVATIVNSC	476			
Db	426 YQMCIQANGSGVLEETCTSKREDOQVALYADGSRFQDQNDQNLITPAIKIKQTVVILSC	485			
QY	477 SAGSGQGRWETVBSGAILNITKQGLADVDAQNPRLRIITVYPTCKRQNMQLPV	530			

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Query Match	42.7%;	Score 1191.5;	DA 1;	Length 540;
Best Local Similarity	47.6%;	Pred. No. 1.26-106;		
Matches	Conservative 84;	Mismatches 177;	Indels 19;	Gaps 106;
QY	9 THQTGGTERTFATLADRYSGGS-FSNEIPL-ROSTIPYSDQKPVLYETVNGSNI 66			
Db	13 TADATVSTFATFATLADRYHPIPLDNRKQPLPS--GRVLSTYSKHALSV 70			
QY	67 TAIIDVYNYLVAAVQAGQSPFLR-DAPGAG--TLFPGYRGS-SLPYSGYDLERA 122			
Db	71 TTAIDVYNAVVGCGKSAAPFPDQDAEATLTFPDQKSTAFPGSGYDRLEQ 130			
QY	123 GHRDIPFGIDLLQSGTALF--FGASTRTQASLTLLQWISAEARNPILMARQY 179			
Db	131 GLENEITGEGLEEDLSALSYRTGCGPPLTASFWCCQWISAEARQYIGERR 190			
QY	260 INSGASTLEPYMYELTSGMOOSQCHSTQYFNKPLALFAGFTLNNRVYAS 239			
Db	191 IRYNRSAADPEVITLSSWGRSLTAIQSGAGFASPIQCGRRGKRPVDSILPI 250			
QY	240 LAIIMFQCARSSSSDPERYMLVPIVYAL--DYVCSASAPFYVYGRNGKCYVDROD 296			

Db 251 IAAWYKCAPSSQ----FSLIIIPVPIVNFADV-CMDPEPIVIVSRGGLCVDWTGEE 305

Qy 257 FHDNQIQALPKSRKNNDDNQIMQIMTIRDGTIRANSGCLATYVYIAQVYIMLEDCTAVREA 356

Db 306 FPGNPFQIQALPKSPKSNDDNQIMQIMTIRDGTIRANSGCLATYVYIAQVYIMLEDCTAVREA 365

Qy 357 TIRQINQGTIIINSRNNILNLAASQISGTTITITQDITITQCCITACGMPARREVIYFGE 425

Db 356 TIRQINQGTIIINSRNNILNLAASQISGTTITITQDITITQCCITACGMPARREVIYFGE 425

Qy 427 RDCIENSGNSGVWVCYSCQSQNQWALYGDPSLRPMQWQDQCTCGSBVSFTVINYSG 476

Db 426 YGICAGNSGKXWLEDCSEKAEQOMALYADDSIRPQQRBNCLTTDANIKTAYVTKLSC 485

Qy 477 SAQSGQRWFMNQGAILINKLIMLVADQANPLFRRIIIVATPKRPNQMLPV 530

Db 486 GPASGQRWFMNQGAILINKLIMLVADQANPLFRRIIIVATPKRPNQMLPV 539

```

US-09-538-973-3
RESULT 8
Sequence 3, Application US/09538873
Patent No. 6566500
INVENTOR: JAMES H. WILSON; ELLEN S. GERSHBERG; JOHN M. WATKINS
APPLICANT: GIBRIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FIELD OF INVENTION: MEDICAL
CURRENT APPLICATION NUMBER: US/09/538, 973
PRIORITY DATE: 09/12/03
EARLIER APPLICATION NUMBER: 60/126, 826
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abinus precatorius
US-09-538-973-3

Query Match      17.0%; Score 474; DB 4; Length 251;
Blast Local Similarity 42.6%; Prd.No. 1..1e-37;
Matches 107; Conservative 37; Mismatches 83; Indels 24; Gaps 5

QY      9 THGTGGEEFFRFTLLADPYASGSFSMEITPLLRSGSTFVSADQAREVLNLTNGSGSITA 68
DB      9 TEGATSSCTKQIETDIALRR-LRGIIHDIFDPDF-TLDGRNKIKIVBLNSISTSEV 66
          |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      69 AIDVMNVVVYVQAGSGCYSLDNARGASATLTFGTSSGLSPNGSYLPOLSRVAGH-RDQ 127
DB      67 GIIVNNVVAARFGISGYFLTRDASSADYLFTGTDGHSDPYGTGCLREMAHQSSOQ 126
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      128 IPIGDILQSVTLAFPGDSFTTQARSITLLIQMISEARFNPTLMRAQYNIGSASF 187
DB      127 IPIQLQALHTSGSFSSGSDGNDEKATLVIIVMWALLARFYINRFYSVDTGTAA 186
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      188 PDVWLETSMTGCGSYTGTHSGVGNPNRLAIPONTVTLVNTVD-V 236
DB      187 PDANIIELENNMDLDRCVQESVQDTFPNQ-VLTIVINEPFVINDISHP 236
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      237 ISALIMLTVQC 247
DB      237 VAVALMLTVQC 247

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Thu Dec 11 16:09:53 2003

us-09-601-667c-4.rail

Page 5

? APPLICANT: WALSH, TERENCE A
? APPLICANT: HEY, TIMOTHY D
? APPLICANT: MORGAN, ALICE ER
? TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
? TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
? NUMBER OF SECTIONS: USING
? CORRESPONDENCE ADDRESS: 91
? ADDRESSEE: ANDREA T. BORUCKI
? STREET: 9330 ZIONSVILLE ROAD
? CITY: INDIANAPOLIS
? STATE: IN
?
? COUNTRY: US
?
? ZIP: 46268
?
? COMPUTER READABLE FORM:
? MEDIAUM TYPE: floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/378,761A
? FILING DATE: 26-JAN-1995
?
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: BORUCKI, ANDREA T
? REGISTRATION NUMBER: 33651
? REFERENCE/DOCKET NUMBER: 38272B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (317) 337-4846
? INFORMATION FOR SEQ ID NO.: 71:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 250 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IS-08-378-761A-71

	Query Match	16.7%	Score 466.5	DB 1	Length 250
	Best Local Similarity	42.6%	Pred. No. 5.76-37		
	Matches 107	Conservative	37	Mismatches 82	Indels 25
				Gaps	6
Qy	THQTGKEFRFTLPLTPYSGFSSNSRPLRSGTTPSPDNRQRYVLELTMQGSITLTA	68			
Dy	9 TBNASGSKQRIALRNL-RGRLHDPVLDPPT-TLERNRYVLELSPTSEIY	66			
Qy	69 AIDVYNLYVAAQKQDSTYELNARQAEHLFTGTASSLPENQSYVDLEETVYGH-RQ	127			
Dy	67 GIDVNAVYVARRPGSTSTFLRAPSASDYFLTGDDHSLPEYGVGLDEEMHOSRQ	126			
Qy	128 IPIGLIDQSTVLAFLFGSTTQTSITLITLIMSSANRPLFLNARQINSGLT	187			
Dy	127 IPIGLQDLHGISFFSGSDNREKRTTIVILQVAANRPFYISNRVRSIGDTNRQ	186			
Qy	188 FVYVLELFTSGQSTGVGHSDVDNPNRIILAIIPGNFVYITVVD				-V 236
Dy	187 FDMNLSLNNH-DNIRGVDSVDITPQ-----VTLVIRNEPVYDLSLHT	235			
Qy	237 ISALNLEFLVC 247				
Dy	236 VAVIALMLEFLVC 246				

US-08-455-286-71
Sequence 71, Application US/08452866
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME RNA

TITLE OF INVENTION: PROTECTOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 TITLE OF INVENTION: USING
 NUMBER OF SEQUENCES: 81
 CORRESPONDING ADDRESS:
 ADDRESSER: ANDREA T. PORCICK
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46248
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 PRIORITY NUMBER: US/08/495,286
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/378761
 FILING DATE: 26-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PORCICK, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 382728
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 337-4846
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRAINDNESS: single
 TOPOLOGY: linear
 MODIFIED: none
 MOTIF: none
 PROTEIN: proceain

	Quary Match	16.7%	Score 466.5	DB 1	Length 250
Bent Local Similarity	42.6%	Pred. No. 5.7e-37			
Matches	107	Conservative 37	Mismatches 62	Indels 25	Gaps 6
Qy	1	1	1	1	1
Db	9	9	9	9	9
Qy	1	1	1	1	1
Db	9	9	9	9	9
Qy	69	69	69	69	69
Db	67	67	67	67	67
Qy	128	128	128	128	128
Db	127	127	127	127	127
Qy	168	168	168	168	168
Db	167	167	167	167	167
Qy	237	237	237	237	237
Db	236	236	236	236	236

RESULT 11
 US-08-356-786-10
 ; Sequence 10, Application US/08356786
 ; Patent No. 5877305
 ; INVENTOR:
 ; APPLICANT: Opreaman, James S.
 ; APPLICANT: Opreaman, Herman
 ; APPLICANT: Houscen, U. L.
 ; APPLICANT: Ring, David B.
 ; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 ; TITLE OF INVENTION: Marker

/ NUMBER OF SEQUENCES: 16
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Edmund R. Plichter, Testa, Hurwitz, & Thibault
 / STREET: Exchange Place, 53 State Street
 / CITY: Boston
 / STATE: Massachusetts
 / COUNTRY: USA
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/356,786
 / FILING DATE:
 / CLASSIFICATION: 424
 / PRIOR ART CITATION DATA:
 / APPLICATION NUMBER: 07/831,967
 / FILING DATE: 06-FEB-1992
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Plichter, Edmund R.
 / REGISTRATION NUMBER: 27,829
 / REFERENCE/DOCKET NUMBER: CRF-053
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (617) 248-7000
 / TELEFAX: (617) 248-7100
 / INFORMATION FOR SEQ ID NO: 10:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 534 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-356-786-10

Query Match 15.0%; Score 418; DB 2; Length 534;

Best Local Similarity 27.8%; Pred. No. 9,6e-32;

Matches 149; Conservative 76; Mismatches 171; Indels 140; Gaps 20;

QY 9 THQTGEEFRPITLLDLYVSSGS--ESNEIPL--RQSTIPVSDAPRYVELTNGGDSI 66
 DB 16 TQATVQSTNFIKAVKRLITGADVREHLEVLRVGLPIN--QFLLVLSNHAELSV 73
 QY 67 TTAIDVTNLVYVAVQAGDSYPLR-DAPRGAE--TFLFTGR--TRSSLPNGSYDLERYA 122
 DB 74 TLALDVTNAYVGVYVAGNSAYPHPDNDQDAITLFTDVQRXYTAFQGNVRLDQA 133
 QY 123 GR-RDQIPLGIDQLGSYPLARF--FGSSTRQASLILLOMISEAAEPNPLMARQ 178
 DB 134 GMLKENIELANGPLEKIAISLYVYSGTQPLFLNRSEFTICQWISBAFQYIEGEMT 193
 QY 179 YINSASFLPYVMALETSGVQSTVQVHSTQGVNPPRLAIPGNFVTLNVDVTA 238
 DB 194 KIRNRSAPDPBSVITLNSWKLSTAIQSNQAGFASPIQDQRNRSKTSYVDSILIP 253
 QY 239 SLALMLFVCGERSSSDVRYMFLTPYI--AD-----DY 271
 DB 254 IIALVYRCAPRESSQ--FSLIRPVYVNPVADVCMBEIQVQSGPELKKRGETVMI 309
 QY 272 TCSASEPFAIVGRNGV-----CVDVDDPDHGNQIQAMPKX-- 310
 DB 310 SCASGTYFANVGMWKAQAPKQLMGMWINTYQGYVADPKERFASLETATYH 369
 QY 311 ---NDPNQMLTKDQSTRNSG--CLTYGTAGVYVAFPCNTNAREKTIWQING 363
 DB 370 LQNN-----LNRDSATYFCARERGA-----YNG 395
 QY 364 NGTINPRSNLVLAASGILK-----TTLVQLDLYTLQ----- 398
 DB 396 QGLVVSASISSSGG 455
 QY 399 --GMLAGNUTAPREVITYGFRDL-----CHESNGSGVWVETVSSQGNMAY 445

DB 456 SLWMLGEPDPTIKELIATVATSSLDGVPFRSSGSGSDVSLT-LSLSSEDPFVY 510

RESULT 12

US-07-901-707-1

/ Sequence 1, Application US/07901707

/ Patent No. 5376546

/ GENERAL INFORMATION:

/ APPLICANT: Bernhard, Susan L.

/ APPLICANT: Bernhard, Susan L.

/ APPLICANT: Carroll, Steve F.

/ APPLICANT: Lane, Julie A.

/ TITLE OF INVENTION: Materials Comprising and Methods of

/ NUMBER OF SEQUENCES: 57

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

/ ADDRESS: Bicknell

/ STREET: Two First National Plaza, 20 South Clark

/ STREET: Street

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60603

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/07/901,707

/ FILING DATE: 19920619

/ CLASSIFICATION: 435

/ PRIOR ART CITATION DATA:

/ APPLICATION NUMBER: US 07/787,567

/ FILING DATE: 04-NOV-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: No. 5376546and, Greca E.

/ REGISTRATION NUMBER: 35,302

/ REFERENCE/DOCKET NUMBER: 27129/30910

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (312) 346-5750

/ TELEFAX: (312) 984-5750

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 267 amino acids

/ TYPE: AMINO ACIDS

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

US-07-901-707-1

Query Match 13.9%; Score 387; DB 1; Length 267;

Best Local Similarity 40.0%; Pred. No. 3.2e-29;

Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 THQTGEEFRPITLLDLYVSSGS--ESNEIPL--RQSTIPVSDAPRYVELTNGGDSI 66
 DB 102 TQATVQSTNFIKAVKRLITGADVREHLEVLRVGLPIN--QFLLVLSNHAELSV 70
 QY 67 TTAIDVTNLVYVAVQAGDSYPLR-DAPRGAE--TFLFTGR--TRSSLPNGSYDLERYA 122
 DB 71 TLALDVTNAYVGVYVAGNSAYPHPDNDQDAITLFTDVQRXYTAFQGNVRLDQA 130
 QY 123 GR-RDQIPLGIDQLGSYPLARF--FGSSTRQASLILLOMISEAAEPNPLMARQ 178
 DB 131 GMLKENIELANGPLEKIAISLYVYSGTQPLFLNRSEFTICQWISBAFQYIEGEMT 190
 QY 179 YINSASFLPYVMALETSGVQSTVQVHSTQGVNPPRLAIPGNFVTLNVDVTA 238
 DB 191 KIRNRSAPDPBSVITLNSWKLSTAIQSNQAGFASPIQDQRNRSKTSYVDSILIP 250

Db 251 IIALWVRCAPPSS 265

RESULT 13

US-07-988-430-1
Sequence 1, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Birmahall, Susan L.
APPLICANT: Betty Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Birmahall, O'Toole, Gerstein, Murray & Street, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 1992-09-09
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-10-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greeta E.
REGISTRATION/DOCKET NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1

Query Match 13.9%; Score 387; DB 1; Length 267;
Best Local Similarity 40.0%; Pred. No. 3,2e-29;
Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

Qy 9 TQOTGEBYRFTILADYSSGS-FSNRIPL-RQSTIPVSDAKPVTALNQGQDRI 66
Db 13 TAGATVQSTYTFIRAVRGRLTGADVHEIPVPRKVGPIR--QRTIWEISNHAELSV 70
Qy 67 TAAIDVTNLYVVAQAGDSYFLR-DAPRGAL--TLLFTGT-TSSLPFGSYDLEARYA 122
Db 71 TAAIDVTNLYVVAQAGDSYFLR-DAPRGAL--TLLFTGT-TSSLPFGSYDLEARYA 130
Qy 123 GH-RQPIPLGIDQLGQVTAIRF--PQSGTQVQASILLICWISBAAPVPLMAAQ 178
Db 131 GNLRENIELGNPLSEALISALVYISGQGLPTLASFILICWISBAAPVPLMAAQ 190

Qy 179 YINSGASPLPDVWLELFTSGQSGTGVSDGQVFNRIPLAIPGCVTLNMDVIA 238
Db 191 RIRYRNSAPDPSVITLNSGRLSTALQBSNQGAFASPIQLQKNSGKSTVYVSLIP 250
Qy 239 SLAIMLFVCGERPSS 253
Db 251 IIALWVRCAPPSS 265

RESULT 14

US-08-218-303-16
Sequence 16, Application US/08218303
Patent No. 5547867
GENERAL INFORMATION:
APPLICANT: Kara, Bhupendra V.
APPLICANT: Hockney, Robert C.
APPLICANT: Falton, John E.
TITLE OF INVENTION: FERMENTATION PROCESS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cushman, Darby & Cushman
Street, 1615 L Street, N.W.
City: Washington
State: Washington
Country: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,303
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,533
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PAK/3893/94908/KCM
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-218-303-16

Query Match 13.9%; Score 387; DB 1; Length 267;
Best Local Similarity 40.0%; Pred. No. 3,2e-29;
Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

Qy 9 TQOTGEBYRFTILADYSSGS-FSNRIPL-RQSTIPVSDAKPVTALNQGQDRI 66
Db 13 TAGATVQSTYTFIRAVRGRLTGADVHEIPVPRKVGPIR--QRTIWEISNHAELSV 70
Qy 67 TAAIDVTNLYVVAQAGDSYFLR-DAPRGAL--TLLFTGT-TSSLPFGSYDLEARYA 122
Db 71 TAAIDVTNLYVVAQAGDSYFLR-DAPRGAL--TLLFTGT-TSSLPFGSYDLEARYA 130
Qy 123 GH-RQPIPLGIDQLGQVTAIRF--PQSGTQVQASILLICWISBAAPVPLMAAQ 178
Db 131 GNLRENIELGNPLSEALISALVYISGQGLPTLASFILICWISBAAPVPLMAAQ 190
Qy 179 YINSGASPLPDVWLELFTSGQSGTGVSDGQVFNRIPLAIPGCVTLNMDVIA 238
Db 191 RIRYRNSAPDPSVITLNSGRLSTALQBSNQGAFASPIQLQKNSGKSTVYVSLIP 250

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.ral

Qy 239 SLAIMFVCGERPS 253
Db 251 IIALWYRCAPPS 265

RESULT 15
US-08-425-336-1
Sequence 1, Application US/08425336
Patent No. 5,210,608
GENERAL INFORMATION:
APPLICANT: Bettef, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS: O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425/336
CLASSIFICATION: 18-24R-1995
ERROR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 13-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
ADDRESS: 1800 North Dearborn Street, Suite 1000
REFERENCE/DOCKET NUMBER: 2,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
ORIGIN: 1 linear
MOLECULE TYPE: protein
US-08-425-336-1

Query Match 13.9%; Score 387; DB 1; Length 267;
Best Local Similarity 40.0%; Pred. No. 3.2e-29;

Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

Qy 9 TQOTGEYFRITLNDYSSGS-FSENIPL-ROSTIPVSDQRPVLVELNOCGDSI 66
Db 13 TQAKVOSTNEIARGLTADVAHEIPVLENVGLPIN-QEFLVELSHNELSV 70
Qy 67 EAIDVTNLYTAKOCDOGYFR-DAPRGAR-TLFTGT-TRSGIPNNSIPDIEVIA 122
Db 71 TLALDVNAYVVGIRGNSAFPHFDNOCEDARATHTLFDVONRYTAFGNDIRLEQLA 130
Qy 123 GH-RDOIFGIDILQSYVALRF--PGSGTRIOASITLTIOMISEARFNPILMBARQ 178
Db 131 GUNRENIEIAGNPLEASIALVYSGTGTOLFTIARSPICITOMISEARFYIEGEMT 190

Qy 179 YINSGASFLPYVMELETSGCOASTOVQNSDQVFNNTILALPFGVTLNNRDYA 238
Db 191 RIRYNNRABDPDSVITLHNSGRSLTALQSNQAFASITDQHRNSKSTYDVSLIP 250
Qy 239 SLAIMFVCGERPS 253
Db 251 IIALWYRCAPPS 265

Search completed: December 11, 2003, 14:11:32
Job time: 19.3644 secs

Thu Dec 11 16:10:02 2003

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.17513 Seconds
(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667c-6

Sequence: 1 DVTGASAEPTVATVGRNKM.....RRIIVATGRKPNQMLPVP 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Database:

1: PIR.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1339.5	94.3	264	2	PD0019	mistletoe lectin I
2	1329	93.6	265	2	JM0090	lectin-I B chain -
3	913	64.3	576	1	RLCSD	ricin D precursor
4	891.5	62.8	263	2	S06330	ricin E - calicor b
5	779.7	56.1	554	1	RLCSAG	agglutinin precurs
6	773.5	54.5	528	1	TLASA	abrin-a precursor
7	759.5	53.8	527	2	S32430	abrin-b precursor
8	758.5	53.4	528	2	S32431	abrin-d precursor
9	558.5	39.3	570	2	S62627	endo-1,4-beta-strep
10	149.5	10.5	477	1	JG05059	chitinase (EC 3.2
11	146.5	10.3	383	2	T34603	protease RFI - R
12	145.5	10.2	377	2	JC7535	arabinofuranosidase
13	145.5	10.2	377	2	JC7535	glucan endo-1,3-pe
14	130	9.2	525	2	A45053	polypeptide N-acet
15	124	8.7	475	2	T35697	actinohivin precu
16	119	8.4	538	2	A88515	probable polypepti
17	107.5	7.6	553	2	A88515	probable hydrolase
18	107.5	7.4	542	2	T42243	probable hydrolase
19	105	7.4	464	2	T35943	probable polypepti
20	104.5	7.0	451	2	T34988	beta transducin-11
21	100	7.0	623	2	T42245	hypothetical prote
22	99.5	6.9	1633	2	S76086	hypothetical prote
23	97.5	6.9	1633	2	AE1996	mosaicocidal toxic
24	95.5	6.7	386	2	AE1996	cytolysin vrbh prote
25	95.5	6.7	870	2	S27514	hypothetical prote
26	94.5	6.7	471	2	A41478	hypothetical prote
27	94	6.6	357	2	T21152	hypothetical prote
28	92	6.5	1067	2	T28663	polypeptide N-acet
29	91	6.4	571	2	I37405	

30	90.5	6.4	545	2	S21582	alpha-galactosidase
31	90	6.3	2229	2	T16199	hypothetical prote
32	90	6.3	4180	2	G83559	hypothetical prote
33	89	6.3	542	2	A49114	protein-tyrosine k
34	89	6.3	1708	2	AE1866	WD-40 repeat prote
35	88.5	6.2	773	2	A47666	structural polypep
36	88.5	6.2	1008	2	T32986	hypothetical prote
37	87	6.1	698	2	A69222	hypothetical prote
38	86.5	6.1	1526	2	AC2239	WD-40 repeat prote
39	86.5	6.1	2252	2	H83452	probable bacterioph
40	86.5	6.1	326	2	AE0930	probable bacterioph
41	86.5	6.1	366	2	T42247	polypeptide N-acet
42	86	6.0	1032	2	T43287	beta-1,3 exoglucan
43	85.5	6.0	157	2	H70902	hypothetical prote
44	85	6.0	157	2	H70902	
45	84.5	6.0	292	2	S58857	botulinum neurotox

ALIGNMENTS

RESULT 1

PD0019

mistletoe lectin I B chain - Viscum album (fragment)

C/Species: Viscum album

C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 07-May-1999

C/Accession: PD0019

R/Eschschburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, B.

Biochem. Biophys. Res. Commun. 247, 367-372, 1998

A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum

A/Reference number: PD0019; MUID:98308123; PMID:9642133

A/Accession: PD0019

A/Protein type: protein

A/Protein family: lectin, RMA N-glycosidase homology

Query Match 94.3% Score 139.5; DB 2; length 264;

Best Local Similarity 95.8% Match No. 1, 4e-105;

Matches 252; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY	1	DVTGASAEPTVATVGRNKM	CVVRDDPFIDNQCIOAFSKSNNDPQMLTKRQGRS	60
Db	1	DVTGASAEPTVATVGRNKM	CVVRDDPFIDNQCIOAFSKSNNDPQMLTKRQGRS	60
QY	61	NSGCTTYGTCAGYVWIDCNVRENTIYQNGTIVPSNLVLAASGKICITTT		120
Db	61	NSGCTTYGTCAGYVWIDCNVRENTIYQNGTIVPSNLVLAASGKICITTT		120
QY	121	VQILDVTLGGWAGNDTPPELTIVGRPLCSNNGSVAFTCSQONO-ANALYSD		179
Db	121	VQILDVTLGGWAGNDTPPELTIVGRPLCSNNGSVAFTCSQONO-ANALYSD		180
QY	180	GSIRPNQDQCTCRSDSVTVINVSAGSGQRWFTNEGALINLQGLANDVAQR		239
Db	181	GSIRPNQDQCTCRSDSVTVINVSAGSGQRWFTNEGALINLQGLANDVAQR		240
QY	240	NPKLRRIIVATKRNQMLPVP		262
Db	241	NPKLRRIIVATKRNQMLPVP		263

RESULT 2

JM0090

lectin-I B chain - European mistletoe

C/Species: Viscum album (European mistletoe)

C/Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 19-May-2000

C/Accession: JM0090

R/Schier M.H. Stoeva, S.; Voelter, W.

Biochem. Biophys. Res. Commun. 246, 566-601, 1998

A/Title: Complete amino acid sequence of the B chain of mistletoe lectin I.

A/Reference number: JM0090; MUID:98289575; PMID:9618256

A/Accession: JM0090

A: Molecule type: protein
 A: Residues: 1-265 <SOL>
 C: Superfamily: ricin, rRNA N-glycosidase homology
 C: Keywords: Glycoprotein
 F: 61, 96, 136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 93.6%; Score 1329; DB 2; Length 265;
 Best Local Similarity 95.5%; Prem 1, 1e-106; Indels 2; Gaps 2;
 Matches 252; Conservative 2; Mismatches 9;

QY 1 DDTCSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 60
 DB 1 DDTCSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 60
 QY 61 NSGCTTGTGTAGVYVMEPCNTAVREATTQWNGNTINPRSNVLAASGKQITLT 120
 DB 61 NSGCTTGTGTAGVYVMEPCNTAVREATTQWNGNTINPRSNVLAASGKQITLT 120
 QY 121 VQTLDTYTLGGWLAGNDTAPREVITVGFQDLQWESNGSVWTCSSQONQ-PRALVGD 179
 DB 121 VQTLDTYTLGGWLAGNDTAPREVITVGFQDLQWESNGSVWTCSSQONQ-PRALVGD 179
 QY 121 VQTLDTYTLGGWLAGNDTAPREVITVGFQDLQWESNGSVWTCSSQONQKVALVD 180
 DB 121 VQTLDTYTLGGWLAGNDTAPREVITVGFQDLQWESNGSVWTCSSQONQKVALVD 180
 QY 180 GSIRKQNDQCLTCGRDSVSTVIVVSCASGSSQGFVTFBGAIIINRGLANDVAK 239
 DB 181 GSIRKQNDQCLTCGRDSVSTVIVVSCASGSSQGFVTFBGAIIINRGLANDVAK 240
 QY 240 NPELRRIITVPAKKNQMA-LPV 262
 DB 241 NPELRRIITVPAKKNQMA-LPV 264

RESULT 3

RICSD
 ricin D precursor - castor bean
 N: Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C: Species: Ricinus communis (castor bean)
 C: Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 A: Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
 S: Halling, C.C.; Halling, A.C.; Murray, B.B.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
 N: J. Biol. Chem. 268:1982-1985, 1993
 A: Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
 A: Reference number: S20513; PMID:92163016; PMID:1171405
 A: Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
 A: Reference number: A24041; PMID:8607214; PMID:299712
 A: Accession: A24041

A: Molecule type: DNA
 A: Residues: 1-576 <HML>
 A: Cross-references: GB:X0179; MID:921082; PIDN:CAA2639.1; PID:921083
 R: Tregear, J.W.; Roberts, L.M.
 Plant Mol. Biol. 18, 515-525, 1992

A: Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
 A: Reference number: S20513; PMID:92163016; PMID:1171405

A: Accession: S20513
 A: Molecule type: mRNA
 A: Residues: 1-576 <HML>
 A: Cross-references: EMBL:X52908; MID:921084; PIDN:CAA27095.1; PID:921085
 R: Lamb, F.I.; Roberts, L.M.; Lord, J.M.
 Eur. J. Biochem. 148, 265-270, 1985

A: Title: Nucleotide sequence of cloned cDNA coding for preproricin.
 A: Reference number: A24614; MID:85179479; PMID:3838723
 A: Accession: A24614

A: Molecule type: mRNA
 A: Residues: 12-75, 'D', '77-550', 'R', 552-576 <LHM>
 A: Cross-references: GB:X02388; MID:921077; PIDN:CAA2630.1; PID:921078
 R: Roberts, L.M.; Halling, A.C.; Murray, B.B.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
 Agric. Biol. Chem. 42, 1267-1274, 1978

A: Title: Isolation and sequences of peptic peptides, and the complete sequence of the cDNA
 A: Reference number: A03372

A: Accession: A03372

A: Molecule type: protein
 A: Residues: 36-97, 'Q', '99-109', 'S', '111-269', 'D', '272-283', 'L', '285-288', '290-302' <YOS>
 A: Note: this paper cites the others in the series providing experimental details for the
 R: Izeki, T.; Funatsu, G.
 J. Biol. Chem. 268, 121-124, 1993

A: Title: Reversed amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A: Reference number: A24010
 A: Accession: A24010
 A: Molecule type: protein
 A: Residues: 315-383, 'PS', '386-576 <ARA>
 R: Funatsu, G.; Kimura, M.; Funatsu, M.
 Agric. Biol. Chem. 43, 2221-2224, 1979

A: Title: Primary structure of Ala chain of ricin D.
 A: Reference number: A03374

A: Accession: A03374
 A: Molecule type: protein
 A: Residues: 315-383, '337-342', '345-362', '364-383', '387', '386-399', 'T', '401', 'D', '403',
 527, 'R', '528-564', 'W', '565-570', 'LT', '572-574', 'P', <RHS>
 A: Note: this paper, one of a series, summarizes the experimental details for the de
 R: Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991

A: Title: Site-directed mutagenesis of ricin A-chain and implications for the mechan
 A: Reference number: A48237; MID:91352006; PMID:1881883

A: Contents: annotation: active site
 R: Robertus, J.D.
 Proteins 10, 251-259, 1991

A: Title: Structure of ricin A-chain at 2.5 angstroms.
 A: Reference number: A48239; MID:91352004; PMID:1881881

A: Contents: annotation: X-ray crystallography, 2.5 angstroms
 C: Comment: The functional molecule is a disulfide-linked dimer of A and B chains, v
 hoo the cell of the A chain; B chains are also responsible for cell agglutination;
 C: Comment: This protein is cytotoxic and very poisonous to animals.
 C: Keywords: duplication; glycoprotein; glycoside; hydrolyase; lectin; RNA binding;
 C: Summary: This protein is cytotoxic and very poisonous to animals.
 F: 1-35/Domains: signal sequence #status predicted <SIG>
 F: 1-36-302/Product: ricin D chain A #status experimental <ACH>
 F: 1-35-576/Product: ricin D chain B #status experimental <BCH>
 F: 1-331-373/Product: ricin D chain B #status experimental <BCH>
 F: 1-45, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F: 1-15, 159, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F: 2-2/Active site: Gln #status experimental
 F: 2-24, 318, 319, 324, 353, 372-394, 465, 466, 500-521/Dsulfide bonds: #status experimental
 F: 294-318, 319, 324, 353, 372-394, 465, 466, 500-521/Dsulfide bonds: #status experimental
 F: 548, 569/Binding site: N-acetyl-galactosamine (Asp, Asn) #status experimental

Query Match 64.3%; Score 933; DB 1; Length 576;
 Best Local Similarity 63.6%; Prem. NO. 3, 4e-69;
 Matches 164; Conservative 32; Mismatches 62; Indels 0; Gaps 0;

QY 5 CSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 64
 DB 318 CSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 64
 QY 65 LTTGYTGVYVMEPCNTAVREATTQWNGNTINPRSNVLAASGKQITLT 124
 DB 378 LTTGYTGVYVMEPCNTAVREATTQWNGNTINPRSNVLAASGKQITLT 124
 QY 125 DDTCSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 184
 DB 438 DDTCSASPEPTVIRVGRNQCVDVDDPHQNGQIQLPWPKSNNDPQWLTKKDTIR 184
 QY 185 KQNDQCLTCGRDSVSTVIVVSCASGSSQGFVTFBGAIIINRGLANDVAK 244
 DB 498 KQNDQCLTCGRDSVSTVIVVSCASGSSQGFVTFBGAIIINRGLANDVAK 244
 QY 245 NPELRRIITVPAKKNQMA-LPV 262
 DB 558 NPELRRIITVPAKKNQMA-LPV 264

RESULT 4

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us-09-601-667c-6.rpr

Page 5

RESULT 8

Nt6022
abrin-c precursor - Indian licoicec
N/contains: rRNA-N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licoicec)
C/Accession: M9722 #sequence_revision 15-Mar-1997 #text_change 20-Aug-1999
R/Mood: K.A., Itochi J.M.; Nanyangrak, E.J.; Patek, M.
Eur J Biochem 199; 723:732-1991
A/RTitle: Preproabrin genomic cloning, characterization and the expression of the A-chain
A/Reference number: S16022; MIDB:9166957; PMID:2050119
A/Accession: S16022
A>Status: preliminary
Molecule type: DNA
A/PResidue: 1-562 <MOO>
C/Comment: References: EMBL:X56677; NID:g16083; FIDN:CMAJ9202.1; PID:g16085
The A and B chains are linked by a disulfide bond, which inhibits protein synthesis by inactivating
the A and B chains respectively. The A chain contains a homocysteine residue, which is essential for toxicity.
C/Superfamily: ricin; rRNA-N-glycosidase homologues; glycoprotein; glycosylase; hydrolase; lectin; pyroglycamic acid
F/33-289/Product: abrin-c chain A #status predicted <ACH>
F/41-280/Domains: rRNA-N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <ECH>
F/337-359;/Product: 403-441,448-483,487-526,529-562/Region: 40-residue repeats
F/337/Modified site: pyrrolysine carboxylic acid (Gln) (in mature form) #status predictsee
F/158/201/AminoAcids/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/124/287/335-337,335-350-binding site: N-acetylglucosamine (Asp) (covalent) #status predicted
F/124/287/335-337,335-350-binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/124/303,320-333,353-380,451-464,490-507/disulfide bonds predicted
F/334,555/Binding site: N-acetylgalactosamine (asp, Asn) #status predicted

Query Match

Score 53.5%; Score 759.5; DB 2; Length 562;

Local Similarity 54.1% Pred.No.2,9e-56;

Matches 139; Conserved 45; Mismatches 72; Indels 1; Gaps 1;

Dy 5 CSMS-EPTVATVEGNKGVTVDDDFHDSQGLWFSSKNNDPQLTREQOTIRNSGS 63
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 303 CSRREPTFLCHGDCKCVUVDITDHNNMLLNKKCRHRNKMLLSDSSTIKSK 362
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 64 CLFTYGTAGYYVIPEDCNTPAVATWIVMGSGGITINPSNVLAASGIQTLLWT 123
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 363 CLTTGGAPGYVMVTIDCTSAVAETWEIMDGIIITNPASVLTLSSASSMKGTILVOT 422
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 124 LDTPLCGMLAKNDTAPEVLTIFPDLCMESNGSVIETVYSOOQMALVGDSGR 183
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 423 NPMQDMRGKNNISIPFYSLISGISLDQAQSMMALADNCNMQRQOMALTFDSIR 482
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 184 PKXMDQCLOTCGDSSTVNTVSCASGSOCPRTFNIGVALINKRCAMQNALPIFS 243
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 483 SYVYNACCLTKKHKGSPFYLMACSMNAQRMFLFNQGISTYLVADMVVVKSPDEL 542
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 244 RLTIIVPATGEPOVMTL 260
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 543 RKLTHNYTGKGMNL 559

RESULT 9

S32431
abrin-d precursor - Indian licoicec (fragment)
N/contains: rRNA-N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licoicec)
C/Accession: S32431 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
R/Mood: T.C.; Lin, J.Y.
J Mol Biol 229; 263:36-1991
A/RTitle: Primary structure of three distinct isoforms determined by cDNA sequencing.
A/Reference number: S32431; MIDB:93137788; PMID:8642113
A/Accession: S32431
A/Molecule type: mRNA
A/PResidue: 1-528 <RDN>

A:Cross-references: GB:M98346
P:Hung, C.; Lee, M.; Lee, T.; Lin, T.
submitted to the EMBL Data Library, March 1993
A:Reference number: S33408
A:Accession: S33408
A:Status: Valid
A:Residues: 171-320, 'L', 322-528 <HD>
A:Cross-references: EMBL:U27122; NID:9141772; PIDN:AA049158.1; PID:9141773
C:Comment: Abirin consists of an A chain, which inhibits protein synthesis by inacti
C:Superfamily: ricin. RNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin
F:1-251/Product: abrin-d chain A #status predicted <ACH>
F:17-246/Domain: RNA N-glycosidase homology <RNG>
F:261-320/Product: abrin-d chain B #status predicted <ECH>
F:17-113/Domain: 44-149, 453-492, 495-528/Region: 40 residue repeats
F:17-Modified site: Asparagine
F:174,117,195,196/Binding site: substrate (Gly, Trp, Glu, Asn) #status predicted
F:154,167/Active site: Glu, Arg #status predicted
F:200,253,261,401,402/Binding site: carboxylate (Asn) (covariant) #status predicted
F:247-269,285-305,339-346,417-430,456-472/Disulfide bond: #status predicted
F:288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 53.4%; Score 758.5; DB 2; Length 528;
Best Local Similarity: 54.1%; Fred. No. 3,26-59; Gaps 1;
Matches 139; Conservative 46; Mismatches 71; Indels 1;

A:Cross-references: GB:M98346
P:Hung, C.; Lee, M.; Lee, T.; Lin, T.
submitted to the EMBL Data Library, March 1993
A:Reference number: S33408
A:Accession: S33408
A:Status: Valid
A:Residues: 171-320, 'U', 322-528 <HD>
A:Cross-references: EMBL:U27122; NID:9141772; PIDN:AA049158.1; PID:9141773
C:Comment: Abirin consists of an A chain, which inhibits protein synthesis by inacti
C:Superfamily: ricin. RNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin
F:1-251/Product: abrin-d chain A #status predicted <ACH>
F:17-246/Domain: rRNA N-glycosidase homology <RNG>
F:261-320/Product: abrin-d chain B #status predicted <ECH>
F:17-113/Domain: 44-149, 453-492, 495-528/Region: 40 residue repeats
F:17-Modified site: Glycylidol 44-149, 453-492, 495-528/Gln #status predicted
F:174,117,195,196/Binding site: substrate (Gly, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
F:200,253,261,401,402/Binding site: carboxylate (Asn) (covariant) #status predicted
F:247-269,286-335,339-346,417-430,456-472/Ismaltide bond: #status predicted
F:288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 53.4%; Score 758.5; DB 2; Length 528;
Best Local Similarity: 54.1%; Fred. No. 3,26-55; Gaps 1;
Matches 139; Conservative 46; Mismatches 71; Indels 1;

Matches 119; Conservative 31; Mismatches 97; Indels 11; Gaps 5;
QY 5 CSASEPTVAVIGRNGKCYVDVDDPHQNOIQMPKSNNDPNQWITTRKDTIRNSGC 64
DB 316 CSVETTRISGMDGLCYVRGHHIDGNPVLRLP--CGNECNQIMTFRTGTITMLKGC 373
QY 65 LTTGVTATVYVIMFDCTAVREATITQIMNGTINPNTVYLAASSGKGTITLVQTL 124
DB 374 L-----TASSVWIDQNTPPKATKRWVSLDGLTHNSGLVLRQALSGTALSLEN 428
QY 125 DTLGGGMLAGNDAPREAVTIGPRDLCMESNGSS--VWETCTSSQCKGKALVGGST 182
DB 429 IHARQGMVIG-DVEPLVTITVGYKQKCLRENGENFWLEDCVANNVQGMALVGGDTI 487
QY 183 RPKQNOQCLTCQSDSVSTVINIVSCAGSSQGVWFTNGAATMLNGLAMVQANPK 242
DB 488 RVNSRKLCTVSDHPEDLDIVLKCR-GSGNQRVWFVNTGITSNPVALIMDVQNDVS 546
QY 243 LRRITITPATKPNQML 260
DB 547 LKRIILIRKTRFNQOMI 564

RESULT 11

endo-1,4-beta-xylosanase (EC 3.2.1.8) A precursor - Streptomyces lividans
N/Alternate names: xylanase A
C/Species: Streptomyces lividans
C/Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
E/Accession: J05089; PS0238
G/Email: R. Koy, C. Taguchi, M. Morosoli, R. Kluepfel, D.
G/Ref: 107, 75, 62, 13, 99
A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A/Reference numbers: J05089; MIMD:92077439; PMID:1745521
A/Accession: J05089
A:Residue type: DNA
A:Residues: 1-477 <SHA>
A:Cross-references: GB:M64551
A/Accession: PS0238
A:Molecule type: protein
A:Residues: 42-92 <SH2>
C/Genetics:
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C/Superfamily: Streptomyces endo-1,4-beta-xylosanase A; Streptomyces endo-1,4-beta-xylosanase
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-477/Product: endo-1,4-beta-xylosanase A #status experimental <MAT>
F:74-341/Domain: Streptomyces endo-1,4-beta-xylosanase A homology <STX>
F:169,277/Active site: GH1 #status predicted

Query Match 10.5%; Score 146.5; DB 1; Length 477;
Best Local 28.2%; Pred. No. 6,4e-05;

Matches 49; Conservative 20; Mismatches 54; Indels 51; Gaps 8;

QY 7 ASEP-----TVRIYGRNGKCYVDVDDPHQNOIQMPKSNNDPNQWITTRKDTIRNSG 61
DB 346 SSEPADGGQIKRGV-SGRCLDVPDASTSDTQQLQMCSSGT--NQGMATPAEELRYV 402
QY 62 G-SCITTYGTATGYVIMFDCTAVREATITQIMNGTINPNTVYLAASSGKGTITLVQTL 120
DB 403 GGRCLDAAGTNSKQVQYSCWGGDNQK--WRANSDSVVGVQSGCLDA----- 450
QY 121 VQTLDTYTGQMLAGNDAPREAVTIGPRDLCMESNGSSVWFTNGAATMLNGLAMVQANPK 174
DB 451 -----VANGTA-----NGLTLQLVTC-SNGSNQW 474

RESULT 12
T34603
xylanase A - Streptomyces coelicolor (fragment)

C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
A/Accession: T34603
R/Murphy, L.; Harris, D.; Parkhill, T.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, January 1998
A/Reference number: Z21548
A/Status: preliminary; translated from GB/EMBL/DDP
A/Molecule type: DNA
A:Residues: 1-383 <QW>
A:Cross-references: EMBL:M021529; PIRN:CAA16468.1; GSPDB:GN00070; SCOPDB:SC10A5.36
X/Experimental source: strain A5(2)
C/Genetics:
A:Suprafamily: Streptomyces endo-1,4-beta-xylosanase A; Streptomyces endo-1,4-beta-xy
F:1-247/Domain: Streptomyces endo-1,4-beta-xylosanase A homology <STX>

Query Match 10.3%; Score 146.5; DB 2; Length 383;
Best Local 28.2%; Pred. No. 8.9e-05;

Matches 49; Conservative 19; Mismatches 55; Indels 51; Gaps 8;

QY 7 ASEP-----TVRIYGRNGKCYVDVDDPHQNOIQMPKSNNDPNQWITTRKDTIRNSG 61
DB 252 SSEPADGGQIKRGV-SGRCLDVPDASTSDTQQLQMCSSGT--NQGMATPAEELRYV 308
QY 62 G-SCITTYGTATGYVIMFDCTAVREATITQIMNGTINPNTVYLAASSGKGTITLVQTL 120
DB 309 GGRCLDAAGTNSKQVQYSCWGGDNQK--WRANSDSVVGVQSGCLDA----- 356
QY 121 VQTLDTYTGQMLAGNDAPREAVTIGPRDLCMESNGSSVWFTNGAATMLNGLAMVQANPK 174
DB 357 -----VANGTA-----NGLTLQLVTC-SNGSNQW 380

RESULT 13

chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus
C/Species: Streptomyces thermoviolaceus
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
A/Accession: J07535
R/Tsujiho, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.;
Bischof, B.; Technol. Biochem. 64, 2445-2453, 2000
A/Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular
A/Reference numbers: J07535; MIMD:21036907; PMID:11193414
A/Accession: J07535
A:Molecule type: DNA
A:Residues: 1-317 <TSU>
A:Cross-references: DDBJ:AB016442
A:Experimental source: strain OPC-520
C/Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin
lysaccharide-binding domain that is important in the efficient hydrolysis of insol
C/Genetics:
A/Genes: ch35

A/Keywords: glycosidase; hydrolase

Query Match 10.2%; Score 145.5; DB 2; Length 377;
Best Local 28.7%; Pred. No. 0.0011;

Matches 41; Conservative 21; Mismatches 68; Indels 13; Gaps 5;

QY 7 ASEPTRIVGRNGKCYVDVDDPHQNOIQMPKSNNDPNQWITTRKDTIRNSGCT 66
DB 33 AQAATISITLGGKCLDVAGDSANQTPVQIDCNQGN--AQGYVSGDITRALGKCLD 90
QY 67 TVGTAT--GVYVIMFDCTAVREATITQIMNGTINPNTVYLAAS--SGIKGTITLVQ 122
DB 91 VDRSTPAAGKQVQMDTSGANQK--WVYPAADIVNPAKQCLDVTRSGANQTRQV 148
QY 123 TLDTYTGQMLA-----GNQATP 140
DB 149 ICTGSGNKNKPNATGSGSTRP 171

RESULT 14

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us-09-601-667c-6.rpr

A45053
protease RPI - *Ratobacter faecitabidus*

C:Species: *Ratobacter faecitabidus*

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999

C:Accession: A45053

C:SHIMOL, H.; Linna, Y.; Ohta, T.; Tadenuma, M.

C: Biol. Chem., 267, 25189-25192, 1992

C:Title: Murakami, O. *Ratobacter faecitabidus* protease I. A yeast-lytic serine

A:Reference number: A45053; PMID:1339445

A:Accession: A45053

A:Status: preliminary

A:Molecule type: DNA, protein

A:Residues: 1-525 <SH1>

A:Cross-references: GB:010753; NID:9216923; PIDN:BA01585.1; PID:d1002060; PID:g912440

A:Experimental source: YIM-50

A>Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

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A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

A:Note: sequence extracted from NCBI backbone (NCBI:120149, NCBI:120151)

Search completed: December 11, 2003, 13:55:42
Job time: 9.17513 sec

FT VARIANT 231 231 N -> S OR T.
RT VARIANT 231 233 MET -> KOP.
RT VARIANT 232 235 GLAM -> SLIV.
SO SEQUENCE 264 AA; 28981 MW; 70DD0326CC6F544 CRC64;
Query Match 94.3%; Score 1339.5; DB 1; Length 264;
Best local similarity 95.8%; DB 1;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 1 DDTGTSASPTVRIYVGRNKCVDVADDDPHGQIQCLMPKSKNDPQWLIRKQGTIS 60
Db 1 DDTGTSASPTVRIYVGRNKCVDVADDDPHGQIQCLMPKSKNDPQWLIRKQGTIS 60
QY 61 NSSCLTGYTGAGVYVIMPCQNVAREATIQIWMNGTINRNSVLAASSIGKTTLT 130
Db 61 NSSCLTGYTGAGVYVIMPCQNVAREATIQIWMNGTINRNSVLAASSIGKTTLT 130
QY 121 VQSLDTLGGTCMLAGNDAPRAVITGVPHDCIMENSGSYVWECUSQD-RALLKGTTL 179
Db 121 VQSLDTLGGTCMLAGNDAPRAVITGVPHDCIMENSGSYVWECUSQD-RALLKGTTL 179
QY 121 VQSLDTLGGTCMLAGNDAPRAVITGVPHDCIMENSGSYVWECUSQD-RALLKGTTL 180
Db 121 VQSLDTLGGTCMLAGNDAPRAVITGVPHDCIMENSGSYVWECUSQD-RALLKGTTL 180
QY 180 GSIRPKNODQCLTCGRQSVYVNIYVSGSSGSSRWVYTMGALINLXGGLADVAOK 239
Db 180 GSIRPKNODQCLTCGRQSVYVNIYVSGSSGSSRWVYTMGALINLXGGLADVAOK 239
QY 240 GSIRPKNODQCLTCGRQSVYVNIYVSGSSGSSRWVYTMGALINLXGGLADVAOK 240
Db 240 GSIRPKNODQCLTCGRQSVYVNIYVSGSSGSSRWVYTMGALINLXGGLADVAOK 240
Db 241 NPKLRILITVPAKGRKNOMLPEV 262
241 NPKLRILITVPAKGRKNOMLPEV 263
RESULT 2
ID RICCI STANDARD; PRT; 576 AA.
AC P02879; P02880;
DT 21-JUL-1986 (Reel. 01, Created)
DT 13-AGE-1987 (Reel. 05, Last sequence update)
DE 13-AGE-1987 (Reel. 05, Last annotation update)
DE Riccin proteinase (catalytic chain (RNA N-glycosidase)
DS (EC 3.2.22) ; Riccin B chain)
OS Ricinus communis (Castor bean)
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae; eucotids I; Malpighiales; Euphorbiaceae; Ricinus.
OC NCBI_Taxid:3989;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8067214; PubMed=22999712;
RA Heilmann R.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L., Weaver R.P., Halling A.C., Murray E.E., Ladin B.F., Houston L.L., "Genomic cloning and characterization of a ricin gene from Ricinus communis.",
RT "Genomic cloning and characterization of a ricin gene from Ricinus communis.",
RL Nucleic Acids Res. 13:8019-8033(1985).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=92163016; PubMed=1371405;
RA "Rigau J.M., Roberts J.M., Ricinus communis: cloning of a functional ricin gene and three ricin pseudogenes.",
RT "Rigau J.M., Roberts J.M., Ricinus communis: cloning of a functional ricin gene and three ricin pseudogenes.",
RL Plant Mol. Biol. 18:515-525(1992).
RN (3)
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=3838723;
RA Lamb A., Roberts J.M., Lord J.M.,
RT "Nucleotide sequence of cloned cDNA coding for preproricin.",
RL Eur. J. Biochem. 148:265-270(1985).
RN (4)
RP SEQUENCE OF 36-302
RX "Yoshitake S., Funatsu G., Funatsu M.,
RT "Isolation and sequences of peptide
RT "sequence of the chain of ricin D." peptides, and the complete
RT Agric. Biol. Chem. 42:1267-1274(1978).
RN (5)
RP SEQUENCE OF 315-576.
RA Funatsu G., Kimura M., Funatsu M.,
RT "Primary structure of Aa chain of ricin D.",
RL Agric. Biol. Chem. 43:2221-2224(1979).
RN (6)
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1688317;
RT "Stratton R., Funatsu M.,
RT "Stratton R., Funatsu M.,
RL Agric. Biol. Chem. 54:157-162(1990).
RN (7)
RP REVIEW.
RX MEDLINE=21480122; PubMed=1595634;
RA Olmstead S., Kozlov J.V.,
RL Toxicon 39:1723-1728(2001).
RN (8)
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=91161483; PubMed=238397;
RA Moutier R., Villi F.,
RT "The three-dimensional structure of ricin at 2.8 A.",
RL J. Biol. Chem. 262:5198-5403(1987).
RN (9)
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=9132004; PubMed=1881881;
RA Katzin B.J., Collins E.U., Robertus J.D.,
RT "Structure of ricin A-chain at 2.5 A.",
RL Proteins 10:251-259(1991).
RN (10)
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=9132005; PubMed=1881882;
RA Rubeher E., Robertus J.D.,
RT "Structure of ricin B-chain at 2.5-A resolution.",
RL Proteins 10:260-269(1991).
RN (11)
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95902010; PubMed=7990130;
RA Pearson S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.",
RL J. Mol. Biol. 244:410-422(1994).
RN (12)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
RX MEDLINE=96314222; PubMed=8780513;
RA Day P.U., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M., Molina-Svahn M.C., Robertus J.D.,
RT "Structure and activity of an active site substitution of ricin A chain.",
RL J. Biochem. 35:11098-11103(1996).
RN (13)
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9086580;
RA Yan X., Hollis T., Svirin M., Day P., Monzingo A.F., Milne G.W., Robertus J.D.,
RT "Structure-based identification of a ricin inhibitor.",
RL J. Mol. Biol. 266:1043-1049(1997).
RN (14)
RP MEDLINE=89355532; PubMed=1287857;
RA Kim Y., Robertus J.D.,
RT "Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography.",
RL Protein Eng. 5:775-779(1992).
RN (15)
RP -I- FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosylase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factor 2, this inactivation results in the arrest of protein synthesis. The A chain can connective to the few ribosomal protein per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal

cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.

-1- Specific activity: Endoanalysis of the N-glycosidic bond at one specific site of the B chain, the 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

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Best Local Similarity 63.68; Pred. No. 1,7e-72;
Matches 164; Conservative 32; Mismatches 62; Indels 0; Gaps 0;

DB 318 CMDEPITRIVRNGDLCVDRGHFNNAIQMCKSTNDQMTLKRNTISNOK 377
QY 5 CASAEPTTIVRNGDLCVDRGHFNNAIQMCKSTNDQMTLKRNTISNOK 64
DB 65 LITVGTAGVYVWIPDCVRENTIWOIKNQNTIPRSNVILASGIGTTLVQTL 124
QY 185 KNOQDQCTGSDSVYVNIYSGASGQGVPTTEGAILIKXIAMVQANPTE 244
DB 378 LITVGTAGVYVWIPDCVRENTIWOIKNQNTIPRSNVILASGIGTTLVQTL 437
QY 125 DYLGGQVLAQNTAPREVTIYGRFLMESNGSVWETCVSSQONQMLYDGSIRP 184
DB 438 IIVASQMLPNNTPQPVITVIGLGLCLNAGQVWIECSSKAEQMLYADGSIRP 497
QY 185 KNOQDQCTGSDSVYVNIYSGASGQGVPTTEGAILIKXIAMVQANPTE 244
DB 498 QQNDNDCLDSKIVRETVKILSGCPASSGQVRMKDQTLINLXGLVLYVADPSLK 557
QY 245 RIITVPGKPNQMLPV 262
DB 558 QILYFHGDNPQIMPL 575

RESULT 3
AGGLRKTCCO STANDARD; PRT; 564 AA.
MD PGGT50.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (PCA) (Contains: Agglutinin A chain (RNA N-glycosidase) (BC 3.2.2.22); Agglutinin B chain).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucroside II; Malvales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID:3989;
RN 11; SEQUENCE FROM N.A.
RX MEDLINE:605949; PubMed:299910.
RA Roberts L.W., Lamb P.J., Papadou J.C., Lord J.M.,
RT "The primary sequence of Ricinus communis agglutinin. Comparison with
RT ricin".
RL J. Biol. Chem. 260:15682-15686(1985).
RN [2]
RP SEQUENCE OF 303-564.
RC TISSUE-Seed;
RA Ataki T., Yoshioke Y., Funatsu G.,
RT "The complete amino acid sequence of the B-chain of the Ricinus
RT communis agglutinin isolated from large-grain castor bean seeds".
RN [3]
RP SEQUENCE OF 303-337.
RX MEDLINE:80178723; PubMed:6768555;
RA "Purification and physicochemical properties of ricins and
RT agglutinins from Ricinus communis".

CC -----1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M98344; AA32624.1; ALT INIT.
DR EMBL; X54872; -; NOT ANNOTATED; CDS.
DR PIR; S32429; T2LSA.
DR PDB; 1ABR; 07-FEB-95; Ricin_B_lectin.
DR InterPro; IPR00372; Ricin_B_lectin.
DR InterPro; IPR00574; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin. 6.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SMO0458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; 3D-structure; Pyridolone carboxylic acid.
FT CHAIN 1 281 ABRIN-A A CHAIN.
FT PEPTIDE 282 281 LINKER PEPTIDE.
FT DOMAIN 282 325 ABRIN-A B CHAIN.
FT DOMAIN 326 403 RICIN-B-TYPE LECTIN 1.
FT REPEAT 403 527 RICIN-B-TYPE LECTIN 1.
FT REPEAT 283 325 1-ALPHA.
FT REPEAT 326 366 1-BETA.
FT REPEAT 369 401 1-GAMMA.
FT REPEAT 414 449 2-ALPHA.
FT REPEAT 453 492 2-BETA.
FT REPEAT 495 528 2-GAMMA.
FT ACT SITE 164 164 BY SIMILARITY.
FT DISULFID 247 289 INTERCHAIN (BY SIMILARITY).
FT DISULFID 286 305 BY SIMILARITY.
FT DISULFID 306 335 BY SIMILARITY.
FT DISULFID 427 436 BY SIMILARITY.
FT DISULFID 456 473 PYRIDOLONE CARBOXYLIC ACID.
FT MOD RES 1 1 N-LINKED (GLYC. ...).
FT CARBOHYD 361 361 N-LINKED (GLYC. ...).
FT CONFLICT 202 202 MISSING (IN REF. 2).
FT CONFLICT 298 298 N -> Y (IN REF. 4).
FT CONFLICT 427 427 M -> L (IN REF. 4).
FT CONFLICT 467 467 T -> P (IN REF. 4).
FT CONFLICT 483 483 V -> L (IN REF. 4).
FT STRAND 5 8
FT TURN 10 11
FT HELIX 12 14
FT STRAND 15 16
FT TURN 17 18
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FT TURN 22 23
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FT TURN 27 28
FT STRAND 29 31
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FT STRAND 497 501

Query Match 54.5%; Score 773.5; DB 1; Length 528;
Best Local Similarity 54.9%; Pred. No. 2.6e-60;
Matches 141; Conservative 45; Mismatches 70; Indels 1; Gaps 1;
QY 5 CSAS-EPTVRIYGRNGVCYVDDPDHGNQIQLPKSKNNDPNQIQIKRQDTRISNGS 63


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CC CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
CC KNOCKOUTS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC site on the 28S rRNA, A AND B CHAINS.
CC -1- SUBUNIT: DISPERSED IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIB SUPRASILY.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIB SUPRASILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -----
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CC -----
DR EMBL: U41299; AAB3475.1;
DR PIR: S37382; S37382.1;
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00356; SHIGARICIN.
DR SMART: SM00458; SHIGA_RICIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PDB: 1def; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 305 563
FT DOMAIN 305 431
FT DOMAIN 434 559
FT REPEAT 316 356
FT REPEAT 357 397
FT REPEAT 400 432
FT REPEAT 448 482
FT REPEAT 483 524
FT REPEAT 527 563
FT ACT_SITE 168 188
FT DISULFID 274 319
FT DISULFID 319 338
FT DISULFID 360 377
FT DISULFID 448 463
FT DISULFID 489 506
FT CARBOHYD 221 221
FT CARBOHYD 368 368
FT CARBOHYD 436 436
FT CARBOHYD 492 492
FT CARBOHYD 537 537
FT CONFLICT 39 39
SQ SEQUENCE 563 AA; 62300 MW; P250CB24621B74 CRC64;
Query Match 38.0%; Score 539; DB 1; Length 563;
Best Local Similarity 41.4%; Pred. No. 1e-39;
Matches 109; Conservative 43; Mismatches 105; Indels 6; Gaps 4;
OY 1 DDVTCASAEPTVR-IVGENMKVCYDPRDDPHDGNQIOLMSKSNDDNOLMTIRKDCGTR 59
DB 228 DSGITLRTSFTKNIYVDSGLCDVRNGHVDLGFQLMPCGNOR--NORPTFSDDIR 355
OY 60 SNGSLTCTTCTAGCTATWIPCTCTVNEATITWIKNGITLNSKNTVYLAASGIRGTL 119
DB 356 SNGKCTPRLNNGNSVIVFNGSTPAENAKIKVPIIDSLINSSGLVWTFAPLASRTIL 415
OY 120 TVQTLDTYAGGAGNDTAPREVIYVGRDLCNSNG--GSWYEWCTVSSQCONPMALY 177
DB 416 LLDNDITVAGSGMTVNVNVPYVSIYGVYKWLQNGENNGNVMEDCEATSLQQOMALY 475

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DR InterPro: IPR000772; Ricin B lectin.
 DR Pfam: PF00331; Glyco_hydro_10; 1.
 DR Pfam: PF00652; Ricin B lectin; 3.
 DR PRINTS: PR00134; GHYDRLASE10.
 DR SMART: SM00633; Glyco_10; 1.
 DR SMART: SM00634; Glyco_hydro_10; 1.
 DR PROSITE: PS00541; Glyco_hydro_10; 1.
 DR PROSITE: PS00231; Ricin B lectin; 1.
 DR Xylan degradation; Hydrolase; glycosidase; signal; lectin;
 3D-structure.
 FT SIGNAL 1 41
 FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
 FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
 FT ACT_SITE 169 169 PROTON DONOR.
 FT ACT_SITE 277 277 NUCLEOPHILE.
 SQ SEQUENCE 477 AA; 51162 MW; 51457ES7EDC68CC CRC64;
 Query March 10.5%; Score 149.5; DB 1; Length 477;
 Best Local Similarity 28.2%; Pred. No. 116-09;
 Matches 49; Conservative 20; Mismatches 54; Indels 51; Gaps 8;
 QY 7 ASP-----TVAIVGAMGVCDVDDPHDNGIQLMGSKNMDNGLTKIKGDTIRSN 61
 DB 346 SSEPPADGQDIKGVG-SGRCLDVPASTSTDTQLQMOCHSGT--NOQVATADAGELAVY 402
 QY 62 G-SCLTYGTAGVYVMPDCTNAYRENTIWMGNTIIPRSNLYLAASGSKGTILL 120
 DB 403 GDKCLDAAGTSGSKVQIYSGWGDNCK--WELNSDGSVGVSGCLDPA----- 450
 QY 121 VQTLDTLGGCMALGNDTPREVTYTGFRDLCHNSGSGSVETVCSQGNCR 174
 DB 451 -----VGNCH-----NGLTLDLYIC-SNSNGNR 474
 RESULT 9
 SPL_RARRA STANDARD; PRT; 525 AA.
 ID SPL_RARRA
 AC 005308; 1-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE Serine protease 1, precursor (SC 3.4.21.-?) (R21).
 OS Bacteroides faecitabidus
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Micrococciaceae; Rarobacteriaceae; Rarobacter.
 CX NCBI_Taxid=13243;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
 RC MEDLINE=9218668; PubMed=1778983;
 RA Shmool H., Tadema M.,
 RT "Characterization of Rarobacter faecitabidus protease I, a
 RT yeast-lytic serine protease having mannose-binding activity,"
 RT J. Biochem. 110:608-613 (1991).
 CC -1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
 CC FUNGUS AND YEAST. SHOWN TO EXHIBIT IN ITS SUBSTRATE
 CC SPECIFICITY AND HAS A HIGH AFFINITY FOR MANNOSE.
 CC MANNOSE-BINDING MAY BE THE NATURAL SUBSTRATE FOR RFI.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
 CC -1- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.
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 CC -----
 DR EMBL: D10753; BAA01585.1; --
 DR PIR: A45053; A45053.
 DR HSRP: P00778; IGBA.
 DR SMART: SM00633; Glyco_10; 1.
 DR SMART: SM00634; Glyco_hydro_10; 1.
 DR PROSITE: PS00541; Glyco_hydro_10; 1.
 DR PROSITE: PS00231; Ricin B lectin; 1.
 DR Xylan degradation; Hydrolase; glycosidase; signal; lectin;
 3D-structure.
 FT SIGNAL 1 41
 FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
 FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
 FT ACT_SITE 169 169 PROTON DONOR.
 FT ACT_SITE 277 277 NUCLEOPHILE.
 SQ SEQUENCE 477 AA; 51162 MW; 51457ES7EDC68CC CRC64;
 Query March 10.5%; Score 149.5; DB 1; Length 477;
 Best Local Similarity 28.2%; Pred. No. 116-09;
 Matches 49; Conservative 20; Mismatches 54; Indels 51; Gaps 8;
 QY 7 ASP-----TVAIVGAMGVCDVDDPHDNGIQLMGSKNMDNGLTKIKGDTIRSN 61
 DB 346 SSEPPADGQDIKGVG-SGRCLDVPASTSTDTQLQMOCHSGT--NOQVATADAGELAVY 402
 QY 62 G-SCLTYGTAGVYVMPDCTNAYRENTIWMGNTIIPRSNLYLAASGSKGTILL 120
 DB 403 GDKCLDAAGTSGSKVQIYSGWGDNCK--WELNSDGSVGVSGCLDPA----- 450
 QY 121 VQTLDTLGGCMALGNDTPREVTYTGFRDLCHNSGSGSVETVCSQGNCR 174
 DB 451 -----VGNCH-----NGLTLDLYIC-SNSNGNR 474
 RESULT 10
 SPL_RARRA STANDARD; PRT; 475 AA.
 ID SPL_RARRA
 AC 004151; 1-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Alpha-1-arabinofuranosidase precursor (SC 3.2.1.55) (Arabinoxidase).
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycetaceae; Streptomyces.
 CX NCBI_Taxid=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2196410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D., Quail M.A., Kieffer H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajendram M.A., Rutherford K., Rutter S., Taylor K.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RA Complete genome sequence of the model actinomycete *Streptomyces*
 RA *coelicolor* A1(2).
 RA Nature 407:693-699 (2000)
 CC -1- SUBCELLULAR LOCATION: Cytoplasm; hydrolysis of terminal non-reducing alpha-L-
 CC arabinofuranoside residues in alpha-D-arabinosides.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AL939125; CAA189.1; -
 DR PIR: T35697; T35697.
 DR InterPro: IPR005193; Glyco_hydro_62.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF03664; Glyco_hydro_62; 1.
 DR Pfam: PF00652; Ricin_B_lectin; 3.
 DR SMART: SM00458; Ricin_1.
 DR PROSITE: PS0231; Ricin_B_lectin; 1.
 DR KEGG: 300000000; Hydrolyase; Glycosidase; Signal; Lectin;
 KM Xylan degradation; Hydrolyase; Glycosidase; Signal; Lectin;
 KM Complete proteome. 37
 FT SIGNAL 1
 FT CHAIN 38 475 POTENTIAL
 FT DOMAIN 39 165 ALPHA-D-ARABINOFURANOSIDASE.
 FT SIGNAL 166 RICIN B-TYPE LECTIN
 SQ SEQUENCE 475 AA; 50045 MW; 475707FE543A6D CRC64;
 Query Match 8.7%; Score 124; DB 1; Length 475;
 Best Local Similarity 24.1%; Pred. No. 0.0019;
 Matches 65; Conservative 33; Mismatches 116; Indels 56; Gaps 13;
 QY 6 SASEPTVAVGNKCVTRDDDFHGNQQLQMPKSNNDPNQMLTKEDGTIRSG-SC 64
 DB 37 AAGSGLAKGNSN-RLDYLQSGSDGALQDLQDQKGT-NQOMSTDTGRILTVGDK 93
 QY 65 LITVGYTA-GYVYVNFQONTAVREACTIVQIMNGTIIIPNSWLT-AASGI-KGTTLT 120
 DB 94 LDVGHATATAGTRVQVMSGSGNQ--WVNSDGTIVVSGSLCEAAGAGPMTGAVQ 151
 QY 121 VQTLDTYTGQGLAGNDTPAREVTI-----YGFEDLCNESNGSVVETCVSSQOQR 173
 DB 152 LMTGCGGNGKMTVGTETPTDGTALPSTYRMSSTGVLAQPKSGVAKLKPFTVTHNGR 211
 QY 174 KALYGGGSIKPKONQDCLTGKDSVSTVINYVSCAGSSGQRYV--FTNIGALINIKR 230
 DB 212 HLYVG-----STSSGSSVGSWVSPFTNMSDMSAGQ 243
 QY 231 GLANDVQANPRLRIIIPATKRNQML 260
 DB 244 N-AMNOAAVAPLT---FFFA---PKNIWV 265
 RESUME 11
 ID ABBB STRLI STANDARD; PRT; 475 AA.
 AC P06453;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (arabinosidase).
 GN ABBB.
 OS Streptomyces lividans.
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 CC Streptomyces; Streptomycesaceae; Streptomyces.
 CC [1]_taxid=1316;
 RN NCBI_TaxID=1316;
 RP SEQUENCE FROM N.A.
 RC STRAIN=66 / 1326;
 RX MEDLINE=9720396; PubMed=9148759;
 RA Vincent P., Shareck F., Dupont C., Morosoli R., Kluepfel D.,
 RA "New alpha-L-arabinofuranosidase produced by *Streptomyces lividans*;
 RA cloning and DNA sequence of the *abbB* gene and characterization of the
 RA enzyme". J. 322:845-852 (1997).
 RL [2]
 RN REVISIONS.
 RP STRAIN=66 / 1326;
 RA Shareck F.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HAS A SPECIFIC ARABINOFURANOSYL-BRANCHING ACTIVITY ON
 CC XILAN FROM GRAMINAE, ACTS SYNERGISTICALLY WITH THE XYLANASES AND
 CC BINDS SPECIFICALLY TO XILAN. FROM SMALL ARABINOXYL-O-LIGOSIDES.
 CC IT LIBERATES ARABINOSIDES AND, AFTER PROLONGED INCUBATION, THE
 CC FORMED ENZYME EXHIBITS SOME XYLANOXYLACTIC ACTIVITY AS WELL.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
 CC arabinofuranoside residues in alpha-D-arabinosides.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M64531; AAC2652.1; -
 DR InterPro: IPR005193; Glyco_hydro_62.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF03664; Glyco_hydro_62; 1.
 DR Pfam: PF00652; Ricin_B_lectin; 3.
 DR SMART: SM00458; Ricin_1.
 DR PROSITE: PS0231; Ricin_B_lectin; 1.
 DR KEGG: 300000000; Hydrolyase; Glycosidase; Signal; Lectin.
 KM Xylan degradation; Hydrolyase; Glycosidase; Signal; Lectin;
 KM Complete proteome. 37
 FT SIGNAL 1
 FT CHAIN 38 475 POTENTIAL
 FT DOMAIN 39 165 ALPHA-D-ARABINOFURANOSIDASE.
 FT SIGNAL 166 RICIN B-TYPE LECTIN
 SQ SEQUENCE 475 AA; 50369 MW; CCA34EB7B85AAD CRC64;
 Query Match 8.5%; Score 121; DB 1; Length 475;
 Best Local Similarity 24.1%; Pred. No. 0.0024;
 Matches 65; Conservative 33; Mismatches 116; Indels 56; Gaps 13;
 QY 6 SASEPTVAVGNKCVTRDDDFHGNQQLQMPKSNNDPNQMLTKEDGTIRSG-SC 64
 DB 37 AAGSGLAKGNSN-RLDYLQSGSDGALQDLQDQKGT-NQOMSTDTGRILTVGDK 93
 QY 65 LITVGYTA-GYVYVNFQONTAVREACTIVQIMNGTIIIPNSWLT-AASGI-KGTTLT 120
 DB 94 LDVGHATATAGTRVQVMSGSGNQ--WVNSDGTIVVSGSLCEAAGAGPMTGAVQ 151
 QY 121 VQTLDTYTGQGLAGNDTPAREVTI-----YGFEDLCNESNGSVVETCVSSQOQR 173
 DB 152 LMTGCGGNGKMTVGTETPTDGTALPSTYRMSSTGVLAQPKSGVAKLKPFTVTHNGR 211
 QY 174 KALYGGGSIKPKONQDCLTGKDSVSTVINYVSCAGSSGQRYV--FTNIGALINIKR 230
 DB 212 HLYVG-----STSSGSSVGSWVSPFTNMSDMSAGQ 243
 QY 231 GLANDVQANPRLRIIIPATKRNQML 260
 DB 244 N-AMNOAAVAPLT---FFFA---PKNIWV 265

DE N-acetylglucosaminyltransferase (GALNac-T1) (ppgamtase 3).
 GN GLY-3 OR ZK688.8.
 OS Caenorhabditis elegans.
 OC Nematoda; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN (1)
 RE SEQUENCE FROM N.A.
 RX MEDLINE=98192620; PubMed=9525933;
 RA Hagen F.K.; Nehke K.;
 RT "cDNA cloning and expression of a family of UDP-N-acetyl-D-
 galactosamine:polypeptide N-acetylglucosaminyltransferase sequence
 homologs from Caenorhabditis elegans."
 RL U. Biol. Chem. 273:8268-8277 (1998).
 RN (2)
 RE SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R.; Ahmedouh R.; Anderson K.; Baynes C.; Berks M.; Coulson A.;
 RA Bontali K.; Combes O.; Durbin R.; Fellous A.; Fieschi A.;
 RA Craxton M.; Dear S.; Du Z.; Durbin R.; Fellous A.; Fieschi A.;
 RA Johnston L.; Jones M.; Kersey J.; Kistner J.; Lister J.; M.
 RA Latreille P.; Percy C.; Rifkin L.; Roopra A.; Saunders D.; Shownkeen R.;
 RA Sims M.; Smailson N.; Smith A.; Smith M.; Sonhammer E.; Staden R.;
 RA Sulston C.; Thierry-Mieg J.; Thomas K.; Vaudin M.; Vaughan K.;
 RA Waterston R.; Watson A.; Wellstock L.; Wilkinson-Spratt J.;
 RA Wohlschlag P.;
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.
 RL Nucleic Acids Res. 22:32-38 (1994).
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN CATALYZES THE INITIAL REACTION IN O-LINKED
 OLIGOSACCHARIDE BIOSYNTHESIS, THE TRANSFER OF AN N-ACETYL-D-
 GALACTOSAMINE RESIDUE TO A SERINE OR THREONINE RESIDUE ON THE
 PROTEIN RECEPTOR.
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide =
 UDP + N-acetyl-D-galactosaminyl-polypeptide.
 CC -1- PATHWAY: Glycolysis; Glyceraldehyde 3-phosphate; Type II membrane protein (Potentilla).
 CC -1- SUBCELLULAR LOCATION: Cytoplasm.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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 CC -----
 DR EMBL: AF031833; AAC13669.1; -;
 DR EMBL: L16621; AAA28224.3; -;
 DR PIR: T42243; T42243.
 DR WormPep: ZK688.8; CE29649.
 DR InterPro: IPR001173; Glyco_transf_2.
 DR Pfam: PF00652; Glyco_transf_2.1.
 DR SMART: SM00458; RICHN_1; RICHN_2.
 DR PROSITE: PS00231; RICHN_B; LECTIN; 2.
 KW Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
 KW Glycoprotein; Lectin.
 FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 14 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 35 612 LUMINAL (POTENTIAL).
 FT DOMAIN 478 612 RICIN B-TYPE LECTIN.

FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
 SC SEQUENCE 612 AA; 66911 MW; 3031C9F5339858 CRC64;
 Query Match 7.6%; Score 107.5; DA 1; Length 612;
 Best Local Similarity 25.8%; Pred. No. 0.071;
 Matches 31; Conservative 21; Mismatches 53; Indels 15; Gaps 5;
 QY 148 PROTEIN-----GSYWTVCYSSQDQNALYDSSIRPKNODQTCGR-DYSTV 202
 DB 492 FTEKVDYNGKQDQAGQIQGQHQGQKQMSYTKSELR--SDQLSSGHTVQIGSE 548
 QY 203 INIVSGSAGSGGQWYFT--NEGALINLKLGLANDVQANPKRLIIVPATKPGQW 259
 DB 549 LTRRSYSKINKYKVEFEDDQATYLHKTKQCVYGAQGVTLDEC---GLSKDQW 604
 RESULT 15
 ID 163 SYNY3 STANDARD; FRT; 1693 AA.
 AC 952563; 1998 (Rel. 36, Created)
 DT 15-JUN-1998 (Rel. 36, Sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical WD-repeat protein sll0163.
 GN Sll0163.
 OS Synechocystis sp. (strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN (1)
 RE SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T.; Tanaka A.; Sato S.; Koiwai H.; Sazuka T.; Miyajima N.;
 RA Kanehisa A.; Nakamura Y.;
 RT "Genomic analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome."
 RL DNA Res. 2:153-166 (1995).
 CC -1- SIMILARITY: Contains 16 WD repeats.
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 CC -----
 DR EMBL: D63999; BAA10064.1; -;
 DR PIR: S76086; S76086.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 16.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 13.
 DR SMART: SM00307; WD40; 16.
 DR PROSITE: PS00082; WD_REPEATS_1; 8.
 DR PROSITE: PS00082; WD_REPEATS_2; 15.
 DR PROSITE: PS00294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat; Complete proteome.
 FT REPEAT 108 1042 WD 1.
 FT REPEAT 1053 1083 WD 2.
 FT REPEAT 1094 1124 WD 3.
 FT REPEAT 1135 1165 WD 4.
 FT REPEAT 1176 1206 WD 5.
 FT REPEAT 1217 1247 WD 6.
 FT REPEAT 1258 1288 WD 7.
 FT REPEAT 1329 1359 WD 8.
 FT REPEAT 1390 1420 WD 9.
 FT REPEAT 1431 1461 WD 10.
 FT REPEAT 1472 1502 WD 11.
 FT REPEAT 1503 1533 WD 12.
 FT REPEAT 1534 1564 WD 13.
 FT REPEAT 1565 1595 WD 14.

FT REPEAT 1596 1616 WD 15.
FT REPEAT 1627 1657 WD 16.
SQ SEQUENCE 1693 AA; 189335 MW; 0977A827A0251CFP CRC64;

Query Match
Similarity 21.8%; Score 97.5; DB 1; Length 1693;

Matches 57; Conservative 33; Mismatches 92; Indels 79; Gaps 12;

QY 3 VTCSASEPTVRIVGRNMCYDV--RDDEP-----DSNQIQIPKSNDEPQIATIK 53
DB 1234 ITSSSDGTARWRHRKCLGLRGRHDHNIHGRFSLDQKIVLY--STDYIARLMT-- 1288
QY 54 RDTTIRNSGCLTY-GYTAGYVMIFCN-----TAVRATIMQWNGTI-INPRS 104
DB 1289 KEGTL-----LTLRGRQKRYDADFSADGRFVFTVSAQDTARQMDISQKDTITLTCHS 1342
QY 105 NLYLAASSGIKGTTLTVQTLDTYL-----QQGMLAGNDTAPREVTIYGF 149
DB 1343 HWVRHAFNPRKQHLTVSADKXALMTTREGCVATADRGQWVREGQFSP----- 1393
QY 150 DLGMSNGSGVWVETCVSSQONORALYDGSIRPKQNDQCLTGRDSVSTVNI----- 205
DB 1394 -----DQQWIVTGSADKTAQLWNVLG-----KKLTTLRGRQDAVAVTRFSP 1434
QY 206 --VSCNASSSGQWVFTNRG 223
DB 1435 DSGYIVTASIDETARVWNRNG 1455

Search completed: December 11, 2003, 14:09:04
Job time : 5.60292 secs

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpt

Page 1

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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18; Search time 20.2717 seconds
(without alignments)
3347.915 Million cell updates/sec

Title: US-09-601-667c-6
Sequence: 1 DDVTCASSEPTFRIVGRNM.....PRIIYPAKPKMQLFVP 263
Perfect score: 1420

Scoring table: ELOSUM62
Gapop 10.0, Gapext 0.5
Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database:

1: SP_bacteria*
2: SP_bacteriia*
3: SP_fungi*
4: SP_human*
5: SP_invertebrate*
6: SP_mammal*
7: SP_mhc*
8: SP_organelle*
9: SP_phase*
10: SP_plant*
11: SP_protent*
12: SP_virus*
13: SP_vertebrate*
14: SP_virus*
15: SP_virus*
16: SP_bacteriia*
17: SP_archaea*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	98.4	531	10 Q8RX6	Q8RX6 vicium albu
2	1189	83.7	265	10 Q8RX2	Q8RX2 vicium albu
3	1160	81.7	565	10 Q8RX3	Q8RX3 vicium albu
4	1155	81.3	265	10 Q8RX1	Q8RX1 vicium albu
5	1060.5	74.7	266	10 Q8RX3	Q8RX3 vicium albu
6	915	64.4	541	10 Q41174	Q41174 ricinus com
7	902.5	63.6	580	10 Q948W4	Q948W4 ricinus com
8	895.5	63.1	580	10 Q948W3	Q948W3 ricinus com
9	895.5	63.1	580	10 Q948W3	Q948W3 ricinus com
10	864	60.8	543	10 Q948W5	Q948W5 ricinus com
11	864	60.8	543	10 Q948W5	Q948W5 ricinus com
12	755.5	53.3	528	10 Q96076	Q96076 abrus prec
13	753.5	53.1	547	10 Q96059	Q96059 abrus prec
14	743	52.3	382	10 Q8A43	Q8A43 abrus prec
15	684	48.2	573	10 Q8W28	Q8W28 iris hollan
16	684	48.2	592	10 Q8W27	Q8W27 iris hollan

17	592.5	41.7	570	10 Q22415	Q22415 sambucus n
18	577	40.6	316	10 Q6R745	Q6R745 sambucus n
19	576	40.6	316	10 Q93W1	Q93W1 sambucus n
20	575	40.5	316	10 Q94554	Q94554 sambucus n
21	565	39.8	564	10 Q9AVR2	Q9AVR2 sambucus n
22	560.5	39.5	604	10 Q9M634	Q9M634 polyonatum
23	558.5	39.3	570	10 Q41358	Q41358 sambucus n
24	558	39.2	563	10 Q41357	Q41357 sambucus n
25	548	38.6	320	10 Q94553	Q94553 sambucus n
26	548	38.6	320	10 Q94553	Q94553 sambucus n
27	545.5	38.4	603	10 Q9M633	Q9M633 polyonatum
28	544.5	38.3	565	10 Q04071	Q04071 sambucus n
29	542.5	38.2	566	10 Q04072	Q04072 sambucus n
30	539	38.0	563	10 Q94552	Q94552 sambucus n
31	538	37.9	320	10 Q04366	Q04366 sambucus n
32	534.5	37.6	307	10 Q8G746	Q8G746 sambucus n
33	534.5	37.6	307	10 Q93543	Q93543 sambucus n
34	452.5	13.7	293	10 Q9S1V9	Q9S1V9 cucumis sat
35	156	11.0	422	16 Q9EWR5	Q9EWR5 streptomyce
36	152	10.7	435	2 Q86411	Q86411 oestrovira x
37	145.2	10.3	377	2 Q86411	Q86411 streptomyce
38	145.2	10.3	377	2 Q86411	Q86411 streptomyce
39	135	9.5	482	2 Q86WV6	Q86WV6 nonvira
40	134.5	9.5	555	16 Q9K438	Q9K438 streptomyce
41	134	9.4	962	16 Q9K473	Q9K473 streptomyce
42	132	9.3	579	16 Q9K474	Q9K474 streptomyce
43	125.5	8.8	476	2 Q9RW45	Q9RW45 streptomyce
44	125.5	8.8	476	2 Q9RW45	Q9RW45 streptomyce
45	116	8.2	1545	16 Q9RDQ1	Q9RDQ1 streptomyce

ALIGNMENTS

RESULT 1
ID Q8RX6 PRELIMINARY: PRT: 531 AA.
AC Q8RX6;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Lectin chain A isoform 1 (EC 3.2.2.23) (RNA N-glycosidase)
DE (fragment)
OS Vicium album (European mistletoe)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Streptophyta; Equisetophyta; Eudicotyledons; core eudicot;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=3972;
RN [1]
RP SOURCE FROM N.A.
RA TISSUE=Leaf;
RA Parmasivam M., Misra V., Srinivasan A., Singh T.P.;
RT "Viscum album (Indian) mRNA for Mistletoe lectin chain A isoform 1 and
RT chain B.";
RC Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -L- SPECIFIC AMBOSIN ON THE 28S RNA.
CC EMBL: AY081149, AY870061, O1 THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR InterPro: IPR001772; Rictin_B_lectin.
DR Pfam: PF00652; Rictin_B_lectin; 6.
DR SMART: SM00458; RICTIN_2.
DR PROSITE: PS00231; RICTIN_B_LECTIN; 2.
KW Hydroxylase; Toxin.
FT NDNTER 1 1
FT CHAIN 1 241 LECTIN CHAIN A ISOFORM 1.
FT CHAIN 2 531 LECTIN B CHAIN
SQ SEQUENCE 531 AA; 58802 MW; 162448BDFE53422 CRC64;
Query Match 98.4%; Score 1397; DB 10; Length 531;
Best Local Similarity 96.1%; Pred. No. 1.1e-114;

Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 60
DB DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 328
QY 61 NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 120
DB NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 388
QY 121 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 180
DB 389 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 448
QY 181 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 240
DB 449 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 508
QY 241 PSLRRIIYPATGKQNMWLPVP 263
DB 509 PSLRRIIYPATGKQNMWLPVP 531

RESULT 2

Q8LK02 PRELIMINARY; FRT; 263 AA.

AC 08LK02; (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Lactin chain B subsp. coloratum. 2 (segment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159376;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.-K.,
Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508918; AM46936.1;
DR InterPro; IPR000772; Rctin_B lectin.
DR Pfam; PF00652; Rctin_B lectin. 5.
DR SMART; SM00458; Rctin_B lectin. 2.
DR PROSITE; PS50231; Rctin_B lectin. 2.
FT PROSITE PS50231; Rctin_B lectin. 2.
FT NON_TER 1
FT TER 263
SQ SEQUENCE 263 AA; 29150 MW; B6858CB7C49C8D1F CRC64;

Query Match 83.7%; Score 1189; DA 10; Length 263;
Best Local Similarity 82.5%; Pred. No. 9,3e-97;
Matches 217; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 60
DB 1 DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 60
QY 61 NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 120
DB 61 NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 120
QY 121 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 180
DB 121 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 180

QY 181 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 240
DB 181 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 240
QY 241 PSLRRIIYPATGKQNMWLPVP 263
DB 241 PSLRRIIYPATGKQNMWLPVP 263

RESULT 3

Q8W243 PRELIMINARY; FRT; 565 AA.

AC 08W243;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE VCA precursor (BC 3.2.2.21) (rRNA N-glycosylase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159376;
RN [1].
RP SEQUENCE FROM N.A.
RA Park W.-S., Lyu S.;
RT Blooming of Viscum album subsp. coloratum (Korean mistletoe).
RT Blooming. Biophys. Res. Commun. 0:0-0(2002).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF369561; XAL0411.1;
DR InterPro; IPR001574; Rctin_B lectin.
DR SMART; SM00458; Rctin_B lectin. 2.
DR PROSITE; PS50231; Rctin_B lectin. 2.
DR Pfam; PF00652; Rctin_B lectin. 6.
DR PRINTS; PR00366; SHIGRACIN.
DR SMART; SM00458; Rctin_B lectin. 2.
DR PROSITE; PS50231; Rctin_B lectin. 2.
KW Hydroxylase; signal; toxin.
FT SIGNAL 1 22
FT CHAIN 23 273
FT CHAIN 309 565
SQ SEQUENCE 565 AA; 62401 MW; 991B3994DAD05F11 CRC64;

Query Match 81.7%; Score 1160; DA 10; Length 565;
Best Local Similarity 82.5%; Pred. No. 8.8e-94;
Matches 217; Conservative 16; Mismatches 26; Indels 4; Gaps 1;

QY 1 DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 60
DB 307 DDVTCASAEPTVRIAGNMGCVADDDPHDGNQIQIOLMPSKSNNDPQMLTIRKDTTRS 362
QY 61 NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 120
DB 363 NSGCLITGTYGAGVYMIPOCNVAREATIQWNGSTINPSSVLAASSGKGTTLT 422
QY 121 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 180
DB 423 VQTLDTYLGQGLAGNDTPAEVYIGFRLCNESSGSSVWETCVSSQONKRALYDGG 482
QY 181 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 240
DB 483 SIREKQNDQCLTCGDSVSTVINTVSCSSGSGQWFTNKGALINLKNGLAMVDAQN 542
QY 241 PSLRRIIYPATGKQNMWLPVP 263
DB 543 PSLRRIIYPATGKQNMWLPVP 565

RESULT 4

Q8LK01 PRELIMINARY; FRT; 263 AA.

AC Q81K01.
 DT 01-OCT-2002 (TRENBERL. 22, Created)
 DT 01-OCT-2002 (TRENBERL. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)
 DE Lectin chain B isoform 3 (fragment).
 DE Viscum album subsp. coloratum.
 OS Bakayocet; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RX MEDLINE=156752; PubMed=1170524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 DO M.-S., Song S.K.;
 RI Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF508919; AAM46937.1;
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 DR NON_TER 1
 FT NON_TER 266
 SQ SEQUENCE 266 AA; 29071 MW; 359C4ADA860F061D CRC64;
 Query Match 81.3%; Score 1155; DB 10; Length 263;
 Best Local Similarity 80.6%; Pred. No. 9.2e-94;
 Matches 212; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 DDVTGASBPETVRIAGNMGCVYRDPDHDGNOIQIMPEKSNNDPQOLMTIRKGTIR 60
 DB 1 DDVTGASBPETVRIAGNMGCVYRDPDHDGNOIQIMPEKSNNDPQOLMTIRKGTIR 60
 QY 61 NSGLCTVGTAGVYVWMEPCNTAVERITWQMGNGITINPRSNLYLAASGIGKTT 120
 DB 61 NSGLCTVGTAGVYVWMEPCNTAVERITWQMGNGITINPRSNLYLAASGIGKTT 120
 QY 121 VQTLQDLYLQGLMAGNDTAPREVTIYGFNDLCMESNGSVWETCVASQONRMAL 180
 DB 121 VQTLQDLYLQGLMAGNDTAPREVTIYGFNDLCMESNGSVWETCVASQONRMAL 180
 QY 181 STPRKONQOCCTGCSBVSIVINIVSCASSGGQWFTNEGAILNKNLAMPVQA 240
 DB 181 STPRKONQOCCTGCSBVSIVINIVSCASSGGQWFTNEGAILNKNLAMPVQA 240
 QY 241 PGLRLLIIPATKPKQWMLPYV 263
 DB 241 PGLRLLIIPATKPKQWMLPYV 263
 QY 241 PGLRLLIIPATKPKQWMLPYV 263
 DB 241 PGLRLLIIPATKPKQWMLPYV 263

RESULT 5
 ID Q81K03 PRELIMINARY; PRT; 266 AA.
 AC Q81K03
 DT 01-OCT-2002 (TRENBERL. 22, Created)
 DT 01-OCT-2002 (TRENBERL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)
 DE Lectin chain B isoform 1 (fragment).
 DE Viscum album subsp. coloratum.
 OS Bakayocet; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RX MEDLINE=2156752; PubMed=1170524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 DO M.-S., Song S.K.;
 RI Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF508919; AAM46937.1;
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 DR NON_TER 1
 FT NON_TER 266
 SQ SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;
 Query Match 74.7%; Score 1060.5; DB 10; Length 266;
 Best Local Similarity 72.6%; Pred. No. 2e-85;
 Matches 159; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 DO M.-S., Song S.K.;
 RI Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF508917; AAM46935.1;
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 5.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 DR NON_TER 1
 FT NON_TER 266
 SQ SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;
 Query Match 74.7%; Score 1060.5; DB 10; Length 266;
 Best Local Similarity 72.6%; Pred. No. 2e-85;
 Matches 159; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

QY 1 DDVTGASBPETVRIAGNMGCVYRDPDHDGNOIQIMPEKSNNDPQOLMTIRKGTIR 60
 DB 1 DDVTGASBPETVRIAGNMGCVYRDPDHDGNOIQIMPEKSNNDPQOLMTIRKGTIR 60
 QY 61 NSGLCTVGTAGVYVWMEPCNTAVERITWQMGNGITINPRSNLYLAASGIGKTT 117
 DB 61 NSGLCTVGTAGVYVWMEPCNTAVERITWQMGNGITINPRSNLYLAASGIGKTT 117
 QY 118 TLVQTLQDLYLQGLMAGNDTAPREVTIYGFNDLCMESNGSVWETCVASQONRMAL 177
 DB 118 TLVQTLQDLYLQGLMAGNDTAPREVTIYGFNDLCMESNGSVWETCVASQONRMAL 177
 QY 177 GDSIRPKNQOCCTGCSBVSIVINIVSCASSGGQWFTNEGAILNKNLAMPVQA 237
 DB 177 GDSIRPKNQOCCTGCSBVSIVINIVSCASSGGQWFTNEGAILNKNLAMPVQA 237
 QY 238 QANPKRLIIPATKPKQWMLPYV 263
 DB 238 QANPKRLIIPATKPKQWMLPYV 263
 QY 241 PGLRLLIIPATKPKQWMLPYV 266
 DB 241 PGLRLLIIPATKPKQWMLPYV 266
 QY 241 PGLRLLIIPATKPKQWMLPYV 266
 DB 241 PGLRLLIIPATKPKQWMLPYV 266

RESULT 6
 ID Q41174 PRELIMINARY; PRT; 541 AA.
 AC Q41174
 DT 01-NOV-1996 (TRENBERL. 01, Created)
 DT 01-NOV-1996 (TRENBERL. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)
 DE Pycnidia A chain (EC 3.2.2.22) (RNA N-glycosidase) (fragment).
 DE Ricinus communis (castor bean).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RX MEDLINE=9238377; PubMed=163311;
 RA Roberts L.M., Tregear J.W., Lord J.M.;
 DO Molecular cloning of ricin."
 RI Targeted Diagn. Ther. 7:81-97(1992).
 RL -1- CARLITIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 OF THE TWO GLYCOSIDIC SITES ON THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF001661; A03206; TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR HSPB; P02879; 1BR6
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Interpro; IPR001406; Somatostrophin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.

DR PFAM: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00318; SOMATROPIN_2; 1.
KW Hydrolase; toxin.
KW Nucleoside.
SQ SEQUENCE 541 AA; 60281 MW; 28782CBF1F2E3D9 CRC64;
Query Match 64.4%; Score 915; DB 10; Length 541;
Best Local Similarity 63.6%; Pred. No. 3,2e-72;
Matches 164; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

QY 5 CSASPTVATVGRNKCVDVDDPHDQIQIOLMPKSNNDPNOLMTIRKDTIRNSGSC 64
DB 283 CNDPEPTVATVGRNGLCVDFADGRHNGNAIQLPCKSNTDANQIMTLKQNTIRNSGKC 342
QY 65 LITVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 124
DB 343 LITVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 402
QY 125 DYLGGQMLAGNDAPREVTIVGPRDLCKESNGSVWETCVSSQONQMALVGGDSIR 184
DB 403 IYAVSQMLPTNPTOPFTTIVGLYGLCLQANSQCVWEDCSSEKALQOMALVYDGSIRP 462

QY 185 KQNPQCLTCGRDSVSTVINIVSCAGSSQGRWFTNCGAILNLNGLAMVDAQAPFLR 244
DB 463 QQRNCLTISDSNIRETVKILICGPAASQGRWFTNCGAILNLNGLVLRSPDELR 522
QY 245 RITTPATKRNQMLPV 262
DB 523 QILVPLADPQIMNDEL 540

RESULT 7
Q94BM4 PRELIMINARY; FRT; 580 AA.
ID Q94BM4
AC Q94BM4
DT 01-DEC-2001 (TEMBELrel. 19, Created)
DT 01-DEC-2001 (TEMBELrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBELrel. 23, Last annotation update)
DE 1-100% identical to the EMBL/Genbank/DBJ databases
DE EC 3.2.2.22 (rRNA N-glycosylase)
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_Taxid:13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q.; Gong Z.Z.; Liu W.Y.;
RT Molecular cloning of three type 2 R1P (ribosome-inactivating protein)
RT genes encoding cinnamomum proteins and study of their expression
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases
RL -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039802; AA02459.1; -
DR InterPro: IPR000772; Ricin_B_Lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; Ricin_B_Lectin; 6.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
KW Hydrolase; signal; toxin.
KW SIGNAL. 32
CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN II.
SQ SEQUENCE 580 AA; 64265 MW; 37E4289CECCEBF CRC64;
Query Match 63.6%; Score 903.5; DB 10; Length 580;

Best Local Similarity 63.9%; Pred. No. 3.6e-71;
Matches 168; Conservative 32; Mismatches 62; Indels 1; Gaps 1;

QY 1 DQVCSASEPTVATVGRNKCVDVDDPHDQIQIOLMPKSNNDPNOLMTIRKDTIRNSG 60
DB 317 NDTCADPEPTVATVGRNGLCVDFADGRHNGNAIQLPCKSNTDANQIMTLKQNTIRNSG 376
QY 61 NSCLTIVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 120
DB 377 NSCLTIVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 436
QY 121 VQNLVYASRQGMALNTEPEVTSIVGNDLCQANQDMVWECSSKAEQKALVYDGS 496
DB 437 VQNLVYASRQGMALNTEPEVTSIVGNDLCQANQDMVWECSSKAEQKALVYDGS 496
QY 181 SIREKQNPQCLTCGRDSVSTVINIVSCAGSSQGRWFTNCGAILNLNGLAMVDAQA 239
DB 497 SIREKQNPQCLTCGRDSVSTVINIVSCAGSSQGRWFTNCGAILNLNGLAMVDAQA 239
QY 240 NPKXRITITTPATKRNQMLPV 262
DB 557 NPSLHITITTPATKRNQMLPV 579

RESULT 8
Q94BM3 PRELIMINARY; FRT; 580 AA.
ID Q94BM3
AC Q94BM3
DT 01-DEC-2001 (TEMBELrel. 19, Created)
DT 01-DEC-2001 (TEMBELrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBELrel. 23, Last annotation update)
DE 1-100% identical to the EMBL/Genbank/DBJ databases
DE EC 3.2.2.22 (rRNA N-glycosylase)
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_Taxid:13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q.; Gong Z.Z.; Liu W.Y.;
RT Molecular cloning of three type 2 R1P (ribosome-inactivating protein)
RT genes encoding cinnamomum proteins and study of their expression
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases
RL -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039803; AA02460.1; -
DR InterPro: IPR000772; Ricin_B_Lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; Ricin_B_Lectin; 6.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
KW Hydrolase; signal; toxin.
KW SIGNAL. 32
CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F0E7F558 CRC64;
Query Match 63.1%; Score 896.5; DB 10; Length 580;
Best Local Similarity 63.5%; Pred. No. 1.5e-70;
Matches 167; Conservative 33; Mismatches 62; Indels 1; Gaps 1;

QY 1 DQVCSASEPTVATVGRNKCVDVDDPHDQIQIOLMPKSNNDPNOLMTIRKDTIRNSG 60
DB 317 NDTCADPEPTVATVGRNGLCVDFADGRHNGNAIQLPCKSNTDANQIMTLKQNTIRNSG 376
QY 61 NSCLTIVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 120
DB 377 NSCLTIVGTAGVYVIMPCYANREATVQIMNGTIIINRSNLYLAASGIGKTTITVOTL 436
QY 121 VQNLVYASRQGMALNTEPEVTSIVGNDLCQANQDMVWECSSKAEQKALVYDGS 496
DB 437 VQNLVYASRQGMALNTEPEVTSIVGNDLCQANQDMVWECSSKAEQKALVYDGS 496
QY 181 SIREKQNPQCLTCGRDSVSTVINIVSCAGSSQGRWFTNCGAILNLNGLAMVDAQA 239
DB 497 SIREKQNPQCLTCGRDSVSTVINIVSCAGSSQGRWFTNCGAILNLNGLAMVDAQA 239
QY 240 NPKXRITITTPATKRNQMLPV 262
DB 557 NPSLHITITTPATKRNQMLPV 579

QY 121 VOTLDYTLGGMLAGNDTAPREVTIVGFDLCNESNGSVWVCVSSQONKMLVQDD 180
DB 437 VOADIVASRQGMLAGNTEPPTVSIVGFNDLCQONMEDIAMVVCSSKAEQKMLVQDD 496
QY 181 STRKONQOCLT-CGRDSVTVINIVCSAGSSGQGRVTFNEGAILNKGLAMVQAQ 239
DB 497 STRKONQOCLTSDNHSQGSIISSCSFSSQGRVTFNDGIIINXGLVQVQSS 556
QY 240 NPKLRETIIVPATGKPNOMLVP 262
DB 557 DPLHQLIIVPATGKPNOMLVP 579

RESULT 9
ID Q41143 PRELIMINARY; PRT; 263 AA.
DT 01-NOV-1996 (TRENBERG, 01, Created)
DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)
DT 01-MAR-2003 (TRENBERG, 23, Last annotation update)
DE Ricin B beta chain (fragment).
GN RICIN B BETA CHAIN.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxId=3983;
RN [1]
RF SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RA Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain.;
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SPECIFIC ADENOSINE TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HSP; P02879; 2A1.
DR Interpro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR PRINTS; PR00161; RIP; 1.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS02311; RICIN_B_LECTIN; 2.
KW Hydroxylase; Toxin.
FT NON_TER 1.
SQ SEQUENCE 549 AA; 60648 MW; 02607BE607C44B0 CRC64;
Query Match 60.8%; Score 864; DB 10; Length 549;
Best Local Similarity 61.0%; Pred. No. 1e-67;
Matches 161; Conservative 32; Mismatches 69; Indels 2; Gaps 1;

QY 1 DDTVCAEEPTVIVGNKGVDRDDPHDQNOIOLMPSKSNDDPNQWLTIRGDTIS 60
DB 285 NDVCADEEPTVIVGNKGVDRDDPHDQNOIOLMPSKSNDDPNQWLTIRGDTIS 344
QY 61 NSCLTYGTAGVYVIFDQNTAVERTWQWNGTINPRSNVLAASGIGTTLT 120
DB 345 MKCLTLNGTSAGDVYVITDKRTVVAASITWQWNGTINPRSNVLAASGIGTTLT 404
QY 121 VOTLDYTLGGMLAGNDTAPREVTIVGFDLCNESNGSVWVCVSSQONKMLVQDD 180
DB 405 VONATIASRQGMLAGNTEPPTVSIVGFNDLCQONMEDIAMVVCSSKAEQKMLVQDD 464

QY 181 STRKONQOCLT-CGRDSVTVINIVCSAGSSGQGRVTFNEGAILNKGLAMVQAQ 239
DB 465 STRKONQOCLTSDNHSQGSIISSCSFSSQGRVTFNDGIIINXGLVQVQSS 556
QY 239 ANPKLRETIIVPATGKPNOMLVP 262
DB 525 DPLHQLIIVPATGKPNOMLVP 579

RESULT 10
ID Q9FV22 PRELIMINARY; PRT; 549 AA.
DT 01-DEC-2001 (TRENBERG, 19, Created)
DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DT 01-MAR-2003 (TRENBERG, 23, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin I precursor
DE (EC 3.2.2.22) (RNA N-glycosidase).
DE Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxId=13429;
RN [1]
RF SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;

50 SEQUENCE 547 AA; 61248 MW; 355A325C354A1BD CRC64;
Query Match 53.1%; Score 753.5; DB 10; Length 547;
Best Local Similarity 53.9%; Pred. No. 5,56-58;
Matches 138; Conservative 41; Mismatches 76; Indels 1; Gaps 1;
QY 5 CSAS-EPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 63
DB 288 CSAS-EPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 63
QY 64 CLTYGYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 123
DB 348 CLTYGYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 123
QY 124 LYTLAGGMLAGNDTAPREVTIYGRDLCSNSGQSVWETVSSQONQPMALYDGSIR 183
DB 408 NDIRMRQGMRTGNDISPEVTISLNGFPLCERHNSNMWLDVDTKEEQMAVYDPSIR 467
QY 184 PRONDOCLTGGDSVSTVINYSCASGSGQWYMEGATILNKGLADVAONKPL 243
DB 468 PRONDOCLTGGDSVSTVINYSCASGSGQWYMEGATILNKGLADVAONKPL 243
QY 244 RRIIYATGKKNQW 259
DB 528 KOIIMPYGNANQW 543
RESULT 14
Q85N43 085N43 PRELIMINARY; PRT; 382 AA.
AC 085N43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Abirin isoform G (EC 3.2.2.22) (tRNA N-glycosidase)
DB (Fragment).
OS Abirus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids I; Fabales; Fabaceae; Papilionoideae; Abirae; Abirus.
RX NCBI_TaxID=3816;
RN (1) SOURCE FROM N.A.
RA Cook J.P., Roberts L.M., Lord M.;
RT "New isoform of Abirin - Abirin G";
RC Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF495828; AAL7444.1; -;
DR InterPro: IPR000772; Rictin_B_lectin.
DR PIR: P00452; Rictin_B_lectin. 6.
DR Pfam: P00452; Rictin_B_lectin. 6.
DR SMART: SMO0458; RICTIN. 2.
DR PROSITE: PS00231; RICTIN B LECTIN. 2.
DR PROSITE: PS00275; SHIGA_RICTIN. 1.
KW Hydrolase; Toxin.
FT CHAIN 1 105 ABIRIN A CHAIN.
FT NON_TER 382 382 ABIRIN B CHAIN.
FT CHAIN 382 382
SQ SSQDENCE 382 AA; 42743 MW; B08A341813AD2EE CRC64;
Query Match 53.2%; Score 743; DB 10; Length 382;
Best Local Similarity 53.6%; Pred. No. 2,96-57;
Matches 135; Conservative 43; Mismatches 74; Indels 0; Gaps 0;
QY 9 EPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 68
DB 128 EPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 187

QY 69 GYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 128
DB 186 GYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 128
QY 129 GYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 128
DB 246 GYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 128
QY 189 RQMRGNDISPEVTISLNGFPLCERHNSNMWLDVDTKEEQMAVYDPSIR 467
DB 306 RQMRGNDISPEVTISLNGFPLCERHNSNMWLDVDTKEEQMAVYDPSIR 467
QY 249 YPATGKPNQW 260
DB 368 WPTGKPNQW 379
RESULT 15
Q82E8 082E8 PRELIMINARY; PRT; 573 AA.
AC 082E8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein IPAR (EC 3.2.2.22) (tRNA N-glycosidase)
DB (Fragment).
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OC Iris.
RX NCBI_TaxID=35876;
RN (1) SOURCE FROM N.A.
RA Van Damme E.J.M., Peumans W.J.;
RT "Iris (iris hollandica var. Professor Blaauw) plants express both type
1 and type 2 ribosome-inactivating proteins in bulb tissue";
RC Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF25084; AAL5093.1; -;
DR InterPro: IPR000772; Rictin_B_lectin.
DR PIR: P00452; Rictin_B_lectin. 6.
DR Pfam: P00452; Rictin_B_lectin. 6.
DR SMART: SMO0458; RICTIN. 2.
DR PROSITE: PS00231; RICTIN B LECTIN. 2.
DR PROSITE: PS00275; SHIGA_RICTIN. 1.
KW Hydrolase; Toxin.
FT CHAIN 1 573
SQ SSQDENCE 573 AA; 63759 MW; 141A3B9AECDF9C CRC64;
Query Match 48.2%; Score 684; DB 10; Length 573;
Best Local Similarity 50.8%; Pred. No. 7,76-53;
Matches 130; Conservative 42; Mismatches 86; Indels 2; Gaps 2;
QY 1 DPTVCASEPPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 60
DB 311 DPTVCASEPPTVAVIGNMGCVYVDDPDHFGNQCGLMPSKSNDDNOLMTIRGCTIRSGSLTY 60
QY 61 NSCLTYGYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 120
DB 371 NSCLTYGYTAGVYVIMFDGNTAVREKTIYQINQNGTIPRSMVLAASGKIGTLTYOT 120
QY 121 NQTHYHAKQWPEKNTIPREVTIYGRDLCSNSGQSVWETVSSQONQPMALYDGSIR 179
DB 430 NQTHYHAKQWPEKNTIPREVTIYGRDLCSNSGQSVWETVSSQONQPMALYDGSIR 179
QY 180 GSIRPNQDOCLTGGDSVSTVINYSCASGSGQWYMEGATILNKGLADVAONKPL 243
DB 490 GSIRPNQDOCLTGGDSVSTVINYSCASGSGQWYMEGATILNKGLADVAONKPL 243

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rspc

Page 8

Oy 240 NPKLRRIIYYPATKXNOMW 259
Db 550 DPLQOIIIMSTTGNPNOMW 569

Search completed: December 11, 2003, 14:01:01
Job time : 21.2717 secs

Thu Dec 11 17:00:23 2003

US-09-601-667C-6.rag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 16:56:51, Search time 43 seconds
(without alignment)

970.816 Million cell updates/sec

Title:

US-09-601-667C-6

Perfect score:

1420

Sequence:

1 DVTCSASEPTWRIYGRNM.....RRITVPATKPKQKMPVP 263

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A: Geneseq_190un03.*

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2: /SID1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SID1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SID1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1420	100.0	263	20	AA192995	Mistletoe lectin B
2	1420	100.0	263	20	AA192996	Mistletoe lectin B
3	1420	100.0	531	20	AA192997	Mistletoe lectin B
4	1420	100.0	531	20	AA192998	Mistletoe lectin B
5	1405	99.0	263	19	AA194662	Mistletoe lectin B
6	1405	99.0	263	19	AA194663	Mistletoe lectin B
7	1405	99.0	263	20	AA194664	Mistletoe lectin B
8	1405	99.0	263	19	AA194665	Mistletoe lectin B
9	1405	99.0	564	18	AA194666	Mistletoe lectin B

10	1406	99.0	564	20	AA194667	Mistletoe lectin B
11	1339.5	94.3	264	20	AA194668	Mistletoe lectin B
12	1339.5	94.3	265	20	AA194669	Mistletoe lectin B
13	1333.5	93.9	264	20	AA194670	Mistletoe lectin B
14	1333.5	93.9	265	20	AA194671	Mistletoe lectin B
15	1332	93.8	267	19	AA194672	Mistletoe lectin B
16	1326.5	93.4	264	20	AA194673	Mistletoe lectin B
17	1326.5	93.4	265	20	AA194674	Mistletoe lectin B
18	1324.5	93.3	265	20	AA194675	Mistletoe lectin B
19	1324.5	93.3	264	20	AA194676	Mistletoe lectin B
20	1306.5	92.0	264	20	AA194677	Mistletoe lectin B
21	1306.5	92.0	265	20	AA194678	Mistletoe lectin B
22	1277.5	90.0	264	20	AA194679	Mistletoe lectin B
23	1277.5	90.0	264	20	AA194680	Mistletoe lectin B
24	1277.5	90.0	264	20	AA194681	Mistletoe lectin B
25	1277.5	90.0	533	20	AA194682	Mistletoe lectin B
26	1277.5	90.0	533	20	AA194683	Mistletoe lectin B
27	1277.5	90.0	533	20	AA194684	Mistletoe lectin B
28	1189	83.7	263	22	AA194685	Mistletoe lectin B
29	1189	83.7	263	22	AA194686	Mistletoe lectin B
30	1189	83.7	263	22	AA194687	Mistletoe lectin B
31	1061.5	78.7	261	22	AA194688	Mistletoe lectin B
32	915	64.4	565	6	AA194689	Mistletoe lectin B
33	915	64.4	565	22	AA194690	Mistletoe lectin B
34	913	64.3	574	8	AA194691	Mistletoe lectin B
35	913	64.3	574	10	AA194692	Mistletoe lectin B
36	913	64.3	574	18	AA194693	Mistletoe lectin B
37	913	64.3	576	18	AA194694	Mistletoe lectin B
38	913	64.3	576	20	AA194695	Mistletoe lectin B
39	913	64.3	576	21	AA194696	Mistletoe lectin B
40	913	64.3	576	22	AA194697	Mistletoe lectin B
41	913	64.3	576	7	AA194698	Mistletoe lectin B
42	913	64.3	576	7	AA194699	Mistletoe lectin B
43	907	63.9	262	10	AA194700	Mistletoe lectin B
44	905	63.7	576	8	AA194701	Mistletoe lectin B
45	904	63.7	262	9	AA194702	Mistletoe lectin B

ALIGNMENTS

RESULT 1
AA192995 standard: Protein: 263 AA.

AA192995: 18-OCR-1999 (first entry)

Mistletoe lectin B protein fragment.

Mistletoe, lectin; antimour; immunostimulant; A-chain; MA; immunity;
lymphoma 26S subunit; non-cytotoxic; T-cell activation; immune response;
cancer; cytotoxicity; antigen; isoform; lectin B.

Vasculum Album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DB-1004210.

03-FEB-1998; 98DB-1004210.

(BIOS-) BIOSN ARZNMETITTEL GRSH.

Morris P, Stiefel T, Voelker W, Wellers P,

WPI, 1999-44535/38.

N-Peds; AA209109.

PT Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9, Fig 7B, 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to and activates T-cells and
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cells and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC recombinant from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.
 SQ Sequence 263 AA:
 Query Match 100.0%; Score 1420; DB 20; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5,4e-130;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DDTVCASAEFTVAVKNNKCVADDDPHDNGQIQLPKSKNDPMQMTIRKDGITRS 60
 DB 1 DDTVCASAEFTVAVKNNKCVADDDPHDNGQIQLPKSKNDPMQMTIRKDGITRS 60
 OY 61 NSGLTGYGTAGVYVAFDCNTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 120
 DB 61 NSGLTGYGTAGVYVAFDCNTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 120
 OY 121 VQTLDTYLGQGMLAGNDTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 180
 DB 121 VQTLDTYLGQGMLAGNDTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 180
 OY 181 SIFPKNQDQCLGCRDSVGTATINIVSCAGSSGQGMVFTNEGALINLKNGLAMDVAQAN 240
 DB 181 SIFPKNQDQCLGCRDSVGTATINIVSCAGSSGQGMVFTNEGALINLKNGLAMDVAQAN 240
 OY 241 PKLRRIITYPATGKRNOMLTPV 263
 DB 241 PKLRRIITYPATGKRNOMLTPV 263
 RESULT 2
 AA125991
 ID AA125991 standard; Protein: 264 AA.
 XX
 AC AA125991;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin B variant protein fragment.
 XX
 KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.
 CS
 XX Viscum album.
 XX
 PN DEL9804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 PR 03-FEB-1998; 98DE-1004210.
 XX
 FX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PI Morris P, Stiefel T, Voelker W, Walters P;
 XX WPI; 1999-44535/38.
 DR N-PDB; AA09115.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 13B, 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The B-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cells and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC recombinant from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.
 SQ Sequence 264 AA:
 Query Match 100.0%; Score 1420; DB 20; Length 264;
 Best Local Similarity 100.0%; Pred. No. 5,5e-130;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DDTVCASAEFTVAVKNNKCVADDDPHDNGQIQLPKSKNDPMQMTIRKDGITRS 60
 DB 1 DDTVCASAEFTVAVKNNKCVADDDPHDNGQIQLPKSKNDPMQMTIRKDGITRS 60
 OY 61 NSGLTGYGTAGVYVAFDCNTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 120
 DB 61 NSGLTGYGTAGVYVAFDCNTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 120
 OY 121 VQTLDTYLGQGMLAGNDTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 180
 DB 121 VQTLDTYLGQGMLAGNDTPAREVTIYGFRLCMBSNCGSVWERTCVSQONRMALVGDG 180
 OY 181 SIFPKNQDQCLGCRDSVGTATINIVSCAGSSGQGMVFTNEGALINLKNGLAMDVAQAN 240
 DB 181 SIFPKNQDQCLGCRDSVGTATINIVSCAGSSGQGMVFTNEGALINLKNGLAMDVAQAN 240
 OY 241 PKLRRIITYPATGKRNOMLTPV 263
 DB 241 PKLRRIITYPATGKRNOMLTPV 263
 RESULT 3
 AA125979
 ID AA125979 standard; Protein: 531 AA.
 XX
 AC AA125979;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin I protein fragment.
 XX
 KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 CS
 XX Viscum album.
 XX
 PN DEL19804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 PR 03-FEB-1998; 98DE-1004210.
 XX
 FX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

XX 03-FEB-1998; 98DE-1004210.
 XX (BIOCS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209103.
 DR Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 7, Fig 1B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to and inactivates the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC free of a large scale, at any time of the year. Recombinant products are
 CC free of contaminants present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 SQ Sequence 531 AA;
 Query Match 100.0%; Score 1420; DB 20; Length 531;
 Best Local Similarity 100.0%; Pred. No. 1.5e-129;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DDVTGASSEPTVIVGSGNMCVVDDEPHDGNQIQMPKSKNNDPQQLWTYKEDGTRIS 60
 DB 269 DDVTGASSEPTVIVGSGNMCVVDDEPHDGNQIQMPKSKNNDPQQLWTYKEDGTRIS 328
 QY 61 NSGCTLYGTAGVYVMAFDQNAFRAATINQINPNSVLYAASGKXTLT 120
 DB 329 NSGCTLYGTAGVYVMAFDQNAFRAATINQINPNSVLYAASGKXTLT 386
 QY 121 VQILDYTLGGMLAGNDTAPREVTIYGFRLDQMSNGSGVWETCVSSQONRVALYGG 180
 DB 389 VQILDYTLGGMLAGNDTAPREVTIYGFRLDQMSNGSGVWETCVSSQONRVALYGG 448
 QY 181 SIREKONDDQLTGGDSVTVINIVSCNAGSSGQWVFTNEGAILNKGLANDVPAQAN 240
 DB 449 SIREKONDDQLTGGDSVTVINIVSCNAGSSGQWVFTNEGAILNKGLANDVPAQAN 508
 QY 241 PKRRIITVPAKGRQWMLPVP 263
 DB 509 PKRRIITVPAKGRQWMLPVP 531
 RESULT 4
 AA255982
 ID AA255982 standard; Protein; 532 AA.
 XX AA255982;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin I (variant) protein fragment.
 XX
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
 XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin I.
 XX
 XX viscum album.

PN DEL9804210-AL.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209106.
 DR Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 4B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to and inactivates the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC free of a large scale, at any time of the year. Recombinant products are
 CC free of contaminants present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 SQ Sequence 532 AA;
 Query Match 100.0%; Score 1420; DB 20; Length 532;
 Best Local Similarity 100.0%; Pred. No. 1.5e-129;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DDVTGASSEPTVIVGSGNMCVVDDEPHDGNQIQMPKSKNNDPQQLWTYKEDGTRIS 60
 DB 269 DDVTGASSEPTVIVGSGNMCVVDDEPHDGNQIQMPKSKNNDPQQLWTYKEDGTRIS 328
 QY 61 NSGCTLYGTAGVYVMAFDQNAFRAATINQINPNSVLYAASGKXTLT 120
 DB 329 NSGCTLYGTAGVYVMAFDQNAFRAATINQINPNSVLYAASGKXTLT 386
 QY 121 VQILDYTLGGMLAGNDTAPREVTIYGFRLDQMSNGSGVWETCVSSQONRVALYGG 180
 DB 389 VQILDYTLGGMLAGNDTAPREVTIYGFRLDQMSNGSGVWETCVSSQONRVALYGG 448
 QY 181 SIREKONDDQLTGGDSVTVINIVSCNAGSSGQWVFTNEGAILNKGLANDVPAQAN 240
 DB 449 SIREKONDDQLTGGDSVTVINIVSCNAGSSGQWVFTNEGAILNKGLANDVPAQAN 508
 QY 241 PKRRIITVPAKGRQWMLPVP 263
 DB 509 PKRRIITVPAKGRQWMLPVP 531
 RESULT 5
 AA664662
 ID AA664662 standard; Protein; 263 AA.
 XX AA664662;
 XX 23-OCT-1998 (first entry)
 XX Mistletoe xMLB variant protein.
 XX
 XX lectin B-chain; mistletoe; xMLB; fusion protein; effector; cytotoxic;
 XX intracellular; processing module; protease recognition; targeting module;

Thu Dec 11 17:00:23 2003

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Page 4

NW		Internal disease; treatment; disorder; cell proliferation; activation;
KX		autoimmune disease; allergy; tumour; ricin; translocation.
XX		Viscum album.
XX		
XX		
PX	Key	Location/Qualifiers
FX	Protein	1..263 "partial protein"
FT		/note= "partial protein"
XX		
PN	M09829540-A2.	
PN	09-JUL-1998.	
PD		
PF	02-JAN-1998; 38NO-BP00009.	
PR	02-JUN-1997; 97EB-0100012.	
PI	(BRAT-) BRAIN BIOCHEMISTRY RES & INFORMATION NE.	
PI	Eck J, Schmidt A, Zinke H.	
DR	Wpi; 1998-388122/33.	
DX	N-PSDB; AAIV51344.	
XX		
PT	Nucleic acid encoding fusion protein containing mistletoe lectin A chain - useful for treatment of proliferative and autoimmune diseases, allergies and tumours	
PS	Disclosure; Fig 1(b); 11sep; German.	
XX	This sequence represents a variant mistletoe lectin B-chain, rMB2. This sequence can be used in the construction of a fusion protein which comprises an effector module that is cytotoxic intracellularly, a processing module covalently bonded to the effector module and containing a protease recognition sequence, and a targeting module covalently bonded to the processing module, able to bind specifically to the surface of a cell so as to mediate internalisation of the fusion protein. Mistletoe lectin protein can be used for treating disorders involving proliferation, such as cancer, by inducing activation of cells, especially autoimmune disease, allergy and tumours	
CC	a.5' by injection or topically, or for ex vivo use at 1 pg to 500 ng/ml, at 1 mg to 500 mg/kg/day, or for ex vivo use at 1 pg to 500 ng/ml.	
CC	Fusion proteins can develop toxic activity in a wide range of target cells. The processing module prevents extracellular dissociation, and fusion proteins based on mistletoe lectin A-chain are far more active than those based on ricin and do have the associated problems of toxicity.	
CC	The protein may be expressed in a non-glycosylated form, particularly in the liver, and which has a long half-life in the blood where it actively assists in translocation of the MB A-chain from the endoplasmic reticulum to the cytoplasm.	
XX		
XQ	Sequence 263 AA:	
	Query Match 99.0%; Score 1406; DB 19; Length 263;	
	Rest Local Similarity 98.9%; Fred. No. 1.3e-128;	
	Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0	
QY	1 DDTGASAEETTRVARNKMDVDPDNDNIOQLMRGNPNDDTTRGGRTS 60	
Db	1 DDVTGSASEETTRVARNKMDVDPDNDNIOQLMRGNPNDDTTRGGRTS 60	
	Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0	
QY	61 NSGCITTGTTAGYAVYIPDNNAVERALTWINGNGTINPRSNIYLAASSGIKGLTL 120	
Db	61 NSGCITTGTTAGYAVYIPDNNAVERALTWINGNGTINPRSNIYLAASSGIKGLTL 120	
QY	121 VQIDLTITLGGKLGAKLVAPRHTLYGRDLDMSSNGSVTFETCYSSQNGRYALKYG 180	
Db	121 VQIDLTITLGGKLGAKLVAPRHTLYGRDLDMSSNGSVTFETCYSSQNGRYALKYG 180	
QY	181 STRPKNQODCLTGSDSYSTVINTVSCKSGSSQGMFNTBEALINKGLADVAQNT 240	
Db	181 STRPKNQODCLTGSDSYSTVINTVSCKSGSSQGMFNTBEALINKGLADVAQNT 240	

Query Match	99.0%	Score 1406	DB 18	Length 264
Best Local Similarity	98.9% <td>Pred. No. 1.3e-128</td> <td></td> <td></td>	Pred. No. 1.3e-128		
Matches 260	Conservative 2	Mismatches 1	Indels 0	Gaps 0
Sequence	264 AA			
Query Match	99.0% <td>Score 1406 <td>DB 18 <td>Length 264 </td></td></td>	Score 1406 <td>DB 18 <td>Length 264 </td></td>	DB 18 <td>Length 264 </td>	Length 264
Best Local Similarity	98.9% <td>Pred. No. 1.3e-128</td> <td></td> <td></td>	Pred. No. 1.3e-128		
Matches 260	Conservative 2	Mismatches 1	Indels 0	Gaps 0
Sequence	264 AA			

RESULT 7

ID	AA901026
ID	AA901026 standard; Protein; 264 AA.
XX	
AC	AA901026;
NC	
DE	Mistletoe M. B-chain protein.
DE	
KW	MU, mistletoe, lectin; MDJ; B-chain; transgenic plant; glycosylation; diene; immunotoxin; large-scale production; diagnosis; therapeutic; cancer.
KX	
XX	Viscum album.
XX	
DM	EP864368-AI.
PD	16-DEC-1998.
XX	
PF	26-JUN-1995; 98EF_010560.
PR	26-JUN-1995; 95EP_0109549.
PR	26-JUN-1995; 98EP_0105660.
XX	
XX	(MADU) MADRUS KOBIN AG.
PI	Baur A., Eck J., Lentzen H., Zinke H. WPI: 1999-026592/03.
DR	N-PSDB; AA974181.
XX	
PT	New transgenic plant expressing mistletoe lectin - useful for producing recombinant lectin in e.g. cancer diagnosis and therapy
PS	
XX	Disclosure; Fig 4b; 30pp; German.
CC	This invention describes a novel transgenic plant transformed with a vector capable of encoding a mistletoe (Viscum album) lectin. proprotein or a biologically active fragment. The specification also describes a polypeptide produced by a plant where the polypeptide exhibits at least one enzymatic modification other than the glycosylation that occurs in Viscum album or the polypeptide is a fusion protein, a mistletoe lectin polypeptide dimer and an immunotoxin comprising the polypeptide or the polypeptide dimer. The plants are used for large-scale production of mistletoe lectin for diagnostic or therapeutic purposes B-pharmaceuticals and this sequence represents the mistletoe lectin B-chain which is used as a marker for pyrimid.
CC	(Updated on 20-MAR-2003 to correct PF field.)
SQ	
Sequence	264 AA;
Query Match	93.0%; Score 1406; DS 20; Length 264;
Best Local Similarity	99.9%; Pred. No. 1.3e-128;
Matches 260:	Conservative 2; Mismatches 1; Indels 0; Gaps 0
Dy	1 DDTYSSASPTTATRYKNGCKVPHDDPFDNDNIDQLMRKSNDPGLMTITVDGRTS 60
Dy	2 DDTYSASSETTRATRYKNGCKVPHDDPFDNDNIDQLMRKSNDPGLMTITVDGRTS 61
Oy	61 NSGCITGYTGTVGYVMIPEDNAVARREKLTMOINGGTIIPRSMLVLAASSGKKSTLL 120
Dd	62 NSGCLTYGTGTVGYVMIPEDNAVAREKLTMOINGGTIIPRSMLVLAASSGKKSTLL 121
Oy	121 VQTLDTLIGGMLAANDPAEVTITYGRDLCMSNGSWETCVSSQDNDFALAYDG 180
Dd	122 VQTLDTLIGGGMLAANDPAEVTITYGRDLCMSNGSWETCVSSQDNDFALAYDG 181
Oy	181 SIIRPNODPGTCAGDSIVYTIISCSAGSSQSQRWTREAITLNKGLAMTDVAQN 240
Dd	182 SIIRPNODPGTCAGDSIVYTIISCSAGSSQSQRWTREAITLNKGLAMTDVAQN 241
Oy	241 PKCRILIIYATGKGNQMDLPVV 263

Db	242	PKIRRIYPTGKQWMPFV	264
RESULT 8			
AAW64560			
AAW64660 standard; Protein; 267 AA.			
AAW64660;			
23-OCT-1998 (first entry)			
Mistletoe rMB protein.			
Lectin B-chain, mistletoe; rMB; fusion protein; effector; cytotoxic;			
intracellular; processing module; protease recognition; targeting module;			
internalisation; treatment; disorder; cell proliferation; activation;			
autoimmune disease; allergy; tumour; ricin; translocation.			
Viscum album.			
W08929540-A2.			
09-JUL-1998.			
02-JUN-1998; 98W0-EP00009.			
02-JUN-1997; 97EP-0100012.			
(BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.			
Eck J, Schmidt A, Zinke H;			
WFJ; 1998-388122/13.			
N-PSDB; NAW51342.			
Nucleic acid encoding fusion protein containing mistletoe lectin A			
protein useful for treatment of proliferative and autoimmune			
diseases, allergies and tumours			
Disclousure; Fig 1b; 115pg; German.			
This sequence represents a lectin B-chain, rMB, isolated from mistletoe.			
This sequence can be used in the construction of a fusion protein which			
comprises an effector module that is cytotoxic intracellularly, a			
processing module covalently bonded to the effector module and			
containing a protease recognition sequence, and a targeting module			
capable of targeting the fusion protein to the internalisation of the fusion			
protein. Such a fusion protein can be used for treating disorders			
involving proliferation and/or elevated activation of cells, especially			
e.g. by injection or topically but especially by intravenous injection,			
at 1 ng to 500 mg/day, or for ex vivo use at 1 pg to 500 ng/ml.			
Fusion proteins can develop toxic activity in a wide range of target			
cells. The processing module prevents extracellular dissociation, and			
fusion proteins based on mistletoe lectin A-chain are 100 more active			
non-specific toxicity. The protein may be expressed in a non-glycosylated			
form that does not bind to sugar receptors in the liver, and which has a			
cell long half-life in the blood. Where the mistletoe lectin B-chain is used,			
it actively assists in translocation of the ML A-chain from the			
endoplasmic reticulum to the cytoplasm.			
Sequence 267 AA;			
Query Match 99.0%; Score 1406; DB 19; Length 267;			
Best Local Similarity 99.9%; Freq. NO. 1,35-125;			
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0			
1 DVTGSSSEPTVRVGRKNGCVADDDPHQNGDQLWPKSNNDPQGLMTIKDDSTRS 60			
1 DVTGSSSEPTVRVGRKNGCVADDDPHQNGDQLWPKSNNDPQGLMTIKDDSTRS 60			

QY 61 NSGCLTYGTYAGVYVMTFDCNTAVREATTIWIWNGITIIIPRSNVLVAASGIGKTTLT 120
DB 61 NSGCLTYGTYAGVYVMTFDCNTAVREATTIWIWNGITIIIPRSNVLVAASGIGKTTLT 120
QY 121 VQTLDTYTLGGMLAGNDTARREVTIYGFDDLCESNGSIVWETCVSSQKQRMALYGDG 180
DB 121 VQTLDTYTLGGMLAGNDTARREVTIYGFDDLCESNGSIVWETCVSSQKQRMALYGDG 180
QY 181 SIRPKXNODQCLTCGRDSVSTIVINIVSCASGSGQRFVTFNEGALINFGSLAMVYQAN 240
DB 181 SIRPKXNODQCLTCGRDSVSTIVINIVSCASGSGQRFVTFNEGALINFGSLAMVYQAN 240
QY 241 PKLRRIIYPAATGKPKQMWLPVP 263
DB 241 PKLRRIIYPAATGKPKQMWLPVP 263

RESULT 9

AAW10021
ID AAW10021 standard; Protein: 564 AA.

AC AAW10021;

DT 18-DEC-1997 (first entry)

DE Prepro mistletoe lectin.

KM Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.

XX Viscum album.

PN EP751221-A1.

PD 02-JAN-1997.

PF 26-JUN-1995; 95EP-0109949.

PR 26-JUN-1995; 95EP-0109949.

XX (MADU) MADATUS KOELEN AG.

XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1997-054678/06.

DR N-PSDB; AAT70473.

PT Nucleic acid encoding prepro form of mistletoe lectin - for

XX therapeutic or diagnostic use

XX Claim 12; Fig 4c; 30pp; German.

CC Mistletoe lectin is a cytotoxic agent that has been used for tumour

CC therapy. It can be used as a cytotoxic and medicament. Nucleic

CC acid fragments can be used in methods for producing mistletoe lectin

CC (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).

XX Sequence 564 AA;

QY Query Match 99.0%; Score 1406; DB 18; Length 564;

DB Best Local Similarity 98.9%; Pred. No. 3.8e-128;

QY Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 DPTGCSAEPPTVIRVGNKCTVDDPHDNGTQLMPSKSNNDNQMTTKEDGTTIS 60

QY 302 DPTGCSAEPPTVIRVGNKCTVDDPHDNGTQLMPSKSNNDNQMTTKEDGTTIS 361

DB 61 NSGCLTYGTYAGVYVMTFDCNTAVREATTIWIWNGITIIIPRSNVLVAASGIGKTTLT 120

QY 362 NSGCLTYGTYAGVYVMTFDCNTAVREATTIWIWNGITIIIPRSNVLVAASGIGKTTLT 421

DB 121 VQTLDTYTLGGMLAGNDTARREVTIYGFDDLCESNGSIVWETCVSSQKQRMALYGDG 180

DB 422 VQTLDTYTLGGMLAGNDTARREVTIYGFDDLCESNGSIVWETCVSSQKQRMALYGDG 481
QY 181 SIRPKXNODQCLTCGRDSVSTIVINIVSCASGSGQRFVTFNEGALINFGSLAMVYQAN 240
DB 482 SIRPKXNODQCLTCGRDSVSTIVINIVSCASGSGQRFVTFNEGALINFGSLAMVYQAN 541
QY 241 PKLRRIIYPAATGKPKQMWLPVP 263
DB 542 PKLRRIIYPAATGKPKQMWLPVP 564

RESULT 10

AAW90127
ID AAW90127 standard; Protein: 564 AA.

AC AAW90127;

DT 20-MAR-2003 (updated)

DT 30-APR-1999 (first entry)

DE Mistletoe lectin prepro-protein.

KM Mistletoe; lectin; ML; transgenic plant; glycosylation;

XX diaphorase; immunotoxin; large-scale production; diagnosis; therapeutic;

XX cancer.

XX Viscum album.

PN EP884388-A1.

PD 16-DEC-1998.

PF 26-JUN-1995; 96EP-0105660.

PR 26-JUN-1995; 96EP-0109949.

XX 26-JUN-1995; 96EP-0105660.

PA (MADU) MADATUS KOELEN AG.

XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1999-026582/03.

DR N-PSDB; AAW74182.

PT New transgenic plant expressing mistletoe lectin - useful for

XX producing recombinant lectin in e.g. cancer diagnosis and therapy

XX Claim 1a; Fig 4c; 30pp; German.

CC This invention describes a novel transgenic plant transformed with a

CC vector capable of encoding a mistletoe (Viscum album) lectin

CC also describes a polypeptide produced by a plant where the polypeptide

CC exhibits at least one enzymatic modification other than the glycosylation

CC that occurs in Viscum album or the polypeptide is a fusion protein, a

CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the

CC polypeptide or the polypeptide dimer. The plants are used for large-scale

CC production of mistletoe lectin for diagnostic or therapeutic purposes

CC (e.g. in cancer therapy). This feature represents the mistletoe lectin

QY (updated on 20-MAR-2003 to correct pf field.)

DB Sequence 564 AA;

QY Query Match 99.0%; Score 1406; DB 20; Length 564;

DB Best Local Similarity 98.9%; Pred. No. 3.8e-128;

QY Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 DPTGCSAEPPTVIRVGNKCTVDDPHDNGTQLMPSKSNNDNQMTTKEDGTTIS 60

QY 302 DPTGCSAEPPTVIRVGNKCTVDDPHDNGTQLMPSKSNNDNQMTTKEDGTTIS 361

DB 61 NSGCLTYGTYAGVYVMTFDCNTAVREATTIWIWNGITIIIPRSNVLVAASGIGKTTLT 120

DB 362 NSGCLTGYAGVYVMIPEDCNVAEATIMQIMNGTIIIPFSNLVLAASSGIGKTLT 421
QY 121 VQTLDTYLAGQMLAGNDTAPREVTIYSGPRDLQESNGSGSVWETCVSSQONQMALYGDG 180
DB 422 VQTLDTYLAGQMLAGNDTAPREVTIYSGPRDLQESNGSGSVWETCVSSQONQMALYGDG 481
QY 181 STPRKQNDQCLTCGRDSVSTVINIVSCAGSSGQWVFTNEGAILNLKGLAMDVAQA 240
DB 482 STPRKQNDQCLTCGRDSVSTVINIVSCAGSSGQWVFTNEGAILNLKGLAMDVAQA 541
QY 241 PMLRRIIIPATGKPNQMLPVP 263
DB 542 PMLRRIIIPATGKPNQMLPVP 564

RESULT 11

AAZ5986
ID AAZ5986 standard; Protein; 264 AA.

AAZ5986;
XX

DT 18-OCT-1999 (first entry)
XX

DB Mistletoe lectin B1 protein fragment.
XX

KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.
XX

OS Viscum album.
XX

PN DE19804210-A1.
XX

PD 12-AUG-1999.
XX

PE 03-FEB-1998; 98DE-1004210.
XX

XX 03-FEB-1998; 98DE-1004210.
XX

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P. Stiefel T. Voelter W. Welters P;
XX

DR WPI; 1999-445335/38.
XX

DR N-PSDB; AA209110.
XX

PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX

XX Claim 9; Fig 8b; 78pp; German.
XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC free from toxins scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B1 protein.
XX

XX Sequence 264 AA;
XX

Query Match 94.3%; Score 1339.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 3.8e-122;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DVTCSASEPTVRIYGRNKGKVDVDDPFDONQIQIMPSKSNQPNQWLTKEDGTIRS 60
DB 1 DVTCSASEPTVRIYGRNKGKVDVDDPFDONQIQIMPSKSNQPNQWLTKEDGTIRS 60
QY 61 NSGCLTGYAGVYVMIPEDCNVAEATIMQIMNGTIIIPFSNLVLAASSGIGKTLT 120
DB 61 NSGCLTGYAGVYVMIPEDCNVAEATIMQIMNGTIIIPFSNLVLAASSGIGKTLT 120
QY 121 VQTLDTYLAGQMLAGNDTAPREVTIYSGPRDLQESNGSGSVWETCVSSQONQMALYGD 179
DB 121 VQTLDTYLAGQMLAGNDTAPREVTIYSGPRDLQESNGSGSVWETCVSSQONQMALYGD 180
QY 180 GSIRPRKQNDQCLTCGRDSVSTVINIVSCAGSSGQWVFTNEGAILNLKGLAMDVAQA 239
DB 181 GSIRPRKQNDQCLTCGRDSVSTVINIVSCAGSSGQWVFTNEGAILNLKGLAMDVAQA 240
QY 240 PMLRRIIIPATGKPNQMLPVP 262
DB 241 PMLRRIIIPATGKPNQMLPVP 263

RESULT 12

AAZ5992
ID AAZ5992 standard; Protein; 265 AA.

AAZ5992;
XX

DT 18-OCT-1999 (first entry)
XX

DB Mistletoe lectin B1 variant protein fragment.
XX

KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.
XX

OS Viscum album.
XX

PN DE19804210-A1.
XX

PD 12-AUG-1999.
XX

PE 03-FEB-1998; 98DE-1004210.
XX

XX 03-FEB-1998; 98DE-1004210.
XX

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P. Stiefel T. Voelter W. Welters P;
XX

DR WPI; 1999-445335/38.
XX

DR N-PSDB; AA209116.
XX

PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX

XX Disclosure; Fig 14b; 78pp; German.
XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of the
CC mistletoe lectin, and its individual chains, in many different isoforms
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B1 protein.
XX

XX Sequence 265 AA;
XX

Query Match 94.3%; Score 1339.5; DB 20; Length 265;
 Best Local Similarity 95.8%; Pred. No. 3.9e-122;
 Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 Sequence 264 AA:

QY 1 DDTVCASAEPTVRIYVGNKMCVYDDPHFGVQIQMPKSNNDPQMLTKKDGTRIS 60
 DB 1 DDTVCASAEPTVRIYVGNKMCVYDDPHFGVQIQMPKSNNDPQMLTKKDGTRIS 60
 QY 61 NSGCLTYGYTAGVYVIMPCNTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 120
 DB 61 NSGCLTYGYTAGVYVIMPCNTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 120
 QY 121 VQTLDTYTLGGQMLAGNDTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 179
 DB 121 VQTLDTYTLGGQMLAGNDTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 180
 QY 180 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNMGALINLKGMLANDVQA 239
 DB 181 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNMGALINLKGMLANDVQA 240
 QY 240 NPKLRRIIYFATGKPNQMLPV 262
 DB 241 NPKLRRIIYFATGKPNQMLPV 263

RESULT 13

AA25988
 ID AAY25988 standard; Protein: 264 AA.
 AC AAY25988;

18-OCT-1999 (first entry)

Mistletoe lectin B3 protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KMWibzyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KMWibzyme-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B3.

Viscum album.

DEL9804210-AL.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelker W, Welters P;

WPI; 1999-44535/38.

N-PSDB; AA209112.

Preparation of mistletoe lectins in heterologous systems,

particularly for use as anticancer agents and immunostimulants

Clain 9; Fig 10B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulant activity. The A-chain (MIA)
 of the mistletoe lectin binds to and inactivates the 26S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms

CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B3 protein.

Sequence 264 AA:

QY 1 DDTVCASAEPTVRIYVGNKMCVYDDPHFGVQIQMPKSNNDPQMLTKKDGTRIS 60
 DB 1 DDTVCASAEPTVRIYVGNKMCVYDDPHFGVQIQMPKSNNDPQMLTKKDGTRIS 60
 QY 61 NSGCLTYGYTAGVYVIMPCNTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 120
 DB 61 NSGCLTYGYTAGVYVIMPCNTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 120
 QY 121 VQTLDTYTLGGQMLAGNDTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 179
 DB 121 VQTLDTYTLGGQMLAGNDTAVREAITWQIMNGTIIIPRSNLVLAASGIGKFTLT 180
 QY 180 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNMGALINLKGMLANDVQA 239
 DB 181 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNMGALINLKGMLANDVQA 240
 QY 240 NPKLRRIIYFATGKPNQMLPV 262
 DB 241 NPKLRRIIYFATGKPNQMLPV 263

RESULT 14

AA25994
 ID AAY25994 standard; Protein: 265 AA.
 AC AAY25994;

18-OCT-1999 (first entry)

Mistletoe lectin B3 variant protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KMWibzyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KMWibzyme-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B3.

Viscum album.

DEL9804210-AL.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelker W, Welters P;

WPI; 1999-44535/38.

N-PSDB; AA209118.

Preparation of mistletoe lectins in heterologous systems,

particularly for use as anticancer agents and immunostimulants

Dislosure; Fig 16B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MIA)
 of the mistletoe lectin binds to and inactivates the 26S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its

CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (e.g., tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe associated with its individual chains, in many different isoforms
 CC and on a large scale. The method also allows the production of products
 CC free from toxins present in natural mistletoe. Recombinant products are
 CC represents a fragment of a variant mistletoe lectin B3 protein.

XX Sequence 265 AA;

Query Match 93.8%; Score 133.5; DB 20; Length 265;

Best Local Similarity 95.4%; Freq. No. 1.5e-121; Indels 1; Gaps 1;

Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

1 DDVTCASSEPTVRIYGRNKKCTVDDPDHQQQLQWESKSNNDPNQMTTTRKDTGRS 60

1 DDVTCASSEPTVRIYGRNKKCTVDDPDHQQQLQWESKSNNDPNQMTTTRKDTGRS 60

61 NSGCLTGYGTAGVYVMIFPCNKVYREATIMQKMGFTIIPRSMVLAASGKGTTLT 120

61 NSGCLTGYGTAGVYVMIFPCNKVYREATIMQKMGFTIIPRSMVLAASGKGTTLT 120

121 VQTLDTYLLQGMALANDTAREEVITVGFEDLCWESNGSVWETCVSSQOMQ-EMALYGD 179

121 VQTLDTYLLQGMALANDTAREEVITVGFEDLCWESNGSVWETCVSSQOMQ-EMALYGD 179

121 VQTLDTYLLQGMALANDTAREEVITVGFEDLCWESNGSVWETCVSSQOMQ-EMALYGD 180

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

RESURF 15

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

241 NPKLRRIIIVPATGKNQMWLPV 263

180 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 239

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

PT Misc-difference 235
 FT /label= D23A
 FT /note= "wild-type Asp is replaced by Ala"
 FT Misc-difference 249
 FT /label= Y249A
 FT /note= "wild-type Tyr is replaced by Ala"

MO9629540-A2.

09-JUN-1998.

02-JAN-1998; 98NC-SP00009.

02-JAN-1997; 97EP-0100012.

(BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.

Bek U, Schmidt A, Zinke H;

WPI; 1998-38812/33.

Nucleic acid encoding fusion protein containing mistletoe lectin A

chain - useful for treatment of proliferative and autoimmune

diseases, allergies and tumors

Claim 14; Page -; 115pp; German.

This sequence represents a mutant form of the mistletoe lectin B-chain,
 rMB. This protein is used in the construction of a fusion protein which
 comprises an effector module that is cytotoxic intracellularly, a
 processing module covalently bonded to the effector module and
 containing a protease recognition sequence, and a targeting module
 containing a signal sequence, which is used to bind specifically to
 the surface of a cell so as to deliver the effector module into the
 cell. Such a fusion protein can be used for treating disorders
 involving proliferation and/or elevated activation of cells, especially
 autoimmune disease, allergy and tumors. The proteins can be
 administered e.g. by injection or topically but especially by intravenous
 injection, at 1 ng to 500 mg/kg/day, or for ex vivo use at 1 pg to 500
 ng/ml. Fusion proteins can develop toxic activity in a wide range of
 target cells. The processing module prevents extracellular dissociation,
 and fusion proteins based on mistletoe lectin A-chain are far more
 active than those based on ricin and do have the associated problems of
 non-specific toxicity. The protein may be expressed in a
 non-toxic host cell, e.g. in the yeast *Saccharomyces cerevisiae*, in
 which has a long half-life in the blood stream. The mistletoe lectin
 B-chain is used. It actively assists in translocation of the MB A-chain
 from the endoplasmic reticulum to the cytoplasm.
 NOTE: This sequence does not appear in the specification but has been
 constructed from the wild-type rMB represented in AM64667.

Sequence 267 AA;

Query Match 93.8%; Score 133.2; DB 19; Length 267;

Best Local Similarity 95.4%; Freq. No. 2.1e-121; Indels 0; Gaps 0;

Matches 252; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

1 DDVTCASSEPTVRIYGRNKKCTVDDPDHQQQLQWESKSNNDPNQMTTTRKDTGRS 60

1 DDVTCASSEPTVRIYGRNKKCTVDDPDHQQQLQWESKSNNDPNQMTTTRKDTGRS 60

61 NSGCLTGYGTAGVYVMIFPCNKVYREATIMQKMGFTIIPRSMVLAASGKGTTLT 120

61 NSGCLTGYGTAGVYVMIFPCNKVYREATIMQKMGFTIIPRSMVLAASGKGTTLT 120

121 VQTLDTYLLQGMALANDTAREEVITVGFEDLCWESNGSVWETCVSSQOMQ-EMALYGD 180

121 VQTLDTYLLQGMALANDTAREEVITVGFEDLCWESNGSVWETCVSSQOMQ-EMALYGD 180

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

181 GSIRKQNDQCTCGDSVSTVINIVSCASSGSGQRVFTREGATILNKNGIANDVAAQN 240

240 NPKLRRIIIVPATGKNQMWLPV 262

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Page 10

Qy 241 FKLRRIIYPATGKPNQWMLPVP 263
Db 241 FKLRRIIYPATGKPNQWMLPVP 263
Search completed: December 11, 2003, 16:57:49
Job time : 45 secs

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 2

OY 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETVCSQONQNALYXDG 180
Db 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETVCSQONQNALYXDG 180
OY 181 SRRPKNODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 240
Db 181 SRRPKNODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 240
OY 241 PKLRRIIYIPATGKPNQMWLPV 263
Db 241 PKLRRIIYIPATGKPNQMWLPV 263

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US2003045208A1
GENERAL INFORMATION:
APPLICANT: BCK, Jurgens
APPLICANT: Schmidt, Arno
APPLICANT: Zehn, Hubert
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER FILING DATE: 1999-07-02
PCT/EP98/00009
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 99.98; Score 1406; DB 9; Length 267;
Best Local Similarity 98.98; Pred. No. 36-134;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 DDTCSASPTVYRIVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRS 60
Db 1 DDTCSASPTVYRIVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRS 60
OY 61 NSCLTYTGYTGYVMTFDQNTAVRATIMQWNGTIIINPSRLVLAASGINKGTLT 120
Db 61 NSCLTYTGYTGYVMTFDQNTAVRATIMQWNGTIIINPSRLVLAASGINKGTLT 120
OY 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETVCSQONQNALYXDG 180
Db 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETVCSQONQNALYXDG 180
OY 181 SRRPKNODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 240
Db 181 SRRPKNODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 240
OY 241 PKLRRIIYIPATGKPNQMWLPV 263
Db 241 PKLRRIIYIPATGKPNQMWLPV 263

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wamnenmacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 576
TYPE: PRT
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match 64.3%; Score 913; DB 12; Length 576;
Best Local Similarity 63.6%; Pred. No. 9-1e-98;
Matches 164; Conservative 32; Mismatches 62; Indels 0; Gaps 0;
OY 5 CSASEPTVYRIVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRSNGSC 64
Db 318 CHDEPTVYRIVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRSNGSC 377
OY 65 LTTGYTGYVMTFDQNTAVRATIMQWNGTIIINPSRLVLAASGINKGTLTVOYL 124
Db 378 LTTGYTGYVMTFDQNTAVRATIMQWNGTIIINPSRLVLAASGINKGTLTVOYL 437
OY 125 DDTCSASPTVYRIVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRS 184
Db 438 IYAVSGQLPTNNQPTFTVIGYGLCLQNSGQWIEDCSSEKKEQNALYADSIIR 497
OY 185 KQNDODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 244
Db 498 QQNDODCLTCGRDSVSVINIVSCSAGSQGRWFTVEGAILINIKKGLANDVAQAN 557
OY 245 RIIYIPATGKPNQMWLPV 262
Db 558 QIIIPATGKPNQMWLPV 575

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Publication No. US2003092109A1
GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.
APPLICANT: Wenger, Robert P.
APPLICANT: Kirschner, David
FILE REFERENCE: US-07/24 action, Characterization, Cloning and Use of a Mushroom
CURRENT APPLICATION NUMBER: US/10/137,077
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/354,322
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Ricinus communis
US-10-137-077-17

Query Match 13.9%; Score 198; DB 15; Length 44;
Best Local Similarity 79.5%; Pred. No. 7.9e-13;
Matches 35; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 12 VAVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRS 55
Db 1 VAVRNGKCVYDDDFDNGIOLMPSKSNNDPQMLTKDITRS 44

RESULT 5
US-C-0-074-527-5
Sequence 5, Application US/10074527

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us-09-601-667c-6.rapp

Page 3

1 Publication No. US200201442661
 2 GENERAL INFORMATION:
 3 APPLICANT: Peter J.
 4 APPLICANT: Meyer, Rachel E.
 5 APPLICANT: Sullivan, Katherine A.
 6 APPLICANT: Millington, David
 7 TITLE OF INVENTION: Uses thereof glycosyltransferase and
 8 FILE REFERENCE: MP1001-0182(RC11M)
 9 CURRENT APPLICATION NUMBER: US/10/074,527
 10 PRIOR FILING DATE: 2002-02-12
 11 PRIOR APPLICATION NUMBER: 60/2659202
 12 INVENTOR: SEQ ID NOS: 9
 13 SOFTWARE: PARASO FOR Windows Version 4.0
 14 SEQ ID NO: 5
 15 LENGTH: 145
 16 TYPE: PRT
 17 ORGANISM: Artificial Sequence
 18 FEATURE:
 19 OTHER INFORMATION: consensus
 20 US-10-074-527-5

Query Match 13.0%; Score 184; BD 14; Length 145;
 Best Local Similarity 23.4%; Pred. No. 1e-10;
 Matches 50; Conservative 21; Mismatches 53; Indels 40; Gaps 7;

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QY      11 TTRVAGNNGCTVDRDDPDDPAGDQOCTIMESKSNNDENQVLTII-KKIDETIR--NNSC 64
DB      7  TILVAGNSRCLDAPNSSESDNSQVLMCHNSGKNGKAKMSLTVDESDETIRSVNNKIC 66
QY      65 LRTFGYAAVYVIMPECHTATSEATVYQVLMKNGSTIIPRNLVLAASQIKGTTLVQTL 124
DB      67 LTVANNSPSEKVLKYCCSATSPDNQKVELNDNLGICN-KILLNVNITEL-----VL 116
QY      125 DVTLAGQMTLAGNDLTAREEVLTIVGFDDLCMEKNSGSAVVEVCYSQKQNCN 174
DB      117 D-----VKESLDT-----QNGKTLILVTC-SGGRNQOQ 142
  
```

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RESULT 6
US-10-156-761-14970
: Sequence 14970, Application US/10156761
: Publication No. US20030119018X1
: GENE INFORMATION:
: APPLICANT: OHSU, SHOSHI
: APPLICANT: KIKU, SHOSHI
: APPLICANT: ISHIKAWA, JIRO
: APPLICANT: HORIKAWA, HIROSHI
: APPLICANT: SHIBA, TADAYOSHI
: APPLICANT: SAKAKI, YOSHIYUKI
: APPLICANT: HATTORI, MASAHISA
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-262
: CURRENT APPLICATION NUMBER: US/10/156,761
: PENDING FILING DATE: 2002-05-29
: PENDING FILING NUMBER: JP 2001-2604089
: PRIOR FILING DATE: 2001-08-30
: PRIOR APPLICATION NUMBER: 05-30-2001-272697
: PRIOR FILING DATE: 2001-08-30
: NUMBER OF SEQ ID NOS: 15109
: SEQ ID NO 14970
: LENGTH: 420
: TYPE: PRT
: ORGANISM: Streptomyces avermitilis
: US-10-156-761-14970

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Query Match 11.9% Score 169 / DB 15 Length 420.
Best Local Similarity 31.9%, Pred.No.1-4=08
Matches 45; Conservative 19; Mismatches 67; Indels 10; Gaps 5;
1 DD--VYCSAAPTIVLGVARNKCCVDYRDDHGNQGLDLPKSKSNDPNOIAIMIKRGTT 58

Db 284 DAKTTCGSSGSGAFITGLAKKCVAGSSSANKAPVQLY - DCGNTTAPQXTVANSQGL 344
QY 59 RNSNCQ - ITYGTATGYVYVAFEDCNTRAREATTQIMQENITIIINRAN - LVTLAASSGI 114
Db 342 RALMKDLDTBHTGATGAGGAGSANKQK - WVTITADQTVNSQNKCLDVTYSINRA 399
QY 115 KGTTLTPTQIIDLVTAGGSGHNG 135
Db 400 NGRRLQIMSGSAAANDQKXKNG 420

RESULT 7
 US-10-156-761-9724
 Sequence 9724, Application US/10156761
 Publication No. US20030119018A1
 INFORMATION:
 APPLICANT: OREN, YANOSH
 APPLICANT: KED, YANOSH
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TAKUYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYMERCELOTIDES
 FILS REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 9724
 LENGTH: 658
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-9724

Query Match	10.4%	Score 147.5	DB 15	Length 658
Best Local Similarity	32.2%	Pred. No. 3.9e-06		
Matches	37	Conservative 18	Mismatches 55	Indels 9
				Gaps 5
QY	17	RKACGCVDEADDPRHAGNQLGALSSANDPNQMLT--IKEDSTIRASGCTTTY--GYTAG	73	
DB	559	QGRGCRDILNNTITITDIAELM--DCKGSGSPSTITSREKELYLKGKCLADINVLGTING	596	
QY	74	VYVIMPCPKTAVETALITMQKNGSTINRSNVLAA--SSGKXTLTWQVLDLTLGG	121	
DB	597	TEVYVIMDCGQANQK--WNINSDPTITVNGAGLDAYNATATNCTSLVLSGCTSDNQK	654	
QY	132	W 132		
DB	655	W 655		

RESULT 8
 US-09-770-621-8
 ? Sequence 8, Application US/09770621
 ? Patent No. US20010024815.51
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: M nyl , Arja
 ? APPLICANT: Velmaander , Tari
 ? APPLICANT: Paserett m, Richard
 ? APPLICANT: Lantto, Raija
 ? APPLICANT: Paloheimo, Maria
 ? APPLICANT: Suominen, Pirkko
 ? APPLICANT: Lantinen, Tarija
 ?
 ? NUMBER OF INVENTIONS: Production and Secretion of Proteins of
 ? SEQUENCE: 39
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: STRAND, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ? STREET: 1100 New York Ave., N.W. Suite 600
 ? CITY: Washington

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Page 4

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/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/770.621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590.563
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332.412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282.001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-311-2600
/ TELEFAX: 202-311-2650
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No. US20010024815A1 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: M64551
/ US-09-770-621-8

Query Match
Best Local Similarity 10.3%; Score 146.5; DB 9; Length 491;
Best Local Similarity 27.2%; Pred No. 3.4e-06;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;

QY 7 ASEP-----TVRIYGNMGCVDRDDPFHGNQIQIAMPKSNNDPNQIATIKD 55
DB 354 SSEPXXXXXXXXXADQGIKGVG-SKICIDVPASTSDGTOLQIMDCISGT--NQWALATRA 410
QY 56 GTIRNSG-SCLTYGTAYVMTFPCNTAVREATIQTQWNGTIIINRSNLTVAASSGI 114
DB 411 GELRYGDKCLDAAGTSGSKQIITSGWGSGNCR--WELNSDSSVVGVSGLCLDA---- 464
QY 115 KGTILVQTIDTYTLGGWLAGNDPAFREVTIYGFADLCWESNGGSVWVETGVSQQNQW 174
DB 465 -----VGNQTA-----NQTLLQIAYTC SINSQNH 488

RESULT 9
US-10-156-761-10246
/ Sequence 10246, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HAYTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
```

```
/ CURRENT APPLICATION NUMBER: US/10/156.761
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 10246
/ LENGTH: 647
/ ORIGIN: Streptomyces avermitilis
/ US-10-156-761-10246

Query Match
Best Local Similarity 10.3%; Score 146.5; DB 15; Length 647;
Best Local Similarity 26.5%; Pred No. 4.9e-06;
Matches 45; Conservative 21; Mismatches 59; Indels 45; Gaps 7;

QY 9 EPTVAIYGRNGCVDRDDPFHGNQIQIAMPKSNNDPNQIATIKDGTIRANSGL--T 66
DB 520 DQGSFVGLAGKCLDAVASSANGTAVGLV--DGNSTAGKMTVRAADSVOLKICLDVT 577
QY 67 TGTGTAYVMTFPCNTAVREATIQTQWNGTIIINRSNLTVAASSGIKTTLVQTIDY 126
DB 578 SASTNDKTKIQLYDCL-----GTAAQKMSYN-----ASTGDVNTNADKCLDV 620
QY 127 TLGGWLAGNDPAFREVTIYGFADLCWESNGGSVWVETGVSQQNQW 176
DB 621 T-----GNSSA-----NQAQAQWISCTGA-AHQKWL 646

RESULT 10
US-10-156-761-8170
/ Sequence 8170, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: ISHIDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HAYTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156.761
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 8170
/ LENGTH: 536
/ TYPE: PRT
/ ORIGIN: Streptomyces avermitilis
/ US-10-156-761-8170

Query Match
Best Local Similarity 9.7%; Score 138; DB 15; Length 536;
Best Local Similarity 30.1%; Pred No. 2.7e-05;
Matches 40; Conservative 19; Mismatches 59; Indels 16; Gaps 6;

QY 14 IIV-ENKWCYVDKDDPFHGNQIQIAMPKSNNDPNQIATIKDGTIRNSG--SCLTY-- 68
DB 409 LVVASSNRCLDAVNTQVAGTKEITWC--GQANQAVTIAAGELRLVGTQCIDAYDN 465
QY 69 GTYTAAYVMTFPCNTAVREATIQTQWNGTIIINRSNLTVAASSGIKTTLVQTIDY 122
DB 466 GTTSGKRVQIYTCGAGNCR--WSLNPVGVTVGSGCLDVTGGDQSSANVGTALSLW 523
QY 123 TLDTTLGGWLAG 135
DB 524 TNGGANGQWRLG 536
```

RESULT 11
US-09-673-457-5
Sequence 5, Application US/09973457
Patent No. US20020164746A1
GENERAL INFORMATION:
APPLICANT: Kadellier-Libermann, Rosana
TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 10448-099001
CURRENT APPLICATION NUMBER: US/09/973,457
PRIORITY FILING DATE: 2001-10-09
PRIORITY FILING DATE: 60/238,849
PRIORITY FILING DATE: 60/238,849
NUMBER OF SEQ IDS: 5
SOFTWARE: PatsSeq for Windows Version 4.0
SEQ ID NO: 5
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
Best Local Similarity 9.6%; Score 136.5; DB 10; Length 135;
Matches 43; Conservative 18; Mismatches 59; Indels 21; Gaps 8;
QY 14 IYGNMCTDY--RDDPHGNGCGLAFKSKNDPNQJLT---KDDTFRNSG--CLTT 67
DB 7 IGVNMLCLDYNGNSKSKNPNVQJMDCHGG--NQMLKLTNBSGDAIRNSDLCLTY 64
QY 68 YGYTAGYVWIFPCNTAVR--EATIWQINGGTIIPRSNLTAAASGIKGTTLVQCTLD 125
DB 65 NG-----TVLYSCDGTDKNDKQKVEVNDGTIRNPK--NSKKGVDSG-----LCIDVMD 113
QY 126 YTLGGQMLAGNDTAPREVTY 146
DB 114 GAKYQJLMTGSGDPRNCKWIF 134

RESULT 12
US-10-074-527-6
Sequence 6, Application US/10074527
Publication No. US2002014246A1
GENERAL INFORMATION:
APPLICANT: Olandt, Peter J
APPLICANT: Meyer, Rachel E
APPLICANT: Olandt, Katherine A
APPLICANT: Miller, Patricia A
TITLE OF INVENTION: 33945, A HUMAN GLYCOSYLTRANSFERASE AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: WPI2001-0481RCP1 (N)
CURRENT APPLICATION NUMBER: US/10/074,527
PRIORITY FILING DATE: 2002-02-12
PRIORITY FILING DATE: 60/269202
PRIORITY FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatsSeq for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
Best Local Similarity 9.6%; Score 136.5; DB 14; Length 135;
Matches 43; Conservative 18; Mismatches 59; Indels 21; Gaps 8;
QY 14 IYGNMCTDY--RDDPHGNGCGLAFKSKNDPNQJLT---KDDTFRNSG--CLTT 67

DB 7 IGVNMLCLDYNGNSKSKNPNVQJMDCHGG--NQMLKLTNBSGDAIRNSDLCLTY 64
QY 68 YGYTAGYVWIFPCNTAVR--EATIWQINGGTIIPRSNLTAAASGIKGTTLVQCTLD 125
DB 65 NG-----TVLYSCDGTDKNDKQKVEVNDGTIRNPK--NSKKGVDSG-----LCIDVMD 113
QY 126 YTLGGQMLAGNDTAPREVTY 146
DB 114 GAKYQJLMTGSGDPRNCKWIF 134

RESULT 13
US-09-770-621-5
Sequence 5, Application US/0970621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vennanper, Jari
APPLICANT: Pagarar m, Richard
APPLICANT: Bantoy, Rajya
APPLICANT: Soodamo, Rajya
APPLICANT: Soodamo, Rajya
APPLICANT: Lahinen, Rajya
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: David A. Swartz
REFERENCE/DOCKET NUMBER: 086
TELEPHONE: 202-371-5600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
ORGANISM: NO. US20010024815A1 Relevant
MOLECULE TYPE: linear polypeptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AN50
US-09-770-621-5

Query Match
Best Local Similarity 9.5%; Score 135; DB 9; Length 480;
Matches 33.0%; Pred. No. 4.8e-05;

Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

QY 12 VRIYGRNMCVVDVDDPHDQNIQLWPKSNNDPQOLMTIKRDTIRSNKS-CLTITYGV 70
DB 370 IRGVASN-RCIDVPGNNTADGTQVLYDCHSGS--NQMWTYSGGEFRIRFNKCLDAGS 426
QY 71 TAGVYVMPCNTAVREATIWMGTGNTIINRSNVLAASSGIXKTLTYQ 122
DB 427 SNGAVQIYSCWGAGNCK-WELRADGTLIVGSGCLDAVGGTGNGTRIQ 476

RESULT 14

US-09-770-621-4
Sequence 4, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Veinamper, Jari
APPLICANT: Pajeterst m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4

Query Match 9.5%; Score 135; DB 9; Length 492;
Best Local Similarity 33.0%; Pred. No. 4, 9e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

DB 370 IRGVASN-RCIDVPGNNTADGTQVLYDCHSGS--NQMWTYSGGEFRIRFNKCLDAGS 426
QY 71 TAGVYVMPCNTAVREATIWMGTGNTIINRSNVLAASSGIXKTLTYQ 122
DB 427 SNGAVQIYSCWGAGNCK-WELRADGTLIVGSGCLDAVGGTGNGTRIQ 476

RESULT 15

US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Veinamper, Jari
APPLICANT: Pajeterst m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDNESS: NO. US20010024815A1 Relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AK50
US-09-770-621-7

Query Match 9.5%; Score 135; DB 9; Length 492;
Best Local Similarity 33.0%; Pred. No. 4, 9e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 7

Db 370 IRGVASH-RCIDVPNGNTADDTOLYDCHSS--NOOWTYSSEPRIFENKCLDAQSS 426
QY 71 TAGVYMIFFDNTAVREKTIWQIMWNTIINPSNVLAASSIGTTLIVQ 122
Db 427 SNAVVGITSCWGANOK-WELRADSTIVGVQSGCLDAVGGSTGKGTRO 476

Search completed: December 11, 2003, 14:48:48
Job time : 17.9484 secs

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rat

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.10564 Seconds
(without alignments)
1222.073 Million cell updates/sec

Title: US-09-601-667C-6

Perfect score: 1420

Sequence: 1 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Trusad Patents.AA.*

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2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
4: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
5: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
6: /cgn2_6/prodata/1/aa/5B.COMB.pep:*

Result No. Score Match Length DB ID Description

1 1406 99.0 263 3 US-08-776-059-43 Sequence 43, Appl

2 1406 99.0 264 3 US-08-776-059-33 Sequence 33, Appl
3 1406 99.0 564 1 US-08-776-059-35 Sequence 35, Appl
4 797 86.1 340 1 US-08-378-761A-77 Sequence 77, Appl
5 184 159.1 340 1 US-08-485-286-77 Sequence 77, Appl
6 152 10.7 133 3 US-08-132-102-14 Sequence 14, Appl
7 152 10.7 435 3 US-09-159-106-11 Sequence 15, Appl
8 152 10.7 435 3 US-08-468-812-8 Sequence 8, Appl
9 146.5 10.3 491 2 US-08-590-563-8 Sequence 8, Appl
10 146.5 10.3 491 4 US-08-770-621-8 Sequence 8, Appl
11 146.5 10.3 491 4 US-08-392-828C-39 Sequence 39, Appl
12 146 10.3 127 3 US-09-330-945-39 Sequence 39, Appl
13 146 10.3 127 3 US-08-468-812-5 Sequence 5, Appl
14 135 9.5 480 2 US-08-468-812-5 Sequence 5, Appl
15 135 9.5 480 2 US-08-590-563-5 Sequence 5, Appl
16 135 9.5 480 2 US-09-770-621-7 Sequence 7, Appl
17 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
18 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
19 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
20 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
21 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
22 135 9.5 480 2 US-08-468-812-4 Sequence 4, Appl
23 124.5 8.8 507 4 US-09-130-337A-25 Sequence 25, Appl
24 105 7.4 114 4 US-09-674-608A-1 Sequence 1, Appl
25 105 7.4 160 4 US-09-674-608A-2 Sequence 2, Appl
26 98.5 6.9 420 2 US-08-282-197C-63 Sequence 63, Appl
27 98.5 6.9 420 2 US-08-282-197C-66 Sequence 66, Appl

SUMMARY

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

28 91 6.4 329 4 US-09-604-957-2 Sequence 2, Appl
29 90 6.3 509 3 US-09-198-955A-6 Sequence 6, Appl
30 90 6.3 509 4 US-09-694-931-6 Sequence 6, Appl
31 89.5 6.3 419 2 US-08-282-197C-64 Sequence 64, Appl
32 89.5 6.3 419 2 US-08-282-197C-67 Sequence 67, Appl
33 88 6.2 1446 4 US-09-252-924A-22312 Sequence 22312, A
34 87.5 6.2 1912 3 US-08-685-467-4 Sequence 4, Appl
35 87.5 6.2 2353 3 US-09-377-355-33 Sequence 33, Appl
36 87.5 6.2 2353 3 US-08-913-942-4 Sequence 4, Appl
37 87.5 6.2 2353 3 US-09-669-974-33 Sequence 33, Appl
38 87.5 6.2 2353 3 US-09-268-347-36 Sequence 36, Appl
39 87.5 6.2 2411 4 US-08-468-812-6 Sequence 6, Appl
40 87 6.1 434 2 US-08-590-563-6 Sequence 6, Appl
41 87 6.1 434 4 US-09-770-621-6 Sequence 6, Appl
42 86.5 6.1 632 4 US-09-252-924A-23096 Sequence 23096, A
43 86.5 6.1 2354 4 US-09-268-347-47 Sequence 47, Appl
44 86 6.1 406 2 US-08-282-197C-52 Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-776-059-43
Sequence 43, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: DEPTEN, Hans
APPLICANT: DEPTEN, Hans
APPLICANT: DEPTEN, Hans
APPLICANT: DEPTEN, Hans
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776_059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SEQUENCE: GenBank Ver. 2.0
SEQ ID NO 1
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-43
Query Match 99.0%; Score 1406; DB 3; Length 263;
Best Local Similarity 98.9%; Fred. No. 6.4e-139;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
2 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
3 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
4 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
5 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
6 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
7 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
8 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
9 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
10 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
11 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
12 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
13 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
14 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
15 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
16 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
17 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
18 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
19 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
20 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
21 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
22 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
23 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
24 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
25 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
26 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263
27 DDTGCSASFPTRIYVGNM.....RRIIVPATKQNMFLVP 263

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RESULT 2
US-08-776-059-33
Sequence 33, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LEWTEZEN, Hans
INVENTOR: LEWTEZEN, Hans
APPLICANT: BALT, Jansen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match
99.0%; Score 1406; DB 3; Length 264;
Best Local Similarity 98.9%; Pred. No. 6,4e-139;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDTTCASSEPTFAIVGNKNCVDRDDFDGNOIOLMFPSKSNDDNQWLTIKRDGTTIS 60
DB 2 DDTTCASSEPTFAIVGNKNCVDRDDFDGNOIOLMFPSKSNDDNQWLTIKRDGTTIS 61
QY 61 NSGCLTYGTAGVYWMIFDQNTAVREATIMQWNGIINPRSNVLAASSGIGKTTIT 120
DB 62 NSGCLTYGTAGVYWMIFDQNTAVREATIMQWNGIINPRSNVLAASSGIGKTTIT 121
QY 121 VQTLIDYTLGQMLAGNTAPREVITVGFRLCMESNGSWWVETCVSSQONRMALYDGG 180
DB 122 VQTLIDYTLGQMLAGNTAPREVITVGFRLCMESNGSWWVETCVSSQONRMALYDGG 181
QY 181 SIREKQNDQCLTCGRDSVTVINIVSCAGSSGQWFTNEGALINRQGLANDVAQAN 240
DB 182 SIREKQNDQCLTCGRDSVTVINIVSCAGSSGQWFTNEGALINRQGLANDVAQAN 241
QY 241 PKLRRIITYPATCKNQWMLPVP 263
DB 242 PKLRRIITYPATCKNQWMLPVP 264

RESULT 3
US-08-776-059-35
Sequence 35, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LEWTEZEN, Hans
INVENTOR: LEWTEZEN, Hans
APPLICANT: BALT, Jansen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match
99.0%; Score 1406; DB 3; Length 264;
Best Local Similarity 98.9%; Pred. No. 6,4e-139;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDTTCASSEPTFAIVGNKNCVDRDDFDGNOIOLMFPSKSNDDNQWLTIKRDGTTIS 60
DB 2 DDTTCASSEPTFAIVGNKNCVDRDDFDGNOIOLMFPSKSNDDNQWLTIKRDGTTIS 61
QY 61 NSGCLTYGTAGVYWMIFDQNTAVREATIMQWNGIINPRSNVLAASSGIGKTTIT 120
DB 62 NSGCLTYGTAGVYWMIFDQNTAVREATIMQWNGIINPRSNVLAASSGIGKTTIT 121
QY 121 VQTLIDYTLGQMLAGNTAPREVITVGFRLCMESNGSWWVETCVSSQONRMALYDGG 180
DB 122 VQTLIDYTLGQMLAGNTAPREVITVGFRLCMESNGSWWVETCVSSQONRMALYDGG 181
QY 181 SIREKQNDQCLTCGRDSVTVINIVSCAGSSGQWFTNEGALINRQGLANDVAQAN 240
DB 182 SIREKQNDQCLTCGRDSVTVINIVSCAGSSGQWFTNEGALINRQGLANDVAQAN 241
QY 241 PKLRRIITYPATCKNQWMLPVP 263
DB 242 PKLRRIITYPATCKNQWMLPVP 264

RESULT 4
US-08-776-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: TREWEN, TERENCE A
INVENTOR: TREWEN, TERENCE A
APPLICANT: HEY, TIMOTHY D
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
NUMBER OF INVENTIONS: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
INFORMATION FOR SEQ ID NO: 77:
TELEPHONE: (317) 337-4846
REFERENCE/DOCKET NUMBER: 38272B
REGISTRATION NUMBER: 33651
ANTAGONIST/INVENTOR ACTION:
NAME: BORUCKI, ANDREA T
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein

US-08-378-761A-77

Query Match
56.1%; Score 797; DB 1; Length 540;
Best Local Similarity 56.6%; Pred. No. 8.5e-75;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;
```

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QY 5 CSASEPTVIVGRNGCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 64
DB 282 CMDEPTIVIVGRNGCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 341
QY 65 LITVGYAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 124
DB 342 LITKSSRQGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 401
QY 125 DYLGGQMLAGNDTAPREVTIYGFRLDCKNSGSGVWETCVSQQQKQFALYQDGSIRP 184
DB 402 IVAVSGMLPTNNQCPFTVITVGLYKQCLQNSGKWLKEDCTSEKAEQOMALYADGSIRP 461
QY 185 KQNDQCLTCGRDSVSTVIVIVSCASSGSGRWFTNEGAILNKNGLMNDVQAQNPRLR 244
DB 462 QQNRDNCITTDANIKQIVYKLSGCPASSGQKRWMPNDGTITLNLVGLVLDVRSDPSLK 521
QY 245 RIIIVPATGRNQMLFV 262
DB 522 QIIIVPRGNMQIMLPL 539

RESULT 5

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/378761
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TIPE: amino acid single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match 56.1%; Score 797; DB 1; Length 540;
Best Local Similarity 56.6%; Pred. No. 8.5e-75;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;

QY 5 CSASEPTVIVGRNGCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 64
DB 282 CMDEPTIVIVGRNGCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 341
QY 65 LITVGYAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 124
DB 342 LITKSSRQGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 401
QY 125 DYLGGQMLAGNDTAPREVTIYGFRLDCKNSGSGVWETCVSQQQKQFALYQDGSIRP 184
DB 402 IVAVSGMLPTNNQCPFTVITVGLYKQCLQNSGKWLKEDCTSEKAEQOMALYADGSIRP 461
QY 185 KQNDQCLTCGRDSVSTVIVIVSCASSGSGRWFTNEGAILNKNGLMNDVQAQNPRLR 244
DB 462 QQNRDNCITTDANIKQIVYKLSGCPASSGQKRWMPNDGTITLNLVGLVLDVRSDPSLK 521
QY 245 RIIIVPATGRNQMLFV 262
DB 522 QIIIVPRGNMQIMLPL 539

RESULT 6

US-09-512-342-14
Sequence 14, Application US/09512342
Patent No. 6388068
GENERAL INFORMATION:
APPLICANT: MASUDA, SHINGO
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/512,342
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 09/378761
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TIPE: amino acid single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-512-342-14

Query Match 13.7%; Score 195; DB 4; Length 293;
Best Local Similarity 28.3%; Pred. No. 3e-12;
Matches 63; Conservative 29; Mismatches 93; Indels 38; Gaps 9;

QY 14 IYGNMNCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 59
DB 41 IYGNMNCVDRDDPHDNOIQIMPSKSNNDPNQIMTKRDTIRNSGSC 341
QY 60 SNNSCUTT--YGTAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 116
DB 90 SNNSCUTT--YGTAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 116
QY 117 TITVGTAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 124
DB 146 TITVGTAGVYVIMPCNTAVREACTIWOJWNGSTIINPSKLVLAASGKGTITVQTL 124
QY 175 ALYDGSIRPQNDQCLTCGRDSVSTVIVIVSCASSGSGRWFTNEGAILNKNGLMNDVQAQNPRLR 217
DB 204 ALYDGSIRPQNDQCLTCGRDSVSTVIVIVSCASSGSGRWFTNEGAILNKNGLMNDVQAQNPRLR 217

Query Match 56.1%; Score 797; DB 1; Length 540;
Best Local Similarity 56.6%; Pred. No. 8.5e-75;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;

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FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DE97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

Query Match 10.7%; Score 152; DB 3; Length 132;
Best Local Similarity 36.3%; Pred. No. 2.9e-08;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 5;

OY 18 NMCVDVADDDPHGNDIGLWPKSKNDPVLATIKSGTIRNSGCTTY--GYAGY 75
DB 14 NMCVDVPMADPTDGNPVQVITGSGN--AAQTTRSGDGVRLAKKLDVRSSTIRGA 71
OY 76 VMFPCNTAVREATIQIY---GNGTIPRSLVLAASSGI--KSTLTVOGTLDTYL 128
DB 72 VQVWTCN-----GTGAQKVAIDGSKALRNPQSLCLDTGAPLRDQGRLOTWTCNGTT 126
OY 129 GCGW 132
DB 127 AQOW 130

RESULT 6
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Petter, Pau
; APPLICANT: Dietz, Ivan
; APPLICANT: Hakkar, Tobias
; APPLICANT: Hegerard, Lisbeth
; TITLE OF INVENTION: Aminoacyl-tRNA synthetase with -1,3-glucanase
; TITLE OF INVENTION: ActiV417
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DE97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match 10.7%; Score 152; DB 3; Length 435;
Best Local Similarity 36.3%; Pred. No. 1.7e-07;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 5;
OY 18 NMCVDVADDDPHGNDIGLWPKSKNDPVLATIKSGTIRNSGCTTY--GYAGY 75
DB 317 NMCVDVPMADPTDGNPVQVITGSGN--AAQTTRSGDGVRLAKKLDVRSSTIRGA 374
OY 76 VMFPCNTAVREATIQIY---GNGTIPRSLVLAASSGI--KSTLTVOGTLDTYL 128
DB 375 VQVWTCN-----GTGAQKVAIDGSKALRNPQSLCLDTGAPLRDQGRLOTWTCNGTT 429

US-08-468-812-8
; Sequence 8, Application US/08468812
; Patent No. 625236
; GENERAL INFORMATION:
; APPLICANT: Weinmayer, Jari
; APPLICANT: Mataly, Arja
; APPLICANT: Fagerström, Richard
; APPLICANT: Lantto, Ralf
; APPLICANT: Paloheimo, Maria
; APPLICANT: Suominen, Pirkko
; APPLICANT: Laitinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura xylinase Sequences and Methods
; NUMBER OF SEQ ID NOS: 25
; CORRESPONDENCE ADDRESS
; ADDRESSER: STEVEN KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

RESULT 9
US-08-468-812-8
; Sequence 8, Application US/08468812
; Patent No. 625236
; GENERAL INFORMATION:
; APPLICANT: Weinmayer, Jari
; APPLICANT: Mataly, Arja
; APPLICANT: Fagerström, Richard
; APPLICANT: Lantto, Ralf
; APPLICANT: Paloheimo, Maria
; APPLICANT: Suominen, Pirkko
; APPLICANT: Laitinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura xylinase Sequences and Methods
; NUMBER OF SEQ ID NOS: 25
; CORRESPONDENCE ADDRESS
; ADDRESSER: STEVEN KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT RELEASE: Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/468.812
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332.412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282.001
; FILING DATE: 29-05-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugisaky, Larry B.
; REGISTRATION NUMBER: 35,086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2640
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acids
; STRANDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match 10.3%; Score 146.5; DB 2; Length 491;
Best Local Similarity 27.28%; Pred. No. 7.3e-07;
Matches 43; Conservative 5; Mismatches 54; Indels 57; Gaps 8;
OY 7 ASFP-----TVRYGKNCVDEDDPHGNDIGLWPKSKNDPVLATIKSGTIRNSGCTTY--GYAGY 55
DB 354 SEEPKXXXXXADGQKIKYG--SRCLDVPDASTSGTGLQKMGCHSGT--NQGMATDA 410
OY 56 GTIRNSG--SCLTYGYAGVYVMFPCNTAVREATIQIYINPRSLVLAASSGI 114

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Db 411 GELIVYEDKCLDAAGTSNGSKVQVYSCWQGNOK--KRLNSDGSVVGVSQCLDA----- 464
Qy 115 KETITVOTDITLQCGMLAGNDIAPREVTITIGFRDLCESNGSVAWEITCVSSQGNRM 174
Db 465 -----VGNCH-----NGLIQLYTC-SNGSNRM 488

RESULT 10
US-08-590-563-8
Sequence 8, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vermaapier, Jari
APPLICANT: Pesonen, Richard
APPLICANT: Lehto, Raimo
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugelsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
NOTICE TYPE: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

Query Match 10.3%; Score 146.5; DB 4; Length 491;
Best Local Similarity 27.2%; Pred. No. 7.5e-07;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;
Qy 7 ASEP-----TVRIIVGNQGVVDRDDDFHGGQLOLMKSGSKNDNDPLATIKRD 55

Db 354 SEEPXXXXXXAGGGQKVG--SGRCLDVPDASTDQLOLMDCHSGT--NQMAATDA 410
Qy 56 GTIRSG-SCLTIVGYTAGVYVIFDCTAVRATIMQIWKSGTIIINRSNVLPAASGI 114
Db 411 GELIVYEDKCLDAAGTSNGSKVQVYSCWQGNOK--KRLNSDGSVVGVSQCLDA----- 464
Qy 115 KETITVOTDITLQCGMLAGNDIAPREVTITIGFRDLCESNGSVAWEITCVSSQGNRM 174
Db 465 -----VGNCH-----NGLIQLYTC-SNGSNRM 488

RESULT 11
US-09-770-621-8
Sequence 8, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vermaapier, Jari
APPLICANT: Pesonen, Richard
APPLICANT: Lehto, Raimo
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/550,563
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugelsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6506593 Relevant
NOTICE TYPE: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M65551
US-09-770-621-8

Query Match 10.3%; Score 146.5; DB 4; Length 491;
Qy 10 ASEP-----TVRIIVGNQGVVDRDDDFHGGQLOLMKSGSKNDNDPLATIKRD 55

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Page 6

Best Local Similarity 27.2%; Pred. No. 7.5e-07;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;

OY 7 ASBP-----TWIVRNKNCVVDVDDPHGNOIQIOWPSKSNDDPQWLTIKD 55
DB 354 SSBPFXXXXXXADGGQIKGV-SGRCLDVPDASTSDTOLMDCHSGT--NQOMATDA 410
OY 56 GTRRNG-SCLTIVGTAGVYVWIPDCVREXETIWMGNTINPSNVLAASSGI 114
DB 411 GELRYVGPCKLDAAGTSMGSKVOIYSCWGDNRK--NRINSDSVYGVQGLCLDA--- 464
OY 115 KGTLYVQTLIDYTLGGQWLMAGNDTAPREVIYGRFLCMESNGSVWETCVSSQONRW 174
DB 465 -----VNGT-----NGLTIDLYTC-SNGSNQW 488

RESULT 12

US-08-392-828C-39
Sequence 39, Application US/08392828C
Patent No. 5795962

GENERAL INFORMATION:

APPLICANT: IWANAGA, SADAKI
APPLICANT: MUTO, TATSUSHI
APPLICANT: SEKI, NORIHI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: ADMINISTRATOR, TESTA, HIRWITZ &
ADDRESSER: THIBRAULT LLP
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/392,828C
FILING DATE: 28-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: FUN-033
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS: 39:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Peptide
LOCATION: 1..127
OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

US-08-392-828C-39

Query Match

Best Local Similarity 28.0%; Pred. No. 1.2e-07;
Matches 46; Conservative 19; Mismatches 53; Indels 46; Gaps 7;

OY 12 VIVRNKNCVVDVDDPHGNOIQIOWPSKSNDDPQWLTIKDGTIRNG-SCLTIVGT 70
DB 6 IKGV-SGRCLDVPDASTSDTOLMDCHSGT--NQOMATDAGELRYVGDCKLDAAGT 62

OY 71 TAGVYVWIPDCVREXETIWMGNTINPSNVLAASSGIKGTLYVQTLIDYTLGG 130
DB 63 SNGSKVOIYSCWGDNRK--NRINSDSVYGVQGLCLDA----- 100
OY 131 GMLAGNDTAPREVIYGRFLCMESNGSVWETCVSSQONRW 174
DB 101 -----VNGT-----NGLTIDLYTC-SNGSNQW 124

RESULT 13

US-09-330-945-39
Sequence 39, Application US/09330945
Patent No. 6077946

GENERAL INFORMATION:

APPLICANT: IWANAGA, SADAKI
APPLICANT: MUTO, TATSUSHI
APPLICANT: SEKI, NORIHI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: ADMINISTRATOR, TESTA, HIRWITZ &
ADDRESSER: THIBRAULT LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/330,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Peptide
LOCATION: 1..127
OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

US-09-330-945-39

Query Match

Best Local Similarity 28.0%; Pred. No. 1.2e-07;
Matches 46; Conservative 19; Mismatches 53; Indels 46; Gaps 7;

OY 12 VIVRNKNCVVDVDDPHGNOIQIOWPSKSNDDPQWLTIKDGTIRNG-SCLTIVGT 70
DB 6 IKGV-SGRCLDVPDASTSDTOLMDCHSGT--NQOMATDAGELRYVGDCKLDAAGT 62
OY 71 TAGVYVWIPDCVREXETIWMGNTINPSNVLAASSGIKGTLYVQTLIDYTLGG 130
DB 63 SNGSKVOIYSCWGDNRK--NRINSDSVYGVQGLCLDA----- 100

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rat

Page 7

QY 131 GMLAGNDTAPREVTIYGFRLDLMESNGSVMWETCVSSQONRW 174
DB 101 --VENGTJA-----NOTGIDLTTC-SNGSNQW 124

RESULT 14
US-08-468-812-5
Sequence 5, Application US/06468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nyl, Aija
APPLICANT: Pajestri m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirko
APPLICANT: Lantinen, Taina
APPLICANT: Kietto, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: OF Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-468-812-5

Query Match 9.5%; Score 135; DB 2; Length 480;
Best Local Similarity 31.0%; Pred No. 1,2e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

QY 12 VRIYGNMVCVDDDFHGNQIOLMPSKSNDDPQMLTIIRDTIRNSG-CLTITGY 70
DB 370 IGVASV-RCIDVPGNADGQVLYDCHSGS--NQMWTYSGGEFRIFGNKCDAGGS 426
QY 71 TAGVYMTFCNTAVREATTQIWNGTIIPRSNVLVAASGIKCTTLTVO 122

DB 427 SNGAVQIYSCWGANOK--WELRADTIVYQSLCLAVAGGTGNGTRLQ 476

RESULT 15
US-08-590-563-5
Sequence 5, Application US/06590563
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nyl, Aija
APPLICANT: Pajestri m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirko
APPLICANT: Lantinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-590-563-5

Query Match 9.5%; Score 135; DB 4; Length 480;
Best Local Similarity 33.0%; Pred No. 1,2e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

QY 12 VRIYGNMVCVDDDFHGNQIOLMPSKSNDDPQMLTIIRDTIRNSG-CLTITGY 70
DB 370 IGVASV-RCIDVPGNADGQVLYDCHSGS--NQMWTYSGGEFRIFGNKCDAGGS 426
QY 71 TAGVYMTFCNTAVREATTQIWNGTIIPRSNVLVAASGIKCTTLTVO 122

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us-09-601-667c-6.ra1

Db 427 SNGAVQIYSCMGANOK-WELRADGTIVGSGICIDVGGGTGTRIQ 476
Search completed: December 11, 2003, 14:11:32
Job time : 9.10564 secs

A/Accession: JMW0090

A:Molecule type: protein
A:Residues: 1-265 <R08>
C:Superfamily: Ricin; RNA N-glycosidase homology
C:Keywords: glycoprotein
F:61.96.135/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 99.3%; Score 1407.5; DB 2; Length 265;
Best Local Similarity 99.6%; Pred. No. 7.3e-111;
Matches 264; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DDTGSASEPTRVHGRNRYRDPDHFQNGQIQMSEKSNDDPQVNTTREGGTR 60
DB 1 DDTGSASEPTRVHGRNRYRDPDHFQNGQIQMSEKSNDDPQVNTTREGGTR 60
QY 61 NSGCLTYGTVAGYVNI FDCNTAVREATTIQQIDWKGITINPRSNVLAASGIGKTTTL 120
DB 61 NSGCLTYGTVAGYVNI FDCNTAVREATTIQQIDWKGITINPRSNVLAASGIGKTTTL 120
QY 121 VQTDVYTLQGMALGNDTAPREVITYGFDQLQMSNGSGVWETGDSQKQKVALYGD 180
DB 121 VQTDVYTLQGMALGNDTAPREVITYGFDQLQMSNGSGVWETGDSQKQKVALYGD 180
QY 181 GSIRKXNDQCLSGRDSVSTINIVSGSGSGQRYETEGATINIKVGLAMPNQA 240
DB 181 GSIRKXNDQCLSGRDSVSTINIVSGSGSGQRYETEGATINIKVGLAMPNQA 240
QY 241 NPCLRRIITYPATKPNQMLPVE 264
DB 241 NPCLRRIITYPATKPNQMLPVE 265

RESULT 3

RICIN D precursor - caenor bean
M:Accession: X52908; NID:921084; PIDN:CAA6939.1; PID:921083
C:Species: Ricinus communis (Castor bean)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C:Accession: A24041; S20513; A26614; A03372; A20100; A03376; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.S.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; PMID:86067214; PMID:2393712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <R08>
A:Cross-references: EMBL:X52908; NID:921084; PIDN:CAA6939.1; PID:921083
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Reference number: A24041; PMID:85179479; PMID:3689723
A:Accession: A24041
A:Molecule type: mRNA
A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LMM>
A:Cross-references: GB:X02388; NID:921077; PIDN:CAA6230.1; PID:921078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of ile of
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 1-109, 'S', 111-269, 'D', 272-283, 'U', 285-288, 290-302 <X08>
A:Note: This paper cites the others in the series providing experimental details for the
R:Aoki, T.; Puntieri, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tyrosine

A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', 386-576 <R08>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein
A:Residues: 213-335, 'R', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'N', 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

Query Match 64.0%; Score 907.5; DB 1; Length 576;
Best Local Similarity 63.8%; Pred. No. 2e-60;
Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 5 CAAEPTVAVGRNRYRDPDHFQNGQIQMSEKSNDDPQVNTTREGGTR 64
DB 318 CAAEPTVAVGRNRYRDPDHFQNGQIQMSEKSNDDPQVNTTREGGTR 64
QY 65 LITTYGYAGYVNI FDCNTAVREATTIQQIDWKGITINPRSNVLAASGIGKTTTL 124
DB 378 LITTYGYAGYVNI FDCNTAVREATTIQQIDWKGITINPRSNVLAASGIGKTTTL 124
QY 125 DYTGGGMLGNDTAPREVITYGFDQLQMSNGSGVWETGDSQKQKVALYGD 180
DB 438 DYTGGGMLGNDTAPREVITYGFDQLQMSNGSGVWETGDSQKQKVALYGD 180
QY 185 PGRNNDICITSDNIRETVKILSCGASGSGQRYETEGATINIKVGLAMPNQA 244
DB 497 PGRNNDICITSDNIRETVKILSCGASGSGQRYETEGATINIKVGLAMPNQA 244
QY 245 NPCLRRIITYPATKPNQMLPVE 264
DB 557 NPCLRRIITYPATKPNQMLPVE 265

RESULT 4

506330
 Ricin E - castor bean (fragment)
 N/Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
 C/Species: Ricinus communis (castor bean)
 C/Accession: J05381
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 Plant Mol. Biol. 9, 287-295, 1997
 A/Title: Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus communis ag
 A/Reference number: 506330
 A/Accession: 506330
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-263 <LMD>
 A/Cross-references: EMBL:M17631; NID:g169714; PDB:AAA3506.1; PDB:g169715
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 A/Title: The complete amino acid sequence of the B-chain of ricin E isolated from small-
 A/Reference number: J05381
 A/Accession: J05381
 A/Status: not compared with conceptual translation
 A/Molecule type: protein
 A/Residues: 1-69, PS, 72-209, 'A', 211-241, 243-250, 'V', 252-263 <NR>
 A/Experimental source: seed
 C/Superfamily: ricin; rRNA N-glycosidase homology
 C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
 F/1-753/Product: ricin B #status experimental <ECH>
 F/17-59, 60-100, 103-141, 148-183, 187-225, 229-263/Region: 40-residue repeats
 F/20-39, 63-80, 151-164, 190-207/Distillate bonds: #status predicted
 F/95, 105/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 61.8%; Score 877; DB 2; Length 263;
 Best Local Similarity 61.7%; Pred. No. 2, 7e-66;
 Matches 161; Conservative 37; Mismatches 61; Indels 2; Gaps 2;
 QY 5 CSASEPTVAIVGNKRVAVDDPDHNDQIOLMPKSNNDPQNLTKRQGTIRNSGC 64
 DB 4 CMDEPPIVAVGNKLCVDRGRFHNGAQLMPCSKNTDNDLWTLKRNITISNGKC 63
 QY 65 LTTGTGAGVYVPCNTAVKATINQWNGTINPNSVLAASSGIGKTLTVQTL 124
 DB 64 LTTGTGAGVYVPCNTAVKATINQWNGTINPNSVLAASSGIGKTLTVQTL 123
 QY 125 DYTGGGMLAGNDTPAEPREVTYGRDLCEMNSGSGVWFCDSQGNQKRAIYDQSTR 184
 DB 124 IYAVSQMLPTNNTQPFVTVGLYKGLCKNSKVMLENC-TEBAEQMALYDQSTR 182
 QY 185 PRONQDCLTSGRDSVSTVNTVSCGASGSGRWVTEBGAITLNLKGLAMPVQANP-K 243
 DB 183 PQQRNDCLTNDANKITVAVKILSCGPSVSGQNNKNDITLNLVNGVLDVRSPPS 242
 QY 244 LKRLITTPATKRNQNMPLPF 264
 DB 243 LKRLITTPATKRNQNMPLPF 263
 RESULT 5
 RICSAG
 agglutinin precursor - castor bean
 N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C/Species: Ricinus communis (castor bean)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 J Biol. Chem. 266, 15682-15686, 1995
 A/Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
 A/Reference number: A24261; PMID:86059449; PMID:2593130
 A/Accession: A24261
 A/Molecule type: mRNA
 A/Residues: 1-564 <ROB>
 A/Cross-references: GB:M12089; NID:g169700; PDB:AAA3869.1; PDB:g169701
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin

A/Reference number: A24210
 A/Accession: A24210
 A/Molecule type: protein
 A/Residues: 303-325, 'P', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V'
 C/Comment: This protein has strong agglutinating activity and weak cytotoxicity com
 C/Superfamily: ricin; rRNA N-glycosidase homology
 C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding;
 F/1-325/Product: agglutinin chain B #status predicted <SIC>
 F/325-280/Product: rRNA N-glycosidase homology #status predicted <ACH>
 F/330-564/Product: agglutinin chain B #status experimental <BOH>
 F/319-361, 363-402, 405-443, 450-489, 492-509, 531-564/Region: 40-residue repeats
 F/104, 147, 231, 232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/34, 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/262, 306, 322-341, 365-382, 453-466, 492-509/Distillate bonds: #status predicted
 F/354, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
 F/357, 437/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/356, 557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 Query Match 55.3%; Score 793.5; DB 1; Length 564;
 Best Local Similarity 55.2%; Pred. No. 96-98;
 Matches 146; Conservative 41; Mismatches 72; Indels 1; Gaps 1;
 QY 5 CSASEPTVAIVGNKRVAVDDPDHNDQIOLMPKSNNDPQNLTKRQGTIRNSGC 64
 DB 306 CMDEPPIVAVGNKLCVDRGRFHNGAQLMPCSKNTDNDLWTLKRNITISNGKC 365
 QY 65 LTTGTGAGVYVPCNTAVKATINQWNGTINPNSVLAASSGIGKTLTVQTL 124
 DB 366 LTTGSKSRQVAVINQSTAVTAVKATINQWNGTINPNSVLAASSGIGKTLTVQTL 425
 QY 125 DYTGGGMLAGNDTPAEPREVTYGRDLCEMNSGSGVWFCDSQGNQKRAIYDQSTR 184
 DB 426 IYAVSQMLPTNNTQPFVTVGLYKGLCKNSKVMLENC-TEBAEQMALYDQSTR 484
 QY 185 PRONQDCLTSGRDSVSTVNTVSCGASGSGRWVTEBGAITLNLKGLAMPVQANP-K 244
 DB 485 PQQRNDCLTNDANKITVAVKILSCGPSVSGQNNKNDITLNLVNGVLDVRSPPS 544
 QY 245 LKRLITTPATKRNQNMPLPF 264
 DB 545 LKRLITTPATKRNQNMPLPF 564
 RESULT 6
 TILSA
 abrin-a precursor - Indian licorice (fragment)
 N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C/Species: Abrus precatorius (Indian licorice)
 C/Date: 31-Dec-1993 #sequence_revision 31-Aug-1997 #text_change 16-Jul-1999
 C/Accession: S32429; U0202; A39761; J01389; S14473; S24133; S74110; S74111
 Kihung, B.H.; Lee, M.C.; Lee, T.C.; Lim, D.T.
 J Biol. Chem. 266, 263-267, 1993
 A/Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protei
 A/Reference number: S32429
 A/Accession: S32429
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-E, 2-558 <HUN>
 A/Cross-references: GB:989344; NID:g166294; PDB:AAA2624.1; PDB:g166295
 A/Note: the coding region for the sequence shown is preceded by an AUG codon
 A/Note: residues 1-8 were derived from the synthesized primer
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 J Biol. Chem. 266, 1095-1097, 1998
 A/Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protei
 A/Reference number: U0202
 A/Accession: U0202
 A/Molecule type: protein
 A/Residues: 1-501, 203-251 <PUN>
 A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid, therefore, 'u'
 Riadin, B.P.; Murray, B.E.; Halling, A.C.; Halling, K.C.; Tilkke, N.; Long, G.L.;
 J Biol. Chem. 266, 6848-6852, 1991

A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; MID:91201323; PMID:2016300
 A:Accession: A39761
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 87,2-251 <SVR>
 A:Cross-references: GB:X54672
 A:Notes: Residues 9 and 10 were derived from the synthesized primer
 R:Kimura M.; Sumizawa T.; Funatsu G.
 Biocell. Biotechnol. Biochem. 57: 166-169, 1993
 A:Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic
 A:Reference number: UC1398; MID:93169023; PMID:7763422
 A:Contents: seeds
 A:Accession: UC1398
 A:Molecule type: protein
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>
 A:Experimental source: seed
 A:Experimental source: seed
 A:Description: Direct molecular cloning of two distinct abrin A-chains.
 A:Reference number: S14472
 A:Accession: S14472
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 'ME', 2-251 <EV2>
 A:Cross-references: EMBL:X54873; MID:916090; PID:CAA38655.1; PID:916091
 R:Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.
 J. Biol. Lett. 309, 115-118, 1992
 A:Title: The complete primary structure of abrin-a B chain.
 A:Reference number: S24133; MID:9257156; PMID:11505674
 A:Accession: S24133
 A:Molecule type: protein
 A:Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CH>
 Eur. J. Biochem. 240, 564-569, 1996
 A:Title: Probing the domain structure of abrin-a by tryptic digestion.
 A:Reference number: S74110; MID:97008945; PMID:8856055
 A:Accession: S74110
 A:Molecule type: protein
 A:Residues: 69-108,154-172 <LIN>
 A:Experimental source: seed
 A:Accession: S74110
 A:Molecule type: protein
 A:Residues: 262-276, 'X', 278-280, 329-348,369-388,399-418 <LIN>
 A:Experimental source: seed
 C:Comment: Abtin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits
 C:Superfamily: ricin; RNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lactin; pyroglyutamic acid
 F:1-251/Product: abrin-a chain A #status experimental <ACH>
 F:1-251/Product: abrin-a chain A #status experimental <ACH>
 F:1-251/Product: abrin-a chain B #status experimental <ACH>
 F:283-328/Product: abrin-a chain B #status experimental <ACH>
 F:1/Modified sites: 969,901,914,459,453,492,493-528/Region: 40-residue repeats
 F:74,113,195,196/Binding site: carbohydrate (Y); Gly, Asn #status experimental
 F:164,167/Active site: Gly, Arg #status predicted
 F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 F:288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:361,401/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 55.1%; Score 781; DB 1; Length 528;
 Seed Local 45; Similarity 55.6%; Pred. No. 7,5e-58;
 Matches 145; Conservative 44; Mismatches 70; Indels 2; Gaps 2;
 QY 5 CSAS-EPTVAVGNKNGVYDDPDDPDHQQOGLPMSKNDPNOILTKRGDTIRNSGS 63
 DB 269 CSRRPEPTVRIQSGDKMCDVYDNGHNRNLTIMWCKDLBEOQLTKSKDITIRNSKG 328
 QY 64 CLTGYGTAGYVWIFDQTNAREALTIQMDNGTITPSPNLYVLAASGKGTLLVQV 123
 DB 329 CLTGYGTAGYVWIFDQTNAREALTIQMDNGTITPSPNLYVLAASGKGTLLVQV 388

QY 124 LDYTLQGMALNDPAREVITVFDICMESNGSVWETFCDSQKQGNALVIGQST 193
 DB 389 NEVIMQGMRTGNNTSPFTSISGSDLDNQAGSNVMAQDSDNKDQ QVALITDGS 447
 QY 184 RFXNODCLTSGRDSVTVINIVSCSAGSGQWVFTMEGALINIKKGLMDVQAQNRK 243
 DB 448 HGVNNTNCLTSSKDKKGSITLLMGCSGMAQSQWVYKQSDISLYDDWMDVYKSDS 507
 QY 244 LRRIITVPANGNQMVLVFP 264
 DB 508 LKQILMTYFNGNQLWILFP 528

RESULT 7
 S32430
 abrin-b precursor - Indian licorice (fragment)
 N:Contains: RNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abus precatorius (Indian licorice)
 C:Date: 30-Sep-1993 #sequence revision 01-Aug-1997 #text-change 20-Aug-1999
 C:Accession: S32430; UC1399
 R:Hung, S.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Biol. Lett. 229, 163-167, 1993
 A:Title: The complete amino acid sequence of the B-chains of abrin-a and abrin-b, toxic
 A:Reference number: S32429; MID:93137388; PMID:8421313
 A:Accession: S32430
 A:Molecule type: RNA
 A:Residues: 1-527 <RNR>
 A:Cross-references: GB:M98345; MID:9166296; PID:AAA2625.1; PID:9166297
 R:Kimura, M.; Sumizawa, T.; Funatsu, G.
 Biocell. Biotechnol. Biochem. 57, 166-169, 1993
 A:Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b,
 A:Reference number: UC1398; MID:93169023; PMID:7763422
 A:Accession: UC1399
 A:Molecule type: protein
 A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'Q', 352-377, 'N', 379-425, 'N', 427, 'D', 42
 A:Experimental source: seed
 A:Experimental source: seed
 C:Comment: ricin; RNA N-glycosidase homology
 C:Superfamily: ricin; RNA N-glycosidase homology
 C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lect
 F:1-250/Product: abrin-b chain A #status predicted <ACH>
 F:7-245/Product: abrin-b chain B #status predicted <ACH>
 F:1-245/Product: abrin-b chain B #status experimental <ACH>
 F:240-527/Product: abrin-b chain B #status experimental <ACH>
 F:240-527/Product: abrin-b chain B #status experimental <ACH>
 F:1/Modified sites: 368-406, 413-448, 452-491, 494-527/Region: 40-residue repeats
 F:71,113,194,195/Binding site: carbohydrate (Y); Gly, Asn #status predicted
 F:164,167/Active site: Gly, Arg #status predicted
 F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 F:288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:361,401/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.4%; Score 771; DB 2; Length 527;
 Seed Local 45; Similarity 55.2%; Pred. No. 5,2e-57;
 Matches 144; Conservative 43; Mismatches 72; Indels 2; Gaps 2;
 QY 5 CSAS-EPTVAVGNKNGVYDDPDDPDHQQOGLPMSKNDPNOILTKRGDTIRNSGS 63
 DB 268 CSRRPEPTVRIQSGDKMCDVYDNGHNRNLTIMWCKDLBEOQLTKSKDITIRNSKR 327
 QY 64 CLTGYGTAGYVWIFDQTNAREALTIQMDNGTITPSPNLYVLAASGKGTLLVQV 123
 DB 328 CLTGYGTAGYVWIFDQTNAREALTIQMDNGTITPSPNLYVLAASGKGTLLVQV 387
 QY 124 LDYTLQGMALNDPAREVITVFDICMESNGSVWETFCDSQKQGNALVIGQST 193
 DB 388 NEVIMQGMRTGNNTSPFTSISGSDLDNQAGSNVMAQDSDNKDQ QVALITDGS 446
 QY 184 RFXNODCLTSGRDSVTVINIVSCSAGSGQWVFTMEGALINIKKGLMDVQAQNRK 243
 DB 447 HGVNNTNCLTSSKDKKGSITLLMGCSGMAQSQWVYKQSDISLYDDWMDVYKSDS 506
 QY 244 LRRIITVPANGNQMVLVFP 264
 DB 507 LKQILMTYFNGNQLWILFP 527

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RESULT 8
S16022
Abirin-c precursor - Indian licorice (fragment)
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C.Accession: S16022
R.Wood, K.A.; Lord, J.M.; Nawrzymca, E.J.; Platak, M.
Eur. J. Biochem. 198, 723-732, 1991
A.Title: Preproabrin: genomic cloning, characterization and the expression of the A-chain
A.Reference number: S16022; PMID:9166957; PMID:2050149
A.Accession: S16022
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-562 <MO>
C.Comment: The A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
C.Superfamily: ricin; RNA N-glycosidase homology
C.Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
P.13-285/Product: abirin-c chain A #status predicted <RCH>
P.141-280/Domain: RNA N-glycosidase homology <RNG>
P.125-562/Product: abirin-c chain B #status predicted <RCH>
F.131-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F.135/Modified site: pyroglutamate carboxylic acid (Glu) (in mature form) #status predicted
F.136,141,1229,1230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F.139,142,1231,1232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F.123,287,395,435,416/Binding site: Arg #status predicted (Asn) (covalent) #status predicted
F.1281-303,320-339,363-380,451-464,490-507/Disulfide bond: #status predicted
F.122,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 54.1%; Score 767; DB 2; Length 562;
Matches 143; Conservative 44; Mismatches 72; Indels 2; Gaps 2;

QY 5 CSAS-BPTVATVGRNKNRVYDDDFHDGNGQQLMPKSNNDPNQMLTKEDGTRNSGS 63
DB 303 GSRNRETVRIGSRDCKCVYDGDJHNNKRIANKCKRLKRNQMLTKSDGTRNSK 362
QY 64 CLTGYTAGVYVWIPDCNRYRRTIYQIINDGTTINPSNLYLAASGIGKTLTYQT 123
DB 363 CLTTEGYPGVYVWIDCTSAVETIYEMNGIINPKRALYLAASSSGITLVQT 422
QY 124 LDYTLQGMALNDTAPREVTIYGPRLDCKNSGSGVWETCDSSQKQKALYGDGSI 183
DB 423 NEYLMRGKMTGNNTSPFVTSIGSYDLCQAGSNVWALADCNKKED-QVALYTGSI 481
QY 184 PRKQNDCTGSRGUSVTVINIVSCSAGSGSRVETNEGALINKKGLADVAQNRK 243
DB 482 RSYQNTNCLTSDHKQSPFLVLMKSGNRAQRKLFKNDSTISLIDRVYDVASDPS 541
QY 244 LRRTIYPATGKPNQMLVY 264
DB 542 LKRIILHPYKPNQIWLTF 562

RESULT 9
S32431
Abirin-d precursor - Indian licorice (fragment)
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C.Accession: S32431
R.Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 283-287, 1993
A.Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. C
A.Reference number: S32429; PMID:9332798; PMID:8421313
A.Accession: S32431
A.Molecule type: mRNA
A.Residues: 1-528 <HUN>

A.Cross-references: GB:M98346
R.Hung, C.; Lee, M.; Lee, T.; Lin, J.
Submitted to the EMBL Data Library, March 1993
A.Reference number: S34408
A.Accession: S34408
A.Molecule type: mRNA
A.Residues: 1-169, C, 171-320, 17, 322-528 <HUN>
C.Comment: The A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
C.Superfamily: ricin; RNA N-glycosidase homology
C.Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin
P.1-251/Product: abirin-d chain A #status predicted <RCH>
P.7-246/Domain: RNA N-glycosidase homology <RNG>
F.261-528/Product: abirin-d chain B #status predicted <RCH>
F.123-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F.174,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F.164,167/Active site: Glu, Arg #status predicted (Asn) (covalent) #status predicted
F.123,229,382,403,492/Binding site: pyroglutamate carboxylic acid (Glu) #status predicted
F.128,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 54.0%; Score 766; DB 2; Length 528;
Matches 143; Conservative 45; Mismatches 71; Indels 2; Gaps 2;

QY 5 CSAS-BPTVATVGRNKNRVYDDDFHDGNGQQLMPKSNNDPNQMLTKEDGTRNSGS 63
DB 269 GSRNRETVRIGSRDCKCVYDGDJHNNKRIANKCKRLKRNQMLTKSDGTRNSK 328
QY 64 CLTGYTAGVYVWIPDCNRYRRTIYQIINDGTTINPSNLYLAASGIGKTLTYQT 123
DB 329 CLTTEGYPGVYVWIDCTSAVETIYEMNGIINPKRALYLAASSSGITLVQT 388
QY 124 LDYTLQGMALNDTAPREVTIYGPRLDCKNSGSGVWETCDSSQKQKALYGDGSI 183
DB 389 NEYLMRGKMTGNNTSPFVTSIGSYDLCQAGSNVWALADCNKKED-QVALYTGSI 447
QY 184 PRKQNDCTGSRGUSVTVINIVSCSAGSGSRVETNEGALINKKGLADVAQNRK 243
DB 448 RSYQNTNCLTSDHKQSPFLVLMKSGNRAQRKLFKNDSTISLIDRVYDVASDPS 507
QY 244 LRRTIYPATGKPNQMLVY 264
DB 508 LKRIILHPYKPNQIWLTF 528

RESULT 10
S62627
Agglutinin I precursor - European elder
C.Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C.Accession: S62627
R.von Damm, R.J.M.; Barre, A.; Ponce, P.; van Leeuwen, F.; Peumans, W.J.
Eur. J. Biochem. 235, 128-137, 1996
A.Title: The NeuAc(alpha-2,6)-Gal/NAc-binding lectin from elderberry (Sambucus r
A.Reference number: S62619; PMID:9620926; PMID:8631319
A.Accession: S62627
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-570 <VAN>
C.Comment: The A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
C.Superfamily: ricin; RNA N-glycosidase homology <RNG>
P.1-251/Product: abirin-d chain A #status predicted <RCH>
P.7-246/Domain: RNA N-glycosidase homology <RNG>
F.261-528/Product: abirin-d chain B #status predicted <RCH>
F.123-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F.174,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F.164,167/Active site: Glu, Arg #status predicted (Asn) (covalent) #status predicted
F.123,229,382,403,492/Binding site: pyroglutamate carboxylic acid (Glu) #status predicted
F.128,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 36.3%; Score 543; DB 2; Length 570;
Matches 143; Conservative 45.9%; Pred. No. 8-20-38;

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	Matches	119;	Conservative	33;	Mismatches	95;	Indels	12;	Gaps	6;
QY	5	CSASEPVAIVAMNARVDVDDPFDHGNQIQAMPSSKSNDDPNQWMTKDDDTIRSNVGC	64							
Db	316	CSAVETKRIISGWDGLCAVDKRGHGYIDNPQVLAPE--CNECQQLMTFRDDGTIRMLKGC	373							
QY	65	LETVGYAGVWMLPDCNPAVENTITQIMDNTIINPSSNLVLAASSGIGKSTLYVOTL	128							
Db	374	-----TASSWVTDKQNPPEKIKMNVSLIDQITINHSSTVPLPQAGKSGVSENN	424							
QY	125	LVTTGSMALGNMTPAPREVITYGRPLQCESNCS--IVNFCPSGSGQGMALYHDS	102							
Db	429	IFARQGMVTV-DVRELVFPIYGVKKQIRBENENFVWLEDCYLMARQQ--EMLYDQST	486							
QY	103	IFPPQNDQCTSGSDSYVTVINIVCSGASGSGQWFTNEGALINLVKGLMDVQADAP	242							
Db	487	IFVNSNRSICVTSSEHSPDLIVLLKCSG--SGNQWVFVNTGTSINPAKLMDVQADRV	545							
QY	243	KLRRIIIVPATGKPNQMTL	261							
Db	546	SLRKILIVFPPGNPNQMT	564							

RESULT 11
JC7535
chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus
C:Species: Streptomyces thermoviolaceus
C:Name: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7535
R:Yasujibo, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inano,
M.; Kato, T. *Biochem. Biophys. Res. Commun.* 244: 103-107, 1998
A:Title: Family 19 chitinases from Streptomyces thermoviolaceus OGC-520: Molecular cloning,
A:Reference number: JC7535; PMID:21036907; PMID:11193414
A:Accession: JC7535
A:Molecule type: DNA
A:Residues: 1-377 <TSU>
A:Cross-references: DDBJ:AB016842
A:Experimental source: strain OGC-520
C:Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation
by anchoring to the cell wall and binding to the efficient hydrolysis of insoluble chitin.
C:Genetics:
A:Gene: ch35
A:Keywords: glycosidase; hydrolase

Query Match	9.78	Score 137.57	D2 2	Length 377
Best Local Similarity	21.33	Pred. No. 0.0057		
Matches	Conservative 33	Mismatches 111	Indels 89	Gaps 10
Qy	7	ASPPVYVVRKMKVYVVDDEPHQNGIQTPKSKNDPMQATKGGTSSNGSCT	66	
Dh	33	AKAAAGSTIGLGGCLDVAAGDAAGNPQVQIDNGSTN--AQGVYDSGDTIRALGKCLD	90	
Qy	67	TVGYTA--GVYVMEPCQANAEATATQWIDNGITINPESNVLVAAS--SGIKGTLATLQ	122	
Dh	91	VDRSTADAGKQVQIMDDTGGANQR--WYVPAHDIYVAPARCLDYTRSNAGFAFQVIM	148	
Qy	123	TLDTYLQAGMLA-----SNQDAAPREVI-----YGRDLCMSNGSIVW	162	
Dh	149	TCGSGSNKKNAIPATGGSTPAGSPGVSAQOFQMFNPENPFYQGLVQALSPFGGA	208	
Qy	163	ETCDSSQKQD-----GKALYGGG	181	
Dh	209	MTQDDITLQKAAALFASNNHNRGGQVQVZELNPAIPFYCDMGSGYCCAPAAVGGG	266	
Qy	182	SIRPKQKQDCLTSIRASDVSFVLTINYSQSAQS--SQRVWFNKAALINKSL	223	
Dh	269	PILDSMN-----YNYAAAGATSTDLNLPVWENDPNA--WKGTL	308	

RESULT 12
J50589
endo-1,4-beta-xy/lanase (EC 3.2.1.8) A precursor - Streptomyces lividans
N/Alternate names: xy/lanase A

C:Species: Streptococcus lividans
C>Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
CAccession: U50589; F50238
R/Shaker_F.; Roy, C., Yaguchi, M., Morosoli, R., Kluepfel, D.
Gene ID: 75-82, 1997 three genes specifying xylanases in Streptococcus lividans.
A:Reference names: U50589, PMID:2407743, PMID:1143521
A:Accession: U50589
A:Molecule type: DNA
A:Residues: 1-477 <SW>
A:Cross-references: GB:M64551
A:Accession: F50238
A:Protein name: Xyloxylysin protein
A:Residues: 42-93 <SRZ>
C:Genetics:
A:Gene: xlnA
C:Function:
A>Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xyians
A:Pathway: xylan degradation
C:Spectralmax: Streptomyces endo-1,4-beta-xylanase A
F142-477/Product: signal sequence status predicted <SIG>
F142-477/Product: endo-1,4-beta-xylanase A #status experimental <EMT>
F142-477/Product: Streptomyces endo-1,4-beta-xylanase A homology <SVY>
I169_237/Active site: Gln #status predicted

1

Query Match	8.9%	Score 125.5	DB 1	Length 477
Best Local Similarity	29.9%	Pred. No. 0.0078		
Matches	40	Conservative 20	Mismatches 61	Indels 13
			Gaps 6	
Cy	7	ASP-----TWRIYINSGMYRVDYRDDFDHSGNQIOLMSEKNNPNDMLTKEDGFIISN	61	
Dy	346	SSSEFADGQAGKGVG--SRCLDTPHATSDGQOLMCHSGT--NQMDATNGSLAVY	402	
Cy	62	G-SCTTAYRATGYGVYVFMFCQNTAVRATVQIMDNGVILNPSNLVLA--SSSGKSTT	118	
Dy	403	GDCLDLAAGTSGSGKTKQIYSQWCGDNQK--WLNSSDSVVGVOGSLCLAVANGTANSTL	460	
Cy	119	LTVQTLDTLYTIGAG	132	
Dy	461	IQLYTCNSGNSQRA	474	

RESULT 13

T34603
xylanase A - Streptomyces coelicolor (fragment)
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text change 28-Jul-2000
C/Accession: T34603
R/Kirby, L.; Harris, D.; Pirikhill, J.; Barrett, B.C.; Rajadream, M.A.
Submitted to the EMBL Data Library, January 1996
A/Accession: T34603 Z21594
A/Species: preliminary; translated from GR/EMBL/DDJ
A/Molecule type: DNA
A/Residues: 1-383 <NR>
A/Cross-references: EMBL:AL021529; PDB: CMA16466.1; GSPDB: QN0070; SCOEBA:SC10A5_31
A/Experimental source: strain AL(2)
C/Genetics:
A/Gene: xlnA; SCOEBA:SC10A5_36C
C/Subfamilly: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-x-
P/I-1-237/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SV>

Query Match Simlarity 8.6%; Score 122.51; Bw 2; Length 383;
Best Local Simlarity 29.3%; Pred. NO.0.0111
Matches 40; Conservative 19; Mismatches 62; Indels 13; Gaps 6

07 7 ASP-----TATGAGNAGAAVYRDRDADFDNGDQGLMAGSANNDDQWTLTKRGKGTISN 61
DB 255 SSESPADGGQIKING--SGRIADLPASTDSFGTOLMGHCSHG--NOVAALNDASLRLAY 308
07 62 G-SCITTYGAVGVTFPCNTANREAIQQLINDGRTIINPSKVLA---SSGIKETT 118

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DB 309 GPKCLDPAAGTNGSKVQIVSCWGDINOK--WRINSDSVVYVQSGCLDAVANGTANGTL 366
QY 119 LTVQTLDTYTLGGCM 132
DB 367 IOLYTCGSKNSQNR 380

RESULT 14

T35697
arabinoxylanase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
C/Accession: T35697
R/Murphy, L.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, January 1998
A/Reference number: Z21548
A/Accession: T35697
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1475 <NDR>
A/Cross-references: EMBL:AL021411; PDB:1AAL5189.1; GSPDB:GN00070; SCOPEDB:SC7H1.02
A/Experimental source: strain AJ(2)
C/Genetics:
A/Genes: abfB; SCOPEDB:SC7H1.02

Query Match

Best Local Similarity 8.1%; Score 115.5; DB 2; Length 475;
Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

QY 6 SASBPTRIVGRKGRVYDDPHDQIOLPSSKSNDDPQLATKDDTIRNSG-SC 64
DB 37 AAGSALRAGNSNRC-LDVLGSGDDGALLQLDYCKGGT--NQWTSITDGRLLVYGRKC 93
QY 65 LTVYGYTA--GVYVMPICNTAVREATIWOIMDNGTINPSNLVLAASG-IKGTLR 120
DB 94 LDVPEHATPGTRVQIWCSSGANGQ--WRVNSDGVVGVESGLCEAAGAGTANGTAVQ 151
QY 121 VQTLDTYTLGGCMLASNDTAREVT---TGFEDLCMESNGSVVETCD-SSQKNGK 174
DB 152 LWTICGSGNQNGTGLTFPDTGALPSTRMSYGVLAQPSKSWYALADPTTVANGR 211
QY 175 MALYGDGS-----IRKNOQDCTSGRDSVS 201
DB 212 HLYGSTRSGSGYGSWVSPFTNWMELMASAGQANNN 247

RESULT 15

A39094
glucan endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - Oerskovia xanthineolytica
C/Species: Oerskovia xanthineolytica
C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
C/Accession: A39094
S/Bastien, P.; Bastien, L.; Sliaty, S.N.
J Biol Chem 263:10581-10583 (1991)
A/Title: Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Express
A/Reference number: A39094; NID:91093212; PMID:1985933
A/Accession: A39094
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1548 <SHE>
A/Cross-references: GB:M60826; GB:M38734; NID:9150444; PDB:1AA25520.1; PDB:9150445
C/Keywords: glycosidase; hydrolase

Query Match

Best Local Similarity 8.0%; Score 114; DB 2; Length 548;
Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

QY 16 GRNGRY-----DVDDPHDQIOLPSSKSNDDPQLATKDDTIRNSGSC--TT 67
DB 422 GTGALRGSTGLDTPVMDPTDNOVL--ATCGRAAQQTGTGDTVRAIKCLDIVAR 479
QY 68 YGTAGVYVMPICN-TAVREATIWOIMDNGT--INPSNLVLAASGCI--KGTTLV 121

DB 480 SGTAGTAVWYTCNGTNGKQRT---YDSATKLNRPSQKCLDAQGAFLRDGKTVL 535
QY 122 QTLDTYTLGGCM 132
DB 536 WTCNQTBNQR 546

Search completed: December 11, 2003, 13:55:43
Job time : 9.20622 secs

FT VARIANT 231 231 N -> S OR T.
 FT VARIANT 231 233 NGU -> KGP.
 FT VARIANT 232 235 GLAM -> SLAM.
 SQ SEQUENCE 264 AA: 28981 MW: 770032626CFES94 CRC64;
 Query Match 100.0%; Score 1418; DS 1; Length 264;
 Best local 100.0%; From 0.3.6e-14;
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVTCSASEPTWYVIGNKNKRVDDDDPHDNGNQLAPSKSNDDPQQLATIKGGITIS 60
 Db 1 DVTCSASEPTWYVIGNKNKRVDDDDPHDNGNQLAPSKSNDDPQQLATIKGGITIS 60
 QY 61 NSCLTGYGTAGYVYVIFDONTAVKRNATINQWNGTIIINPSSMLVLAASGGIKQTILT 120
 Db 61 NSCLTGYGTAGYVYVIFDONTAVKRNATINQWNGTIIINPSSMLVLAASGGIKQTILT 120
 QY 121 VQTLDYTLQCGMLAGMDTAPRENTTYGFRQLCHESVGSVWETDSSGQNGKALYGD 180
 Db 121 VQTLDYTLQCGMLAGMDTAPRENTTYGFRQLCHESVGSVWETDSSGQNGKALYGD 180
 QY 181 GSIRPKNOPOCLTSGPDSVSTYINIVSCSAGSGQWVEFGHIIINQKGLANDYQA 240
 Db 181 GSIRPKNOPOCLTSGPDSVSTYINIVSCSAGSGQWVEFGHIIINQKGLANDYQA 240
 QY 241 NPETKRITTYPATGKKNQWMLPVF 264
 Db 241 NPETKRITTYPATGKKNQWMLPVF 264
 RESULT 2
 RICI RICCO STANDARD; PRT: 576 AA.
 ID RICI RICCO STANDARD; PRT: 576 AA.
 AC P02879; P02880; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 42, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ricin precursor [contains: Ricin A chain (RNA N-glycosidase)
 (EC 3.2.2.22); Ricin B chain).
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Euphorbiales; Euphorbiaceae; core eudicots; Rosidae;
 OC Euphorbiales; Malpighiales; Euphorbiaceae; Ricinus.
 OC NCBI_TaxID:3988;
 RX MEDLINE-86067214; PubMed-2399712;
 RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
 RA Weaver R.F.;
 RT "Genomic cloning and characterization of a ricin gene from Ricinus
 communis."
 RT "Plant Cell Tissue and Organ Culture Res. 13:8019-8033(1985)."
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92163016; PubMed-1374405;
 RA Tregear J.W., Roberts L.W.;
 RT "The lectin gene family of Ricinus communis: cloning of a functional
 ricin gene and three lectin pseudogenes."
 RT Plant Mol. Biol. 18:515-525(1992).
 RN [3]
 RP SEQUENCE OF 12-576 FROM N.A.
 RX MEDLINE-85179479; PubMed-3389723;
 RA Halling K.C., Roberts L.W., Lord J.M.;
 RT "Molecular cloning and characterization of a ricin gene from Ricinus
 communis."
 RT Eur. J. Biochem. 148:265-270(1985).
 RN [4]
 RP SEQUENCE OF 36-302.
 RA Yoshitake S., Funatsu G., Funatsu M.;
 RT "Isolation and sequences of peptic peptides, and the complete
 sequence of the chain of ricin-D."
 RT Agric. Biol. Chem. 42:1267-1274(1978).
 RN [5]
 RP SEQUENCE OF 315-576.
 RA Funatsu G., Kimura M., Funatsu M.;
 RT "Primary structure of the A chain of ricin D."
 RT Agric. Biol. Chem. 43:2221-2224(1979).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
 RX MEDLINE-9034423; PubMed-1366517;
 RA Kimura Y., Kusonou H., Tada M., Takagi S., Funatsu G.;
 RT "Structural analyses of sugar chains from ricin A-chain variant."
 RT Agric. Biol. Chem. 54:157-162(1990).
 RN [7]
 RP REVIEW.
 RX MEDLINE-21480122; PubMed-1159563;
 RA Olsnes S., Kozlov J.V.;
 RT "Ricin."
 RT Toxicol. 39:1723-1728(2001).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE-87165983; PubMed-3558397;
 RA Montfort W., Villafraña J.E., Morzinger A.F., Ernst S.R., Katzin B.,
 RA Rutenber E., Xiong N.H., Hamlin R., Robertus J.D.;
 RT "The three-dimensional structure of ricin at 2.8 A."
 RT J. Biol. Chem. 262:5358-5403(1987).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE-91352004; PubMed-1681881;
 RA Katzin B.J., Collins E.J., Robertus J.D.;
 RT "Structure of ricin A-chain at 2.5 A."
 RT Proteins 10:251-259(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RX MEDLINE-91352005; PubMed-1681882;
 RA Rutenber E., Robertus J.D.;
 RT "Structure of ricin B-chain at 2.5-A resolution."
 RT Proteins 10:260-269(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE-95082010; PubMed-7990110;
 RA Weston S.A., Tucker A.D., Thatcher D.R., Detryshite D.J.,
 RA Pappitt R.A.;
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."
 RT J. Mol. Biol. 244:410-422(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
 RX MEDLINE-9517222; PubMed-760513;
 RA Doherty D., Smith R., Robertus J.D., Morzinger A.F., Pascal J.M.,
 RA Molina-Sanchez M.C., Robertus J.D.;
 RT "Structure and activity of an active site substitution of ricin A
 chain."
 RT Biochemistry 35:11098-11103(1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE-97240820; PubMed-9068280;
 RA Yan X., Hollis T., Svanth M., Day P., Morzinger A.F., Malne G.W.,
 RA Robertus J.D.;
 RT "Structure-based identification of a ricin inhibitor."
 RT J. Mol. Biol. 266:1049-1049(1997).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE-93165632; PubMed-1287657;
 RA Kin Y., Robertus J.D.;
 RT "Analysis of several key active site residues of ricin A chain by
 mutagenesis and X-ray crystallography."
 RT Protein Eng. 5:775-779(1992).
 CC 1- FUNCTION: Ricin is highly toxic to animal cells and to a less
 extent to plant cells. The A chain is responsible for inhibiting
 protein synthesis through the catalytic inactivation of 60S
 ribosomal subunits. The B chain is responsible for the binding of
 specific adenine residues from an exposed loop of 28S ribosomal
 RNA. As this loop is involved in the binding of elongation
 factors, the modified ribosomes are unable to support protein
 synthesis. The A chain can inactivate a few thousand ribosomes
 per minute, thus inactivating them faster than the cell can make
 new ones. A single A-chain molecule can therefore kill an animal

CC		cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.
CC	-1	GALACTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific aspartate on the alpha chain.
CC	-1	DOMAIN: This chain is composed of two domains; each domain consists of a homologous subdomains (alpha, beta, gamma).
CC	-1	PM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC	-1	SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC	-1	SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	-1	MOTION: REF. 1 AND REF. 5 SUGGESTIONS HAVE A HIGH NUMBER OF CONFLICTS WITH THE MOTION OF THE OTHER CHAINS.
CC	-1	DATABASER: NAME=protein Spotlight!
CC	-1	NORMBASE Issue 31 of February 2003!
CC		WWW= http://www.ebi.ac.uk/spottlight/articles/sp1t031.html .
CC	--	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sdb.ch/aboutance/ or send an email to license@sdb-sib.ch).
CC	EMBL:	X03179; CAA6639.1; -
CC	EMBL:	X53908; CAA37095.1; -
CC	EMBL:	X02388; CAA6230.1; -
CC	PIR:	A12892; CAA01058.1; -
CC	PIR:	A42041; RLCSDD.
CC	PDB:	2MAI; 31-JUN-94.
CC	PDB:	1M9J; 31-JUN-94.
CC	PDB:	1YB8; 31-OCT-93.
CC	PDB:	1YF7; 14-JUN-98.
CC	PDB:	1IEU; 14-JUN-98.
CC	PDB:	1ETC; 31-OCT-93.
CC	PDB:	1OB8; 16-JUN-97.
CC	PDB:	1OBT; 16-JUN-97.
CC	PDB:	1BR5; 02-SEP-98.
CC	PDB:	1BR6; 02-SEP-98.
CC	PDB:	1IIS; 16-JAN-02.
CC	PDB:	1IIA; 16-JAN-02.
CC	CSD:	1G3H; EMBD PDB379.
CC	InterPro:	IPR0007722; Ricin_B_lectin.
CC	InterPro:	IPR001574; RIP.
CC	RefSeq:	PF00652; Ricin_B_lectin. 6.
CC	RefSeq:	PF00181; RIP. 1.
CC	PRINTS:	PR00396; SHIGARICIN.
CC	SMART:	SM00459; RICIN_2.
CC	PROSITE:	PS00775; SHIGA_RICIN_1.
CC	Gene Ontology:	hydrolase, protein synthesis inhibitor, Toxin, Repeat;
CC	KEGG:	c00001; cecili; 35
CC	FT	CHAIN 1 302
CC	FT	PEPTIDE 303 314
CC	FT	CHAIN 315 314
CC	FT	DOMAIN 321 448
CC	FT	DOMAIN 451 575
CC	FT	REPEAT 331 373
CC	FT	REPEAT 374 414
CC	FT	REPEAT 415 449
CC	FT	REPEAT 450 489
CC	FT	REPEAT 490 530
CC	FT	REPEAT 531 570
CC	FT	ACT SITE 212 212
CC	FT	DISULFID 294 318
CC	FT	DISULFID 334 353
CC		INTERCHAIN.

	Query Match	Bit Score	Expect	Score	Pos. 1	Length	576:
B. Local similarity	61.9%						
Matches	166:	Conservative	33:	Mismatches	60:	Indels	1:
QY	5	CSASPEPVATVYGRNGMVRVDQDPEHFGNQVQLMPSEKKNNDPVQMLTKRSDGTRNSASC	64				
Dh	318	CHDPPEPVATVYGRNGICVDVGRFHNSNAQLMPCKENSDANQMLTKRSDGTRNSKNC	377				
QY	65	LTFTYTAQVYVWLPDQNTVVEATITWQIMNGTINPNSLWLAASSGIKQTLLTYDTL	124				
Dh	378	LFTYTSPEVYVWLPDQNTVVEATITWQIMNGTINPNSLWLAASSGIKQTLLTYDTL	437				
QY	125	DYVGLGSLAQNPLDPAENYITVYFQDLCWENSGSVYVWVCCSQQKQGNALVYGGSGIR	184				
Dh	438	IYVSGVQGLPNNITGPVTTITVGLYSLCLQNSQGVWIEDC-SSEKAEQNALVYGGSGIR	496				
QY	185	PKRNDQCCITSGRSVSVTVINVSQSGASGSRNVTMEGALINIKNGALDVQAMFEL	244				
Dh	497	FOQNDMDCLTSGSINIEVTVKLVISGPAISQGRWFKQDQITLINTVGLVYDVAASDPL	556				
QY	245	RRILITVPATGKPKQMLVLP	264				
Dh	557	KQILITVPATGKPKQMLVLP	576				
RESULT 3							
AGGL RICCO							
ID	AGGL RICCO	STANDARD:	PRG:	564 AA.			
AC	P06750:						
DT	01-JAN-1988 (Rel. 06, Created)						
DT	01-JUN-1988 (Rel. 06, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Agglutinin (P29932.222), Agglutinin A chain (IRNA N-						
OS	Ricinus communis (Castor bean)						
OC	Ricinus communis (Castor bean)						
OC	Spermatocytis, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,						
OC	Euphorbiales, Magnoliopsida, eudicotyledons, core eudicots, Rosidae;						
OC	eucotids I; Malpighiales; Euphorbiaceae; Ricinus.						
OX	NCBI_TaxID=3988;						
EN	[1]						
EN	SEQUENCE FROM N.A.						
RK	MEDLINE=8059449; PubMed=2999130;						
RK	Roberts L.N., Lamb F.I., Fappin D. J. C., Lord J. M.;						
RT	ricin", primary sequence of Ricinus communis agglutinin. Comparison with						
RT	ricin".						
RT	J. Biol. Chem. 260:15682-15686(1985).						
RN	[2]						
RN	SEQUENCE OF 303-564.						
RC	TISSUE=Seed.						
RC	Araki, T., Yoshioaka Y., Funatsu G.;						
RT	"The complete amino acid sequence of the B-chain of the Ricinus						
RT	communis agglutinin isolated from large grain castor bean seeds".						
RL	Biochim. Biophys. Acta 871:217-285(1986).						
RL	SEQUENCE OF 303-327.						
RN	MEDLINE=8018723; PubMed=6768555;						
RK	Lin T.T.-S., Li S.G.-L.;						
RT	"Purification and physicochemical properties of ricins and						
RT	agglutinins from Ricinus communis".						

NL	Eur. J. Biochem.	105:433-439(1980).
CC	-1. CATALYTIC ACTIVITY. Endohydrolysis of the N-glycosidic bond at one specific asenine on the 26S rRNA.	
CC	-1 SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.	
CC	-1 SIMILARITY: Contains 2 ricin B-type lectin domains.	
CC	This Swiss-ProT entry is complete; it is produced through a collaboration between the Swiss Institute of Biomedicine and the EMBL institution.	
CC	the European Bioinformatics Institute. There are no restrictions on way CC use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/).	
CC	or send an email to license@sib-sb.ch .	
DR	EMBL, M13089; AAA33869.1; -	
DR	EMBL, X40466; AA822584.1; -	
DR	HSP, A02873; RLCSA8.	
DR	GlycoSignalDB, P0C7P0, -	
DR	InterPro, IPR001574; Ricin_B_lectin.	
DR	InterPro, IPR001574; RIP.	
DR	Pfam, PF00652; Ricin_B_lectin, 6.	
DR	Pfam, PF00161; Rip, 1.	
DR	PRINTS, PR00396; SHIGARICIN.	
DR	SMART, SMO0458; RICIN, 2.	
DR	PROSITE, PS50231; RICIN B LECTIN, 2.	
DR	PROSITE, PS00275; SHIGA_RICIN, 1.	
KM	Ricin defense; Hydroxase; Protein synthesis inhibitor; Toxin; Repeat; Plant protein; Lectin; Signal.	
FT	SIGN.	
FT	CHAIN	
FT	PROPEP	
FT	CHAIN	
FT	DOMAIN	
FT	DOMAIN	
FT	REPEAT	
FT	REPEAT	
FT	REPEAT	
FT	REPEAT	
FT	REPEAT	
FT	REPEAT	
FT	ACT SITE	
FT	DISULFID	
FT	DISULFID	
FT	DISULFID	
FT	DISULFID	
FT	CARBOND	
FT	CARBOND	
FT	CARBOND	
FT	CONFLICT	
FT	CONFLICT	
FT	CONFLICT	
FT	CONFLICT	
FT	CONFLICT	
SO	SEQUENCE	
Query Match	564 AA; 62851 MW; D455F2A72P609759 CHC64;	
Best Local Similarity	55.3%; Score 783.5; DB 1; Length 564;	
Matches 146;	Conservative 41; Mismatches 72; Indels 1; Gaps 1	
OY	CAASPPVAVRVRGRNRVDGDDPDGNGDIOGWKPSNDNMDPTXGGDTISNSGC 64	
Db	306 CMNPFPVIRIVRGKCDVTVEGEFFDNPIGLMPCKSNITWMLRLADSTIRANXC 365	
OY	LTVGYTAGVYVMIFPCNTAFRAATITWINDGIINPNSLVLAASGIKETLTAYQT 124	
Db	366 LVTSKSPROGVYVIAVAQVATQRQIWDNRRIINPSSQLVAATSGISTELTAYTN 425	
OY	125 DYTLQGMLAGNOTFAREVVIYGFBDLCMESNGSVWEVTDSDSRQNGMAVLGDGSIR 164	

Db	146	IVANOVCOMP1NNR20PEFTT1VGLKVCQKQNSAKTVLEQC-TSEKAEQOONALVAA3SIR	494
Oy	195	FRANQDDCTSGRSNYSVYINIVSQCASGSGQRWFTMEALINLNGADVAQANPKU	244
Db	485	FOONDDICLTVDNINAGVYKVLISGSPASQGRWPNKDITLNLNGLVLEVRADPSL	544
Oy	245	RAT1TTPARGKQNGQMLPEF	264
Db	545	KQIVHPHPRNGLNQWLELTF	564
RESULT 4			
ID	ABRA_ABRER	STANDARD	ERT, 528 AA.
CC	P11140; P28589;		
PT	01-JUN-1989 (Rel. 11, Created)		
PT	01-JUN-1994 (Rel. 29, Last sequence update)		
DE	Abbrin-2003 (Ref. 1), last annotation update		
DE	Abbrin-2003 (Ref. 1), last annotation update		
DE	Abbrin-2003 (Ref. 1), last annotation update		
DE	(Ref. 2, 2022). Abbrin-a chain		
OC	Abnra preacortius (Indian iicorice) (Crab's eye).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eucotids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrua;		
EN	NCBI_TaxID=3816;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=93112799; PubMed=842113;		
RP	PMID=842113; PMID=842113; PMID=842113; PMID=842113; PMID=842113;		
RT	"Primary structure of three distinct isoforms determined by cDNA		
RT	sequencing. Conservation and significance."		
RL	J. Mol. Biol. 229:263-267 (1993).		
RL	[2]		
RP	SEQUENCE OF 1-251.		
RC	TISSUE=Seed;		
RC	Funastru G., Teguuchi Y., Kamenosono M., Yanaka M.;		
RA	The complete amino acid sequence of the A-chain of abrin-a, a toxic		
RA	protein from the seed of Funastru G. (1993).		
RA	Appl. Biochem. Chem. 52:1095-1097 (1980).		
RL	[3]		
RP	SEQUENCE OF 1-251 FROM N.A.		
RC	TISSUE=Leaf;		
RA	MEDLINE=91201329; PubMed=2016300;		
RA	Evensen G., Mathiesen A., Sundan A.;		
RT	"Direct molecular cloning and expression of two distinct abrin		
RT	A-chains."		
RL	J. Biol. Chem. 266:6848-6852 (1991).		
RP	SEQUENCE OF 262-528.		
RP	MEDLINE=92311656; PubMed=1505674;		
RA	Chen Y.-L., Chow L.-P., Tsangata A., Lin J.-Y.;		
RT	"The complete primary structure of abrin-a b chain."		
RL	FEBS Lett. 309:115-118 (1992).		
RP	[5]		
RP	X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).		
RA	MEDLINE=95331188; PubMed=7608980;		
RA	Tanakov T.H., Lu D.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;		
RA	Crytal Biol. 250:54-57 (1995).		
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN		
CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL		
CC	SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.		
CC	ABRIN-A IS MORE TOXIC THAN RGIN.		
CC	-1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT		
CC	FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT		
CC	PREFERS ENDOCYTOSIS.		
CC	-1- CATALYTIC ACTIVITY: Endohealydrolase of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		
CC	-1- DOMAIN: THE A CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN		
CC	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA)		
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-		
CC	INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.		

CC	-1 SIMILARITY: Contains 2 rich B-type lectin domains.	
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CC	EMBL; M98344; AAA32624.1; ALT INIT.	
DR	EMBL; X54872; -) NOT ANNOTATED_CDS.	
DR	PIR; S32429; TZLSA.	
DR	PIR; IAB; 07-FEB-95.	
DR	InterPro; IPR00772; Ricin_B_lectin.	
DR	InterPro; IPR001574; RLP.	
DR	Pfam; PF00163; RBL_1_lectin; 6.	
DR	Pfam; PF00163; RBL_1_lectin; 6.	
DR	PRINTS; PR00386; SHTGALICIN.	
DR	SMART; SM00458; RICIN; 2.	
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.	
DR	PROSITE; PS00275; SHIG_RICIN; 1.	
KW	Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;	
KW	Glycoprotein; Lectin; 3D-structure; Pyroglutamate carboxylic acid.	
FT	CHAIN	1 251
FT	PERITIDE	252 261
FT	LINKER	262 269
FT	DOMAIN	273 408
FT	DOMAIN	403 527
FT	REPEAT	283 325
FT	REPEAT	326 366
FT	REPEAT	369 401
FT	REPEAT	414 449
FT	REPEAT	453 492
FT	REPEAT	495 528
FT	ACT_SITE	164 164
FT	DISULFID	264 369
FT	DISULFID	326 346
FT	DISULFID	329 346
FT	DISULFID	417 430
FT	DISULFID	456 473
FT	MOD_RES	1 1
FT	CARBOHYD	361 361
FT	CARBOHYD	401 401
FT	CONFLICT	202 202
FT	CONFLICT	298 298
FT	CONFLICT	427 427
FT	CONFLICT	457 457
FT	CONFLICT	483 483
FT	STRAND	5 8
FT	TURN	10 11
FT	HELIX	14 28
FT	STRAND	32 33
FT	TURN	34 35
FT	STRAND	36 38
FT	TURN	42 43
FT	HELIX	47 49
FT	TURN	51 57
FT	STRAND	61 61
FT	TURN	70 72
FT	STRAND	75 79
FT	STRAND	83 86
FT	TURN	88 89
FT	TURN	92 93
FT	HELIX	94 97
FT	TURN	100 101
FT	STRAND	103 106
FT	TURN	110 115
FT	HELIX	115 116
FT	TURN	124 126
FT	STRAND	129 129
FT	HELIX	131 142
FT	TURN	143 144

Query Match	Match	Score	DB	Length	529	Indels	Gaps
FT	HELI	148	167				
FT	STRAND	168	168				
FT	HELI	169	180				
FT	TURN	181	182				
FT	STRAND	185	185				
FT	HELI	189	196				
FT	TURN	197	197				
FT	HELI	198	200				
FT	STRAND	202	223				
FT	TURN	222	223				
FT	STRAND	226	231				
FT	TURN	232	233				
FT	HELI	235	239				
FT	STRAND	240	240				
FT	STRAND	243	243				
FT	STRAND	248	248				
FT	STRAND	256	268				
FT	STRAND	276	280				
FT	HELI	282	284				
FT	STRAND	286	289				
FT	HELI	290	292				
FT	TURN	296	297				
FT	STRAND	299	303				
FT	HELI	311	313				
FT	STRAND	315	317				
FT	TURN	319	320				
FT	STRAND	322	325				
FT	TURN	326	327				
FT	STRAND	328	332				
FT	TURN	337	338				
FT	STRAND	340	344				
FT	TURN	346	348				
FT	HELI	351	353				
FT	STRAND	355	355				
FT	STRAND	357	358				
FT	TURN	360	361				
FT	STRAND	364	366				
FT	TURN	374	376				
FT	STRAND	371	374				
FT	TURN	380	381				
FT	STRAND	383	383				
FT	STRAND	385	387				
FT	HELI	393	395				
FT	STRAND	398	399				
FT	STRAND	406	408				
FT	STRAND	410	411				
FT	HELI	413	415				
FT	STRAND	421	421				
FT	TURN	427	428				
FT	STRAND	424	428				
FT	TURN	432	433				
FT	HELI	435	437				
FT	STRAND	439	441				
FT	TURN	443	444				
FT	STRAND	447	449				
FT	TURN	450	451				
FT	STRAND	452	459				
FT	STRAND	464	465				
FT	STRAND	472	475				
FT	TURN	474	475				
FT	HELI	478	480				
FT	STRAND	483	484				
FT	TURN	486	487				
FT	STRAND	490	492				
FT	TURN	493	496				
FT	STRAND	497	501				

DB 269 CSNRFFTVAGIGRDKWCVDYDNGVHNGRIILWKKCKRERENQWLTLSKXTHSNK 328
QY 64 CLTYGYAGVYVIMPCNTAVRENTIWIQWNGTIIINPNSNVLVAASGIGKTLTYQT 123
DB 329 CLTYGYAPGSYVWYIDCTSAVAEATWEIWMNGTIIINPKSALVVAASSSWGTLTYQT 388
QY 124 LDYTLGQWLAGVDAPEEYTYGRDLNLSNGSGVWVECTDSQKQGMALYDQSI 183
DB 389 NEXLMRGWKGNNISPTVISISYDLCNQSNGVWVAQDSNKEQ-QMALYDQSI 447
QY 184 RPKQNDQCTSGSDSYVTVINIVSGASGSGCWPTNEGALINLNGALNDVQAQPK 243
DB 448 RSYQNTNCLTSKHKQSGSTILMGCSNGVAGRWYKPDGSLYLDVQWVDVKSQDS 507
QY 244 LRRIIYPATKQKQWMLPVF 264
DB 508 LKQILMFTYKQKQWMLPVF 528
RESULT 5
ABR ABRP STANDARD: PRT: 527 AA.
AC 006077: P81374: Created
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ABrin-b precursor (Contains: ABrin-b A chain (rRNA, N-glycosidase))
DE (EC 3.2.2.22); ABrin-b B chain)
DE ABrin precursors (Indian ilicoidae) (Crab's eye).
DE Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryotes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucotyledon; Fabales; Fabaceae; Papilionoideae; Abraceae; Abrus.
OC NCBI_TaxID=3816;
RX SEQUENCE FROM N.A.
RX MEDLINE=9132798; PubMed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
RT "Primary structure of three distinct isobryins determined by cDNA
RT sequencing. Conservation and significance.";
RL J. Mol. Biol. 229:263-267 (1993).
RM SOURCE OF 260-527.
RM TISSUE=Seed.
RX MEDLINE=91169023; PubMed=7763423;
RA Kimura M., Sumizawa T., Funatsu G.;
RT "The complete amino acid sequences of the B-chains of abrin-b and
RT abrin-b, toxic proteins from the seeds of Abrus precatorius";
RL Biochem. Biotechnol. Biochem. 57:166-169 (1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- FUNCTION: THE A CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANES THAT
CC PRECEDES ENDOCYTOSIS
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC This SWISS-PROT entry is annotated. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL laboratory
CC the European Bioinformatics Institute. The data are available on-line
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CC or send an email to license@ebi.ac.uk.

DR EXEL: N93945; AAA2625.1; -.
DR PIR: S23430; S23430.
DR HSBP: B11140; IABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00488; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGARICIN; 1.
DR PROSITE: PS00275; SHIGARICIN; 1.
DR GlycoProfile: GlycoProfile; Protein synthesis inhibitor; Toxin; Reprec;
KW Glycoprotein; Lectin; Pyrolytic amino acid.
FT CHAIN 1
FT PEPTIDE 251 260
FT CHAIN 2
FT CHAIN 261 527
FT DOMAIN 272 399
FT DOMAIN 402 526
FT REPEAT 282 324
FT REPEAT 325 365
FT REPEAT 366 400
FT REPEAT 413 448
FT REPEAT 452 491
FT REPEAT 492 527
FT REPEAT 528 564
FT DISULFID 246 268
FT DISULFID 328 345
FT DISULFID 416 429
FT DISULFID 455 472
FT MOD RES 1 1
FT CARBOHD 110 110
FT CARBOHD 360 360
FT CARBOHD 480 480
FT CONFLICT 282 282
FT CONFLICT 291 291
FT CONFLICT 350 351
FT CONFLICT 378 378
FT CONFLICT 426 426
FT CONFLICT 428 428
FT CONFLICT 431 431
FT CONFLICT 484 484
FT CONFLICT 491 491
FT CONFLICT 493 493
FT CONFLICT 502 502
FT CONFLICT 503 503
FT CONFLICT 513 513
FT CONFLICT 516 516
SQ SEQUENCE 527 AA; 5914 MW; 32534890CS94944 CRC64;
Query Match 54.4%; Score 771; DB 1; Length 527;
Best Local Similarity 55.2%; Pred. No. 1,7e-58;
Matches 144; Conservative 43; Mismatches 72; Indels 2; Gaps 2;
DB 5 CSNRFFTVAGIGRDKWCVDYDNGVHNGRIILWKKCKRERENQWLTLSKXTHSNK 63
DB 268 CSNRFFTVAGIGRDKWCVDYDNGVHNGRIILWKKCKRERENQWLTLSKXTHSNK 327
QY 64 CLTYGYAGVYVIMPCNTAVRENTIWIQWNGTIIINPNSNVLVAASGIGKTLTYQT 123
DB 329 CLTYGYAPGSYVWYIDCTSAVAEATWEIWMNGTIIINPKSALVVAASSSWGTLTYQT 387
QY 124 LDYTLGQWLAGVDAPEEYTYGRDLNLSNGSGVWVECTDSQKQGMALYDQSI 183
DB 389 NEXLMRGWKGNNISPTVISISYDLCNQSNGVWVAQDSNKEQ-QMALYDQSI 446
QY 184 RPKQNDQCTSGSDSYVTVINIVSGASGSGCWPTNEGALINLNGALNDVQAQPK 243
DB 448 RSYQNTNCLTSKHKQSGSTILMGCSNGVAGRWYKPDGSLYLDVQWVDVKSQDS 506
QY 244 LRRIIYPATKQKQWMLPVF 264


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DR InterPro: IPR000772; Ricin B lectin.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR PRINTS: PR00134; GHYDRLAS10.
DR SMART: SM00523; Glyco_10; 1.
DR SMART: SM00523; Glyco_10; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00231; Ricin B lectin; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 PROTON DONOR.
FT ACT_SITE 169 189
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 51162 MW; 514VFE37BDG68CC CRC64;

Query Match
  8.9%; Score 125.5; DB 1; Length 477;
  Best local similarity 28.9%; Pred. No. 0.0022;
  Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;

QY 7 ASBP-----TVAIGNRNRYVDVDDPDHGNQIQIOWPSKSNDDNQLTIKRDGTIRSN 61
DB 346 SSEPPADGQIKVIG--SQRCLVDPASTDGTOLWCHSGT--NQQAAATDAGSLAVY 402
QY 62 G-SCLTGYTA-GYVYVMEPCNTAVRENTIQTWINDGTTINPRSNLYIAA--SSGIKETT 118
DB 403 GDKCLDAAGTSGSKVQIISGAGDNK--WALNSGSAVGVSGLCLDVGANSTANFTL 460
QY 119 LVTQTLDTYTLGGW 132
DB 461 IOLYTCNSNSNGW 474

RESULT 9
ID ASBP_STRCO STANDARD; PRT; 475 AA.
AC 059161; 1998 (Rel. 37, Created)
DT 12-DEC-1998 (Rel. 37, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID:1902;
RN (1)
RS SEQUENCE FROM N.A.
RX STRAIN: 326/10; PubMed:1200953.
RA Bentley S.D., Cole S.K., Corbett K., Harris D.G., Chail M.A., Kisser H.H.,
RA Thomson N.P., James K.D., Harris D.G., Chail M.A., Kisser H.H.,
RA Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietorek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).
RI NCBI_TaxID:1902;
CC - CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinuronoside residues in alpha-D-arabinosides.
CC - PATHWAY: Xylan degradation.
CC - SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL_HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL39125; CA6189.1; .
DR FRL: J35697; J35697; Glyco_hydro_62.
DR InterPro: IPR00123; Ricin B lectin.
DR Pfam: PF00652; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR SMART: SM00458; Ricin; 1.
DR PROSITE: PS00231; Ricin B lectin; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW Complete proteome.
FT SIGNAL 1 37
FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
FT DOMAIN 39 166 RICIN B-TYPE LECTIN.
SQ SEQUENCE 475 AA; 50045 MW; 47E107FE341C6D0 CRC64;

Query Match
  8.1%; Score 115.5; DB 1; Length 475;
  Best local similarity 24.1%; Pred. No. 0.016;
  Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

QY 6 SASPTVRIYGRNRYVDVDDPDHGNQIQIOWPSKSNDDNQLTIKRDGTIRSN-SC 64
DB 37 AAGSGALKRAGSNRC-LDVIGGSDGDAIQLQIDCWGRT--NQQMTSTDTGRLTYGDKC 93
QY 65 LTTGYTA--GYVYVMEPCNTAVRENTIQTWINDGTTINPRSNLYIAA--IKETTTL 120
DB 94 LVTGTAHTRPOTVQIWSGAGANQ--WRVNSDGTIVYSGCLDPAKGRANGTAVV 151
QY 121 VQTLDTYTLGGW 132
DB 152 LVTGNGAGNQWGLVTPPTDGLCSPTYSRSTGVLAKRSGWALXKDTTTHN 211
QY 175 WALYCDGS-----IRKQNDQCLTSRGRSVS 201
DB 212 HLYVSTSGSGSYSMVSPFTNMSDMSAQQMNN 247

RESULT 10
ID E13B_ARNSP STANDARD; PRT; 546 AA.
AC 059146; 1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) (1->3)-beta-
DE glucan endohydrolase (1->3)-beta-glucanase).
OS Actinobacter sp. (strain YCM03).
OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Actinobacter.
OX NCBI_TaxID:167;
RN (1)
RS SEQUENCE FROM N.A.
RA Natarade T., Hasegawa H., Doi A., Doi K.;
RA Submitted (DEC-1993) to the EMBL/Genbank/DBJ databases.
RT FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
RT IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
RT SIMILARITY).
CC - CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC - SUBCELLULAR LOCATION: Periplasmic (by similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL_HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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DR Pfam: PM00652; Ricin B lectin; 3  

DR SMART: SMO0458; RICIN_1.  

KW PROSITE; PS02031; RICIN B LECTIN; 1.  

KR HYDROLASE; Glycosidase; Signal; Peptidase; Cell wall; Lectin.  

FT SIGNAL 37 548  

FT CHAIN 1 36 POTENTIAL.  

FT DOMAIN 422 436 GLUTAMINE ENDO-1,3-BETA-D-GUCOSIDASE;  

FT DOMAIN 37 430 ROSES BETA-D-GUCANSE ACTIVITY, BUT IS  

FT FT UNABLE TO LYSE VIABLE CELLS.  

FT FT ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT  

FT FT FOR THE BETA-D-GUCANSE FUNCTION.  

SO SEQUENCE 548 AA; 5808 MW; 412B5A4A2AC049D CRO64;  

Query Match  

Best Local Similarity 81.3%; Score 114; DB 1; Length 548;  

Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7.  

Db 16 GENBANK-----PRADPHRQNCGLMPKSNDDPVCGLTIKSGPTGNSGC--TT 67  

Db 422 GGALRIISTLCIDPMADPDITNVOYL -ATGSNAAGCTRGIDVTBALSKLDVAR 479  

Query 68 YVYRAGVYMVFECF-TVEAEATWQMONT--IINRSNIYLAASGI--KGTLTV 121  

Db 480 SCFLDGAWMYLWCNTGAQXT-----YDSATRLARNPSGSCADGGAPLRDGOXVL 535  

Query 122 CTLLDYTLGGW 132  

Db 536 WTCNLTDAEKN 546  

RESULT 12  

ASP_STRLI STANDARD; PRT; 475 AA.  

ID ASP_STRLI  

AC P96463;  

DT 15-DEC-1998 (Rel. 37, Created)  

DT 15-DEC-1998 (Rel. 37, Last sequence update)  

DT 28-FEB-2003 (Rel. 41, Last annotation update)  

DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).  

DE Alpha-D-glucanase lydinans  

DE Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;  

OC Streptomycinae; Streptomyces  

CC NCBI_TaxId=1916;  

RN [1]  

RX SEQUENCE FROM N.A.  

RC STRAIN=56 / 1326;  

RA MEDLINE=97220396; PubMed=9148739;  

RA "Lincent F., Sharpeck F., Dupont C., Morcossi R., Kluepfel D.;  

RT cloning and DNA sequence of the ald5 gene and characterization of the  

RT enzyme";  

RL Biochem. J. 322:845-851(1997).  

RP REVISIONS:  

RC STRAIN=66 / 1326;  

RA Sharpeck F.;  

RL Submitted (Oct-1998) to the EMBL/GenBank/DDBB databases as ACTIVITY ON  

RL -1. FULL-LENGTH DNA SPECIFICALLY INHIBITS SPECIFICALLY WITH THE XYLANS AND  

RL BINDS SPECIFICALLY TO XYLAN. FROM SMALL ALKALI-SOLUBLE XYLANSIDES,  

RL IT LIBERATES ARABINOSE AND AFTER PROLONGED INCUBATION, THE  

RL PURIFIED ENZYME EXHIBITS SOME XYLANOXYLYTIC ACTIVITY AS WELL.  

RL -1. CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-  

RL arabinofuranoside residues in alpha-L-arabinosides.  

CC -1. PATHWAY: xylan degradation.  

CC -1. SUBCELLULAR LOCATION: Secreted.  

CC -1. SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.  

CC -1. SIMILARITY: CONTAINS 1 RICIN B TYPE LECTIN DOMAIN.  

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DR EMBL; M6451; AAC6524.1; 7
DR InterPro; IPR005193; Glyco_hydro_62.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF03664; Glyco_hydro_62; 1.
DR SMART; SM00454; Ricin_B_lectin; 3.
DR PROSITE; PS50231; Ricin_B_LECTIN; 1.
DR Kxylan degradation; Hydroxylase; Glycosidase; Signal; Lectin.
FT SIGNAL 1 37
FT CHAIN 38 475
FT DOMAIN 39 166
FT SEQUENCE 475 AA; 50669 MW; C3DB148E7BF854D CMC64;
Query Match
Best Local Similarity 24.4%; Evid. No. 0.029
Matches 52; Conserved 35; Mismatches 104; Indels 25; Gaps 10

Qy 6 SAEPTATVYGMKSNVAVRDPPDFDQNGOICLWMSKSNDDQWLTKRPRTYSNG-SC 64
Db 37 AASGALRAGASNNC-LDVLSGSDGDLGLLYCNGWT--NQWSTDTGSLTVYGDKC 93
Qy 65 LTVGYTA-GVYVIFEDCTAVREANTWQINDGTTINPESNLYL-AASSGI-KGTLT 120
Db 94 LDVPMKAPRGRVQLMSGSGNQV--WVNSDLYVTSGLCLADQDQDTNNGNQ 151
Qy 121 VQRLVYTLGGWLANDVAPRYT----LYGPDCLMSNGSGIWTGDD-SQKQK 174
Db 152 LPMCGGNGDQVETGLTGTPDTCALPSTYSMSSTGVLAQPSKSVVALDDFTVTHNR 211
Qy 175 WALYGDGSS-----IRPKVQDCLTSGSDVS 201
Db 212 HLVTSTSSSSYGVSPPTWMDASAGQANRN 247

RESULT 13
SPL PARFA
ID SPL PARFA STANDARD; PRT; 525 AA.
AC 005308;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT Serine protease I precursor (SC 3.4.21.-) (Rpt).
OS Rarobacter faecitabidus.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OS Rarobacter faecitabidus; Rarobacteraceae; Rarobacter.
NCBI_TaxID=13243;
KX SEQUENCE FROM N. A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
RC STRAIN-YLM-50;
RC MEDLINE-93094226; PubMed-1339445;
RA Shimoel H., Iimura Y., Obara T., Tadenuma M.;
RT Molecular structure of Rarobacter faecitabidus protease I, a yeast-
lytic serine protease having mannose-binding activity.";
J Biol. Chem. 267:25195-25195 (1992).
RU [3]
SQ SEQUENCE OF 212-247.
RA MEDLINB-92138668; PubMed-1778983;
RA Shimoel H., Tadenuma M.;
RT "Characterization of Rarobacter faecitabidus protease I, a yeast-lytic serine protease having mannose-binding activity.";
J. Biochem. 110:608-613 (1991).
RL 1. FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD LIVING YEAST CELLS. SIMILAR TO ELASINASE IN ITS SUBSTRATE SPECIFICITY AND HAS A LECTIN-LIKE AFFINITY FOR MANNOSE.
CC 1. SUBCELLULAR LOCATION: THE N-TERM SUBSTRATE FOR RPL.
CC 1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
CC 1. SIMILARITY: CONTAINS 1 Ricin B-type lectin domain.

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CC      or send an email to license@sb-stb.ch).
CC
CC      EMBL D10753, P040385.1; ..
CC      DR PIR: A45053; A45053.
CC      DR HSBP: P00778; 1GBA.
CC      DR MEROPS: S01.276; -.
CC      DR InterPro: IPR004236; AL protease.
CC      DR InterPro: IPR001316; Endopeptidase2A.
CC      DR InterPro: IPR001772; Rcin.B lectin.
CC      DR InterPro: IPR001254; Ser. protease_TY.
CC      DR Pfam: PF02933; AL_protease_1.
CC      DR Pfam: PF00632; Rcin.B lectin_3.
CC      DR PRINTS: PR00661; ALCTIPASE.
CC      DR SMART: SM00458; RCIN; 1.
CC      DR PROSITE: PS00134; TRYPSIN_SER; 1.
CC      DR PROSITE: PS50231; RCIN_B_LECTIN; 1.
CC      DR PROSITE: PS50231; RCIN_B_LECTIN; 1.
CC      KW Hydroxylase, serine protease, Nannose-binding, signal, zymogen,
CC      Lectin.
CC      FT SIGNAL 1 32 POTENTIAL.
CC      FT PROPEP 1 211 POTENTIAL.
CC      FT CHAIN 212 525 SERINE PROPEPSE 1.
CC      FT DOMAIN 396 525 RCIN B-TYPE LECTIN.
CC      FT DOMAIN 401 525 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
CC      FOR PROPEASE FUNCTION.
CC      FT DISULFD 223 239 BY SIMILARITY.
CC      FT DISULFD 310 320 BY SIMILARITY.
CC      FT DISULFD 346 376 BY SIMILARITY.
CC      FT DISULFD 412 431 BY SIMILARITY.
CC      FT DISULFD 432 452 BY SIMILARITY.
CC      FT DISULFD 482 512 BY SIMILARITY.
CC      FT ACT_SITE 218 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      FT ACT_SITE 270 270 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      SQ SEQUENCE 525 AA; 55654 MW; DA2BCF7D330EB61 CRC64;
CC
CC      Query Match 7.8%; Score 111; DB 1; Length 525;
CC      Best Local Similarity 31.1%; Pred. No. 0.044;
CC      Matches 33; Conservative 17; Mismatches 46; Indels 12; Gaps 5
CC
CC      Db 399 DVT-----TSVGVQNNCKIDVPSDFDQKQLQVWNCNGT-  

CC      2 DPTVCASEPRVAVGNCNKPDPDPPDQVQICLAPSSANNQDQVITRGITISN 61  

CC      63 GSCQ-  

CC      451 GKCLDARAWATHTNGTQVQVQNCNHI-  

CC      DDb 451 GKCLDARAWATHTNGTQVQVQNCNHI-  

CC      63 GSCQ-  

CC      451 GKCLDARAWATHTNGTQVQVQNCNHI-  

CC      RESULT 14  

CC      P040385.CABE1  

CC      AC D34676; G09003; STANDARD; PROT; 612 AA.  

CC      ID P34076; G09003; STANDARD; PROT; 612 AA.  

CC      DT 01-FEB-1994 (Rel. 28, Created)  

CC      DT 28-FEB-2003 (Rel. 41, Last sequence update)  

CC      DT 28-FEB-2003 (Rel. 41, Last annotation update)  

CC      DE Polypeptide N-acetylglucosaminyltransferase 3 (EC 2.4.1.41)  

CC      (Protein-UDP-N-acetylglucosaminyltransferase) (unp-catalytic polypeptide)  

CC      N-acetylglucosaminyltransferase (GALNAC-T1) (ppGlnase 3f).  

CC      GN GLY-3 OR ZK688.8  

CC      OS Caenorhabditis elegans  

CC      OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  

CC      NCBI_TaxID=6239; Caenorhabditis;  

CC      RE SEQUENCE FROM N.A.

```

RC STAIN-BRISTOL N2;
RX MEDLINE=98192620; PubMed=9525933;
RA Hagen P.K., Nehrkke K.;
RT "cDNA cloning and expression of a family of UDP-N-acetyl-D-
galactosamine polypeptide N-acetylgalactosaminyltransferase sequence
homologs from Caenorhabditis elegans";
RL Biol. Chem. 273:8269-8277 (1998).
RP SEQUENCE FROM N2.
RN STAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Milson R., Ainscough R., Anderson K., Baynes C., Barker M.,
RM Bonfield J., Busch O'F., Connell W., Copsey T., Coulson A.,
RS Richardson L., Dear S., Dol G., Duthie R., Favello A., Fraser A.,
RV Johnson L., Gardner A., Green P., Hawkins T., Hillier L., Jlee M.,
RW Paterson V., Percy C., Rifkin L., Roopra A., Saunders D., Stephens R.,
RX Parsons T., Lightning T., Lloyd C., Mortimer S., Garside D.,
RY Sims M., Smaldon N., Smith A., Smith M., Somhammer E., Stead R.,
ZZ Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RT Wolfman P.;
RU "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RV Nature 368:32-38(1994).
RN REVISIONS.
RP Revisions.
RL Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: THIS PROTEIN CATALYZES THE INITIAL REACTION IN O-LINKED
GLYCOSAMINOGLYCAN BIOSYNTHESIS, THE TRANSFER OF AN N-ACETYL-D-
GALACTOSAMINE RESIDUE TO A SERINE OR THREONINE RESIDUE ON THE
PROTEIN RECEPTOR.
CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide =
UDP + N-acetyl-D-galactosaminyl-polypeptide.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein [Potential].
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaborator
between the Swiss Institute of Bioinformatics and the EMBL consortium -
the European Bioinformatics Institute. There are no restrictions on way
it can be used by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by for commercial
or send an email to license agreement (see http://www.isb-sib.ch/aboutus/
--
DR EMBL AF013933; AAC13669.1; --
DR EMBL U15621; AAA28224.3; --
DR PIR T42243; T42243.
DR WormRep ZK688.8; CEZ9643.
DR InterPro IF000173; Glyco_trans_2.
DR Pfam PF005017; RicinB_Lectin.
DR Pfam PF00652; RicinB_Lectin_1.
DR Pfam PF00652; RicinB_Lectin_2.
DR SMART SMO0458; RICIN_1.
DR PROSITE PS00231; Ricin_B_Lectin; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
KW Glycoprotein; Lectin.
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAINS 1 34 POTENTIAL.
FT DOCKIN 35 612 POTENTIAL.
FT DOCKIN 478 612 POTENTIAL.
FT CARBOHYD 146 146 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAc...) (POTENTIAL).
SQ SEQUENCE 612 AA; 68911 MW; 3031CZF933FE958 CRC64;

Query Match

Best Local Similarity 26.4%; Prod. No. 0.33;

Matches 32; Conservative 23; Matches 50; Indels 16; Gaps 6.

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0Y 148 FRILMNSN- ---SSWVETCSGONKQKALYSDSS:REKNOQDGLTSGE-DUST 202
Db 492 FFEKCVTQKKDDQAFQIQCHGAGQQA-MSLTKQKFR--SDCLTSGHYQVGS 547
0Y 203 VINIYSGASAGSGSWMT---NEBALIKKGLAADQAQNPMLKRIITIPANSGPNOM 559
Db 548 ELKLRFSVSKINMVFVDDQAGTLTKRTKGKQVGLQVRLVDEC---GLGKDDM 603
0Y 260 W 260
Db 604 W 604

RESULT 15
AGAL ASPNG STANDARD PRT, 545 AA.
Db 1 AGAL ASPNG
Db 2 P28351, 1992 (Ref. 24, Created)
Db 3 01-DEC-1992 (Ref. 24, Last sequence update)
Db 4 16-OCT-2001 (Ref. 40, Last annotation update)
Db 5 Alpha-galactosidase A precursor (EC 3.2.1.22) (Melibiose).
Db 6 AGAL.
Cc Aspergillus niger.
Cc Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
Cc Eumetazoa; Trichocnemeae; mitosporic Trichocnemeae; Aspergillus.
Cc NCBI_Taxid=5061;
Cc 11.
Cc SEQUENCE FROM 'A', AND SEQUENCE OF 32-59.
Cc 1.
Cc 2.
Cc MEDLINE=92318923; PubMed=1201016;
Cc van der Helder I.P., Rosell A.M.M., van Zullen C.M., Punt P.J.,
Cc R. van den Hondel C.A.M.T.J.,
Cc "Cloning and expression of a member of the Aspergillus niger gene
Cc family encoding alpha-galactosidase."
Cc Mol. Gen. Genet. 233:404-410(1992).
Cc 1.
Cc ACTIVITY: IN A NISER.
Cc 1.
Cc 1. FUNCTION: REPRESSES A MINOR EXTRACELLULAR ALPHA-GALACTOSIDASE
Cc 1.
Cc 1. PPM: C-METINIL SEF/HR-RCH REGION MAY PROVIDE POSSIBLE SITES
Cc 1. FOR O-GLYCOSYLATION
Cc 1.
Cc 1. SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASIS.
Cc 1.
Cc 1. SIMILARITY: CONTAINS 1 RICHIN B-TYPE LECTIN DOMAIN.
Cc 1. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
Cc 1.
Cc This SWISS-PRO entry is copyright. It is produced through a collaboration
Cc between the Swiss Institute of Bioinformatics and the EMBL outstation.
Cc The European Bioinformatics Institute. There are no restrictions on its
Cc use. It is made available on the WWW and for commercial use. It is not
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Cc use. It requires a license agreement (see http://www.ebi.ac.uk/announcements
Cc or send an email to license@ebi.ac.uk).
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FT CAROHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 545 AA; 60148 MW; 20CSN710CE95D59C CRG64;

Query Match 7.1%; Score 100.5; DB 1; Length 545;
Best Local Similarity 19.9%; Pred No 0 36; Indels 45; Gaps 8;
Matches 46; Conservative 43; Mismatches

QY 22 VVRRDDDFDQNOIQWPSKSNDDPNQWTKRQGTIRNSGCLTYGYTA----- 72
DB 342 LDIILRLSINAGDRILTLVANKNT-----TVTRDIPVQWLGLETDCITYAEDLMDKRTQ 395
QY 73 ---GVYVIFPCNTAVENATIQ---IWDNFTINFRSNLVLAASGIGKTTLVQTL 124
DB 396 KISDHIRELASHRTAVRSLPQGGSSVFTGLVFNTPASGCLTAAS---NSSVAFQSC 452
QY 125 DYLGGQWLAGNDIAPRPRTIYGRFDLCHESNGSIVWETGDSQKQKQKALYDGSRT 184
DB 453 NGRTSQIWOVTPSGVIRPVG--CTTQCLAADNVLVLQACDSTDSQKRTVPTGNTLK 509
QY 185 PKXQDQCLTSGRDSVSTVINIVSCSGSAGSCRWVETBGAIIINIKNGIAM 235
DB 510 -NAKTDGCLTEGS-----VQWKSC-----IYERDQVFTLPBGVOL 544

Search completed: December 11, 2003, 14:09:04
Job time : 4.6201 secs

Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

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Oy 1 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 60
Db 269 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 328
Oy 61 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 120
Db 329 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 388
Oy 121 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 180
Db 389 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 447
Oy 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
Db 448 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQS 507
Oy 241 NPKLRILITTPATGKPNQWMLPV 263
Db 508 NPKLRILITTPATGKPNQWMLPV 530
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RESULT 2

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O8LKQ2 ID Q8LKQ2 PRELIMINARY; PRT; 263 AA.
AC Q8LKQ2;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DB 121-VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD
OS VASCUM ALBUM SUBSP. COLORATUM.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
CX NCBI_Taxid=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
RT cDNA cloning and sequence analysis of the lectin genes of the Korean
mistletoe (Viscum album coloratum).
RM [2]. Cells 12(215-220(2002)).
RN [2]
```

SEQUENCE FROM N.A.

```
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF508918; AAM46936.1;
DR Interpro; IPR000772; Ricin B lectin.
DR Pfam; PF00652; Ricin B lectin.5.
DR SMART; SM00458; RICIN_B_Lectin; 2.
DR PROSITE; PS50231; RICIN_B_Lectin; 2.
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FT NON_TER 263
FT SEQUENCE 263 AA; 29150 MW; B685BDB7C19C8D1F CRC64;
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Query Match 79.4%; Score 112.5; DB 10; Length 263;
Best Local Similarity 79.5%; Pred. No. 2.4e-86;

Matches 209; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

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Oy 1 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 60
Db 1 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 60
Oy 61 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 120
Db 61 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 120
Oy 121 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 180
Db 121 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 180
Oy 241 NPKLRILITTPATGKPNQWMLPV 263
Db 241 NPKLRILITTPATGKPNQWMLPV 263
```

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Oy 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
Db 180 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQS 239
Oy 241 NPKLRILITTPATGKPNQWMLPV 263
Db 240 NPKLRILITTPATGKPNQWMLPV 262
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RESULT 3

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O8W243 ID O8W243 PRELIMINARY; PRT; 565 AA.
AC O8W243;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 23, Last annotation update)
DB VCA precursor (EC 3.2.2.23) (VCA N-glycosidase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
CX NCBI_Taxid=159976;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Park W.-B., Lyu S.-I.;
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe).
RT Biochem. Biophys. Res. Commun. 0:0-0(2002).
CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERASE OF THE N-GLYCOSIDIC BOND AT ONE
-1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -2- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL; AF508918; AAM46936.1;
DR Interpro; IPR001574; Rib_1_lectin.
DR Pfam; PF00652; Ricin B lectin; 6.
DR PRINTS; PR00396; SHIGARICIN.
```

```
DR SMART; SM00458; RICIN_B_Lectin; 2.
DR PROSITE; PS50231; RICIN_B_Lectin; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1
FT CHAIN 23
FT CHAIN 23 272 POTENTIAL.
FT CHAIN 39 565 VCA ALPH. CHAIN.
FT SEQUENCE 565 AA; 62401 MW; 59183994D00C5F11 CRC64;
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Query Match 78.5%; Score 112.5; DB 10; Length 565;
Best Local Similarity 80.6%; Pred. No. 7.6e-85;

Matches 212; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

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Oy 1 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 60
Db 307 DDTVCASSEPTVAVGNKGVVDVDDDPFDGNGQIQLPKSKSNNDPNQMTIKEDGTRIS 362
Oy 61 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 120
Db 363 NSGCLITTYGTAGVYVWIPDCNTAVREKATINQINDGTTINPSRLVLAASGIGKFTLT 422
Oy 121 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 180
Db 423 VOTLDVTLGGQWLAGNDTAPREVTIYGRFLCMESNGSGVVECTDSQKQKMAIYGD 481
Oy 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
Db 482 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQS 541
Oy 241 NPKLRILITTPATGKPNQWMLPV 263
Db 542 NPKLRILITTPATGKPNQWMLPV 564
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AC		Q8IKO1_1	(TREMELBEL_22, Created)
AD	01-OCT-2002	(TREMELBEL_22, Last sequence update)	
DY	01-OCT-2002	(TREMELBEL_22, Last annotation update)	
DT	01-MAR-2003	(TREMELBEL_23, Last annotation update)	
DB	Lectin chain B isoform 3 (Fragment).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;		
CC	Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;		
NCBI_TaxId=159976;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21566752; PubMed=11710524;		
RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,		
LA	Do M.-S., Song S.K.;		
DR	GenBank cloning and sequence analysis of the lectin genes of the Korean		
DR	mistletoe (<i>Vincetoxicum</i>) ^{1,2} .		
PT	CELLS 121:215-220(2001).		
SQ	SEQUENCE 263 AA; 29071 MW; 3f9CADA860F061D CRCE4;		
Query Match	77.0%; score 1091.5; DB 10; Length 263;		
Best Local Similarity	77.6%; Pred. No. 1.7e-83;		
Matches 204;	Conservative 22; Mismatches 36; Indels 1; Gaps 1		
QY	1 DVTYGSASPEPTKATGNGMARDPDDPHDGNQLQMSNSNDPNGLTKKGTIRS 60		
Db	1 DDCITTSREFTWTALVGNLQVDVHGKFRIDNLIQMGCSNYRDLMTIRKDGINS 60		
QY	61 NSGCITLYTGAGYYVAIPCDPAVEAKETIMQINDGNTIMPNSLVMAASSGGKITLT 120		
Db	61 NSKCITLYGRGMQWTVMICNTAFAREIITIMQENGIVNPSSVLGAASSSRITLT 120		
QY	121 VOTLLYLQGMLAGNDAPAEVTTTYGPRDLCMENSGSWVETDSQSNQGMVALYD 180		
Db	121 VQTQAATSLQDGLASHRDPAEFTVITATINYSCSGASQRYTFNKGAILNKMLNGLAAYD 179		
QY	181 GSIRPKNOGCLTSDRSBVSATVINITSCSGASQRYTFNKGAILNKMLNGLAAYD 240		
Db	180 GSIRPKNQRCNCLTCQDSVSTVINITSCSGASQGYTFNKGAILNKMLNGLAVLAYDS 229		
QY	241 NPFLRRRIITYPATSKRNQMWTLPY 263		
Db	240 NPSLRRIITYPATSKRNQMWTLPV 262		
RESULT 5			
ID	O8IKO3	PRELIMINARY; PRT; 266 AA.	
AC	O8IKO3;		
DT	01-OCT-2002 (TREMELBEL_22, Created)		
DT	01-OCT-2002 (TREMELBEL_23, Last sequence update)		
DT	01-MAR-2003 (TREMELBEL_23, Last annotation update)		
DE	Lectin chain B isoform 1 (Fragment).		
OS	Viscum album subsp. coloratum.		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
CC	Santalales; Viscaceae; Viscum.		
NCBI_TaxId=159976;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21566752; PubMed=11710524;		

Query	Subject	Score	Length	Matches	Conservative	Indels	Gaps
QY	1 DVTYTSASEPTAVRVERNGKRVVDVDEDPHGNQGLDLPKSKNDPEQWLTQIKEDTIRS	70.9%	Score 1005; DA 10;	266;			
Db	1 DVTYTSASEPTAVRVERNGKRVVDVDEDPHGNQGLDLPKSKNDPEQWLTQIKEDTIRS	69.9%	Pred. No. 3e-76;				
	Matches 186; Conservative 31; Mismatches 45; Indels 4; Gaps 2						
QY	61 NSGCTITGYATGYKVMYKPGCNATKATQITMDGCTINPSKVT--ASGSGT	117					
Db	121 TPLDTLGSAGGQMAASNTARAVIYIGRPHCMETSGKRWGVCVSGKQWQ-RAL	179					
QY	118 TLVDTLDTLGSAGGQMAASNTARAVIYIGRPHCMETSGKRWGVCVSGKQWQ-RAL	177					
Db	121 TPLDTLGSAGGQMAASNTARAVIYIGRPHCMETSGKRWGVCVSGKQWQ-RAL	179					
Db	61 NSGCTITGYATGYKVMYKPGCNATKATQITMDGCTINPSKVT--ASGSGT	120					
QY	178 YGSGIRPEKQKQDQCTISGSDYSTVITNIVSGSGASGQKVFNTBGAALIKNGIANDV	237					
Db	160 YGSGIRPEKQKQDQCTISGSDYSTVITNIVSGSGASGQKVFNTBGAALIKNGIANDV	239					
QY	238 AASNPRLRITFSTYGNQWMLPV	245					
Db	240 AASNPRLRITFSTYGNQWMLPV	245					
RESULT 6							
QY	Q41174 PRELIMINARY; PER; 541 AA.						
Db	Q41174 PRELIMINARY; PER; 541 AA.						
QY	01-NOV-1996 (TREMUR). 01. Created						
Db	01-NOV-1996 (TREMUR). 01. Last sequence update						
QY	01-MAR-2003 (TREMUR). 23. Last annotation update						
Db	01-MAR-2003 (TREMUR). 23. Last annotation update						
QY	Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)						
Db	Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)						
QY	Ricinus communis (Castor bean).						
Db	Ricinus communis (Castor bean).						
QY	Eukaryotic, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;						
Db	Eukaryotic, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;						
QY	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;						
Db	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;						
QY	eurosid 1; Malvales; Euphorbiaceae; Ricinus.						
Db	eurosid 1; Malvales; Euphorbiaceae; Ricinus.						
QY	111 _taxid=398;						
Db	111 _taxid=398;						
QY	SEQUENCE FROM N.A.						
Db	SEQUENCE FROM N.A.						
QY	MEDLIN-9238377; PubMed35311;						
Db	MEDLIN-9238377; PubMed35311;						
QY	Roberts L.M., Tregear J.W., Lord J.M.,						
Db	Roberts L.M., Tregear J.W., Lord J.M.,						
QY	"Molecular cloning of ricin."						
Db	"Molecular cloning of ricin."						
QY	Targeted Disgn. Ther. 7:81-97(1992).						
Db	Targeted Disgn. Ther. 7:81-97(1992).						
QY	-1. CATALYTIC ACTIVITY; ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE						
Db	-1. CATALYTIC ACTIVITY; ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE						
QY	SPECIFIC ADENOSINE ON THE 28S RNA.						
Db	SPECIFIC ADENOSINE ON THE 28S RNA.						
QY	-1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.						
Db	-1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.						
QY	HSGL; 54099; AAA22502.1; -						
Db	HSGL; 54099; AAA22502.1; -						
QY	InterPro: IPR000772; Ricin_B_lectin.						
Db	InterPro: IPR000772; Ricin_B_lectin.						
QY	InterPro: IPR001574; RIP.						
Db	InterPro: IPR001574; RIP.						
QY	InterPro: IPR001400; Semioctocarpin.						
Db	InterPro: IPR001400; Semioctocarpin.						
QY	Pfam: PF00652; Ricin_B_lectin; 6.						
Db	Pfam: PF00652; Ricin_B_lectin; 6.						

DR Pfam: PF00161; R1P; 1.
DR PRINTS: PRO0396; SHIGA.RICIN.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
DR PROSITE: PS00275; SHIGA_R1CIN; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
DR HYDROLASE; Toxin.
FT NON_TER 1
SEQUENCE 541 AA; 60281 MW; 2873CDSEPIFZ89D9 CRC64;

Query Match 54.1%; Score 909.5; DB 10; Length 541;
Best Local Similarity 63.8%; Pred. No. 7,1e-66;
Matches 166; Conservative 34; Mismatches 59; Indels 1; Gaps 1;

QY 5 CSASEPTVRIYGRNGKRVVDVDDPHGQNIQLMPKSKNDPVQLATIKRGGTIRNSGC 64
DB CMDEPTVRIYGRNGLCVDVDRFHNGNAIQMPCKSNTPANQLMTLKRNTIRNSGC 342
QY 65 LITVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGIKGTLIVOTL 124
DB LITVGSQGVWVIDQNTARADATIMQINDGIIINRSNVLAASSGKTLIVOTN 402
QY 125 DYTIGQWLAGNDPAREVTIVGFRDLQMSNGSVVPTCDSSQKQKALYGDGSR 184
DB IYVSGQWLPNTPTQPTVITVGLXGLQANSQGWLEDC-TSEKAEQWALYADSSIR 461
QY 185 PRQNDQCLTSGRDSVSTVIVVSCGASGSGQWFTNBSGAILNKNGLANDVQAAMP 244
DB PCQRNDQCLTSDSIRKSTVIVVSCGASGSGQWFTNBDITLNLVGLVDRSDPSL 521
QY 245 LRRTIIVPATKNGKQWMLPVF 264
DB KQRTIIVPATKNGKQWMLPVF 541

RESULT 7

Q41143 PRELIMINARY; PRT; 263 AA.
ID Q41143
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DR R1CIN B beta chain (fragment).
GN R1CIN B BETA CHAIN
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Ricinus.
NX NCBI_TaxID=3988;
RE [1]
SEQUENCE FROM N.A.
KA Latin B.F., Murray E.E., Halling A.C., Halling K.C., Tikakazeze N.,
RA "O'Sullivan, Thomas L.L., Weaver R.F., encoding ricin B, a hybrid ricin-Ricinus
RT "Chen, C.-C., 1996, Ricin B, a hybrid ricin-Ricinus communis agglutinin gene from
RL Plant Mol. Biol. 9:287-295 (1997).
DR EMBL: M17631; AA653506.1; -.
DR HSSP: F02879; ZAA1.
DR InterPro: IPR000772; Ricin B lectin.
DR InterPro: IPR001400; Somatotropicin.
DR Pfam: PF00652; Ricin_B.Lectin; 6.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SEQUENCE 263 AA; 29134 MW; AB880FDD1D1E144 CRC64;

Query Match 61.8%; Score 877; DB 10; Length 263;
Best Local Similarity 61.7%; Pred. No. 1,5e-65;
Matches 161; Conservative 37; Mismatches 61; Indels 2; Gaps 2;

QY 5 CSASEPTVRIYGRNGKRVVDVDDPHGQNIQLMPKSKNDPVQLATIKRGGTIRNSGC 64

DB 4 CMDEPTVRIYGRNGLCVDVDRFHNGNAIQMPCKSNTPANQLMTLKRNTIRNSGC 63
QY 65 LITVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGIKGTLIVOTL 124
DB LITVGSQGVWVIDQNTARADATIMQINDGIIINRSNVLAASSGKTLIVOTN 123
QY 125 DYTIGQWLAGNDPAREVTIVGFRDLQMSNGSVVPTCDSSQKQKALYGDGSR 184
DB IYVSGQWLPNTPTQPTVITVGLXGLQANSQGWLEDC-TSEKAEQWALYADSSIR 182
QY 185 PRQNDQCLTSGRDSVSTVIVVSCGASGSGQWFTNBSGAILNKNGLANDVQAAMP-R 243
DB PCQRNDQCLTSDSIRKSTVIVVSCGASGSGQWFTNBDITLNLVGLVDRSDPSL 242
QY 244 LRRTIIVPATKNGKQWMLPVF 264
DB KQRTIIVPATKNGKQWMLPVF 263

RESULT 8

Q94BW4 PRELIMINARY; PRT; 580 AA.
ID Q94BW4
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin II precursor
(EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NX NCBI_TaxID=13429;
RE [1]
SEQUENCE FROM N.A.
KA Yang Q. Gong Z.Z., Liu X.Y.;
RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT gene encoding cinnamomin proteins and study of their expression
RT patterns."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039802; AKR2459.1; -.
DR InterPro: IPR000772; Ricin_B.Lectin.
DR InterPro: IPR001400; Somatotropicin.
DR Pfam: PF00652; Ricin_B.Lectin; 6.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PRO0396; SHIGA.RICIN.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
DR HYDROLASE; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT SIGNAL 1 32
SEQUENCE 580 AA; 64285 MW; 37E429BCECCE0CFP CRC64;

Query Match 61.8%; Score 876; DB 10; Length 580;
Best Local Similarity 63.3%; Pred. No. 5e-65;
Matches 167; Conservative 33; Mismatches 63; Indels 2; Gaps 2;

QY 1 DDVTCASAPTVRIYGRNGKRVVDVDDPHGQNIQLMPKSKNDPVQLATIKRGGTIR 60
DB MERCLITNGSADDTWIDCKRFTVASTVQWFMKFTINPQSAIVLAASGNPRITLL 436
QY 317 NDDVTCDEPTVRIYGRNGLCVDVDRFHNGNAIQMPCKSNTPANQLMTLKRNTIR 376
DB NDDVTCDEPTVRIYGRNGLCVDVDRFHNGNAIQMPCKSNTPANQLMTLKRNTIR 376
QY 61 NSCLTIVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGIKGTLIVOTL 120
DB NSCLTIVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGKTLIVOTN 123
QY 121 VDTLITVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGIKGTLIVOTL 180
DB VDTLITVGTAGYVWIPDQNTAREATIQIMDNGTIINRSNVLAASSGKTLIVOTN 180
QY 437 VQNIYIARQWMLPATKNGKQWMLPVF 495
DB GSIRPRQNDQCLTSGRDSVSTVIVVSCGASGSGQWFTNBSGAILNKNGLANDVQA 239

Db 496 GSIRPHODRCLITSDHSGSIIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 555
 QY 240 AMPCLRRITIIYPATKRNQMWLPY 263
 Db 556 SPSPLHQIILIMPATKRNQMWLP 579

RESULT 9

Q94BM3 PRELIMINARY; PRT; 580 AA.

AC Q94BM3 (TREMBLrel. 19, Created)
 DN 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin III precursor
 DB (EC 3.2.2.2) (RNA N-Glycosylase)
 OS Cinnamomum camphora (camphor tree)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxId=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomin proteins and study of their expression
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AY039803; AA02460.1; -
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; R1P.
 DR Pfam: PF00652; R1P; 1.
 DR Pfam: PF00161; R1P; 1.
 DR PRINTS: SM00458; SHIGARICIN.
 DR SMART: SM00458; R1CIN; 2.
 DR PROSITE: PS00231; R1CIN_B_LECTIN; 2.
 DR HYDROLASE; Signal; 1; 32.
 FT SIGNAL 1 32
 FT CHAIN 33 580 POTENTIAL
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMIN III
 SQ SEQUENCE 580 AA; 64421 MW; 9400109107P8558 CRC64;

Query Match 61.3%; Score 869; DB 10; Length 580;
 Best Local Similarity 62.9%; Pred. No. 1.9e-64;
 Matches 169; Conservative 33; Mismatches 63; Indels 2; Gaps 2;

QY 1 DDTTCASAEPTIVYENKRDYRDDPHDQICLMPKSNNDQWLTKDGTGS 60
 Db 317 NDTCADPEPTVLSGNSGICVDKCKRKNRNPIDLMFCQKSDVQQLWTFRDGATIS 376
 QY 61 NSCLITNGYSAGDYVWIDCRFTVPAISVQFPMNGIINQSAVLVSAESGNRTLT 120
 Db 377 NGCLITNGYSAGDYVWIDCRFTVPAISVQFPMNGIINQSAVLVSAESGNRTLT 436
 QY 121 VQTLDTYLAGQMLAGNDIAPREVTIYGRDLCASNSGSAWYFPCSSQKQKVALYGD 180
 Db 437 VQDLTYASQKMLAGNDIAPREVTIYGRDLCQKQNDAMWVVESSKAEQ-KVALYGD 495
 QY 181 GSIRPHODRCLITSDHSGSIIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 239
 Db 496 GSIRPHODRCLITSDHSGSIIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 555
 QY 240 AMPCLRRITIIYPATKRNQMWLPY 263
 Db 556 SPSPLHQIILIMPATKRNQMWLP 579

RESULT 10
 Q94BV22 PRELIMINARY; PRT; 549 AA.

AC Q94BV22
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinnamomin IEC 3.2.2.22 (RNA
 DE N-glycosylase) (fragment)
 DB Cinnamomum camphora (camphor tree)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxId=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RT Molecular cloning of cinnamomin A-, B-chain and the expression,
 RT purification, characterization and mutagenesis of the A-chain.
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AF02873; 2AAT
 DR HSPB: P02873; 2AAT
 DR InterPro: IPR000772; R1CIN_B_lectin.
 DR InterPro: IPR001574; R1P.
 DR Pfam: PF00652; R1CIN_B_lectin; 5.
 DR Pfam: PF00161; R1P; 1.
 DR PRINTS: SM00396; SHIGARICIN.
 DR SMART: SM00458; R1CIN; 2.
 DR PROSITE: PS00231; R1CIN_B_LECTIN; 2.
 DR HYDROLASE; Toxin; 1.
 FT SIGNAL 1 1
 FT NON-TER 1 1
 SQ SEQUENCE 549 AA; 60648 MW; 02607BE607C44B0 CRC64;

Query Match 58.6%; Score 830.5; DB 10; Length 549;
 Best Local Similarity 60.0%; Pred. No. 3e-61; 71; Indels 3; Gaps 2;
 Matches 159; Conservative 32; Mismatches 71; Indels 3; Gaps 2;

QY 1 DDTTCASAEPTIVYENKRDYRDDPHDQICLMPKSNNDQWLTKDGTGS 60
 Db 285 NDTCADPEPTVLSGNSGICVDKCKRKNRNPIDLMFCQKSDVQQLWTFRDGATIS 344
 QY 61 NSCLITNGYSAGDYVWIDCRFTVPAISVQFPMNGIINQSAVLVSAESGNRTLT 120
 Db 345 NGCLITNGYSAGDYVWIDCRFTVPAISVQFPMNGIINQSAVLVSAESGNRTLT 404
 QY 121 VQTLDTYLAGQMLAGNDIAPREVTIYGRDLCASNSGSAWYFPCSSQKQKVALYGD 180
 Db 405 VQDLTYASQKMLAGNDIAPREVTIYGRDLCQKQNDAMWVVESSKAEQ-KVALYGD 463
 QY 181 GSIRPHODRCLITSDHSGSIIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 238
 Db 464 GSIRPHODRCLITSDHSGSIIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 523
 QY 239 AMPCLRRITIIYPATKRNQMWLPY 263
 Db 524 SPSPLHQIILIMPATKRNQMWLP 548

RESULT 11
 Q94BW5 PRELIMINARY; PRT; 581 AA.

AC Q94BW5
 DN 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor
 DB (EC 3.2.2.2) (RNA N-Glycosylase)
 OS Cinnamomum camphora (camphor tree)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxId=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;

RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamom protein and study of their expression
RT patterns "JUN-2001" to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039801; AK82458.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00161; Ricin_B_lectin; 5.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR Hydrolase; Signal; Toxin.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 581 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
SQ SEQUENCE 581 AA; 64215 MW; 688F8F89A3D196 CRC64;
Query Match 581 AA; Score 830.5; DB 10; Length 581;
Best Local Similarity 54.8%; Pred No. 1e-55;
Matches 159; Conservative 32; Mismatches 71; Indels 3; Gaps 2;
QY 1 DPTVCSAEPYRIVGNRGRVDVDDPHQNOQLMPKSNNDPQOLMTIRKDGTRIS 60
DB 317 NDDTADPEPTVIRISGRNGCDVDKXNNKNIQLMPKSNNDPQOLMTIRKDGTRIS 376
QY 61 NSCLTYGYTAGVYVIMPCNTAVRENTIQTWNGTINRSNLTVAASSGKQTLTVT 120
DB 377 NKKCLTNGISASGVYVIMPCNTAVRENTIQTWNGTINRSNLTVAASSGKQTLTVT 436
QY 121 VOTDITAGCGLACNTAPRATVYGRPCVMSGSGVYVYTCSSQRCRNLAYKQ 180
DB 437 VQNTVYASRQGLASGNTPEPTGISVGFNDLQNGAGQMTVEEESKATQ KVALTPD 495
QY 181 GSIRKQND--QCLTSGDSVSVYVIVYSCGASGQVFTNBAIINIKNGIAMDVA 238
DB 496 GSIRHODPGPACPLDNRHOGSIIIISSCSFGSGRVRVPMDDGYVNLKGLAMDVA 555
QY 239 QANPEKRIIIVPATGKNOMLVP 263
DB 556 GSNVSHQIILIPATGKNEHMLD 580
RESULT 12
ID Q06076 PRELIMINARY; PRT; 528 AA.
AC Q06076;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 23, Last annotation update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Abtin-d (EC 3.2.2.22) (rRNA N-glycosidase) (fragment).
OS Abtin precatorius (Indian Ilicorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Embryophyta; Embryophyta; core eudicots; Rosidae;
OC eucoside I; Fabales; Fabaceae; Papilionoideae; Aboaceae; Abrus.
OC NCBI_Taxid:3816;
RN [1] Textid:3816;
RP SEQUENCE FROM N.A.
RX MEDLINE=93132798; PubMed=8423113;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isobins determined by cDNA
RT sequencing: conservation and significance";
RL J. Mol. Biol. 229:263-267(1999).
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: N93146; AA3266.1; -
DR HSPF; P1140; 1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.

DR Pfam: PF00652; Ricin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGARICIN; 1.
KM Hydrolase; Toxin.
FT NON_TER 1 1
FT NON_TER 528 528
SQ SEQUENCE 528 AA; 58870 MW; 62ED42F88F860F8 CRC64;
Query Match 528 AA; Score 764; DB 10; Length 528;
Best Local Similarity 54.8%; Pred No. 1e-55;
Matches 143; Conservative 45; Mismatches 71; Indels 2; Gaps 2;
QY 5 CSAS-EPYRIVGNRGRVDVDDPHQNOQLMPKSNNDPQOLMTIRKDGTRIS 63
DB 269 CSRYEPYRIVGNRGRVDVDDPHQNOQLMPKSNNDPQOLMTIRKDGTRIS 328
QY 64 CLTYGYTAGVYVIMPCNTAVRENTIQTWNGTINRSNLTVAASSGKQTLTVT 123
DB 329 CLTYRIPENYVIMPCNTAVRENTIQTWNGTINRSNLTVAASSGKQTLTVT 388
QY 124 LDPTLACGNTACNTAPRATVYGRPCVMSGSGVYVYTCSSQRCRNLAYKQ 183
DB 389 NEVLAHQMTNNTSPEPTGISVGFNDLQNGAGQMTVEEESKATQ QVALTVTGGI 447
QY 184 PRKQNDQCLTSGDSVSVYVIVYSCGASGQVFTNBAIINIKNGIAMDVAQAKR 243
DB 448 RSVQNTNCLTSGKQSGPYVLAACSGNAAQSCPLKNDISIVLYDQWMDVAGSDS 507
QY 244 LRLIIVPATGKNOMLVP 264
DB 508 LKQIILIPATGKNEHMLD 528
RESULT 13
ID Q8S443 PRELIMINARY; PRT; 382 AA.
AC Q8S443;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Abtin isoform G (EC 3.2.2.22) (rRNA N-glycosidase)
DB (fragment).
OS Abtin precatorius (Indian Ilicorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Embryophyta; Embryophyta; core eudicots; Rosidae;
OC eucoside I; Fabales; Fabaceae; Papilionoideae; Abroaceae; Abrus.
OC NCBI_Taxid:3816;
RN [1] Textid:3816;
RP SEQUENCE FROM N.A.
RX TISSUE=Leaf;
RA Cook J.P., Roberts L.M., Lord M.;
RT "New isoform of Abtin - Abtin G";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF479626; AL077434.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; Ricin_B_lectin; 5.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGARICIN; 1.
KM Hydrolase; Toxin.
FT NON_TER 1 1
FT NON_TER 382 382
SQ SEQUENCE 382 AA; 42743 MW; 808AB341813AD2EE CRC64;
ABTIN A CHAIN.
ABTIN B CHAIN.

Query Match 52.9%, Score 750.5, DB 10, Length 382,
Best Local Similarity 54.3%, Pred. No. 9, 4e-55,
Matches 139, Conservative 42, Mismatches 74, Indels 1, Gaps 1;
QY 9 EPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGCTIT 68
DB 128 EPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGCTIT 187
QY 69 GTTAGYVWIPDCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 128
DB 188 GYDGVYWIYDCTSAVBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 247
QY 129 GQWLAGNTAPRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 188
DB 248 RQWRTGNDISPTVTSINGSDICMAHSMWMLADCTRRKED-QWALYDGSIRPVON 306
QY 189 QDQCTSGSDSVTVINISGSGSGSQWFTTTEALITKGLANDYQANPELARI 248
DB 307 TNNCTISDQKQSTIVMGSGNMGASQWFTNDGSGVSLVDWMDYVDSGSPSLQII 366
QY 249 IYPATGKRPQWMLPVF 264
DB 367 LWPYTKRPQWMLPVF 382
RESULT 14
QY 10 Q8M288 PRELIMINARY, PRT, 547 AA.
AC Q8M288
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproa9glutinin (EC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Abrys precatorius (Indian lileoide) (Creb's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Adrue.
RX NCBL_taxid=3816;
RP SEQUENCE FROM N.A.
RA MEDLINB-20102702, PubMed=10636890,
RA Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Huang M.T.,
RA Lin J.Y.,
RT "Primary Structure and Function Analysis of the Abrys precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Proofs of Amphiphilic
RT alpha-Helix H Impacts Protein Synthesis Inhibitory Activity.";
RT J. Biol. Chem. 275:1897-1901(2000).
CC -1- CATALYTIC ACTIVITY: ENDOPHYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AF190173, A128309.1, -.
DR HSBP: P11140, IABR.
DR InterPro: IPR000772, Ricin_B_lectin.
DR InterPro: IPR001574, RIP.
DR Pfam: PF00652, Ricin_B_lectin, 6.
DR Pfam: PF00161, RIP, 1.
DR PRINTS: PR00396, SHIGARICIN.
DR SMART: SM00458, RICIN, 2.
DR PROSITE: PS00231, RICIN_B_LECTIN, 2.
DR PROSITE: PS00275, SHIGARICIN, 1.
KW Ricinase; toxin.
SQ SEQUENCE 547 AA, 61248 MW, 355432623541AD CRC64;
Query Match 52.9%, Score 750, DB 10, Length 547,
Best Local Similarity 54.0%, Pred. No. 1, 6e-54,
Matches 141, Conservative 41, Mismatches 77, Indels 2, Gaps 2;
QY 5 CSAS-EPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGS 63
DB 288 CSSEHPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGS 347

QY 64 CLTYGYTAGYVWIPDCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOT 123
DB 348 CLTYGYTAGYVWIPDCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOT 407
QY 124 LDYTAGQWLAGNTAPRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 183
DB 408 NDRRQSGKRTGNDISPTVTSINGSDICMAHSMWMLADCTRRKED-QWALYDGSIR 466
QY 184 RPKWNOQCTSGSDSVTVINISGSGSGSQWFTTTEALITKGLANDYQANPELARI 243
DB 467 RPKWNOQCTSGSDSVTVINISGSGSGSQWFTTTEALITKGLANDYQANPELARI 526
QY 244 LRRTIYPATGKRPQWMLPVF 264
DB 527 LKQIILWPYTKRPQWMLPVF 547
RESULT 15
QY 10 Q8M288 PRELIMINARY, PRT, 573 AA.
AC Q8M288
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein Itax (EC 3.2.2.22) (rRNA N-glycosidase).
GN LECTINAR.
OS Itax hollandica (Dutch Itax).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Itidaceae;
OC Itis.
RX NCBL_taxid=35876;
RP SEQUENCE FROM N.A.
RA Van Damme E, J.M., Pennane M.J.,
RT "Itis (Itax hollandica var. Professor Blaauw) plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";
RT Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOPHYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AF256084, AAL55093.1, -.
DR InterPro: IPR000772, Ricin_B_lectin.
DR InterPro: IPR001574, RIP.
DR Pfam: PF00652, Ricin_B_lectin, 6.
DR Pfam: PF00161, RIP, 1.
DR PRINTS: PR00396, SHIGARICIN.
DR SMART: SM00458, RICIN, 2.
DR PROSITE: PS00231, RICIN_B_LECTIN, 2.
DR PROSITE: PS00275, SHIGARICIN, 1.
KW Hydroxylase; toxin.
SQ SEQUENCE 573 AA, 63759 MW, 1414392942CD4F5C CRC64;
Query Match 47.9%, Score 679.5, DB 10, Length 573,
Best Local Similarity 50.2%, Pred. No. 1, 4e-48,
Matches 139, Conservative 40, Mismatches 89, Indels 3, Gaps 3;
QY 1 DQVTSSEPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGS 60
DB 311 EDPTSPSEPTVRIYVNGKGVYDDEPHDNGIQIAPSSKNDPQWITIKRGTISNGS 370
QY 61 NSGCLTYGYTAGYVWIPDCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOT 120
DB 371 NSGCLTYGYTAGYVWIPDCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOT 429
QY 121 VQYLYTAGQWLAGNTAPRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 179
DB 430 MQYLYTAGQWLAGNTAPRBAKTIWQINDGTIIPRSNLYAASSGKGTITVOTDYL 488
QY 180 DSGIRPQWNOQCTSGSDSVTVINISGSGSGSQWFTTTEALITKGLANDYQANPELARI 239
DB 489 DSGIRPQWNOQCTSGSDSVTVINISGSGSGSQWFTTTEALITKGLANDYQANPELARI 548

Thu Dec 11 16:10:05 2003

Page 8

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Qy      240 ANPLRRIIITPATGNGNKKLWVF 264
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Db      549 SDPLQIILWSTGNGNKKWFTTF 573
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 Job time : 20.3487 secs

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 26.0964 Seconds
[without alignments]
1506.345 Million cell updates/sec

Title: US-09-601-667C-7
Perfect score: 1418
Sequence: 1 DWTCSAASEPTVRIKRNQM.....RRIITVPAKGNQNMPEVF 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database: A: Geneseq_13jun03.*

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	length	DB	ID	Description
1	1418	100.0	264	20	AAV25985	Mistletoe lectin B
2	1418	100.0	264	20	AAV25982	Mistletoe lectin B
3	1412	99.6	264	20	AAV25988	Mistletoe lectin B
4	1412	99.6	264	20	AAV25994	Mistletoe lectin B
5	1405	99.1	264	20	AAV25989	Mistletoe lectin B
6	1405	99.1	264	20	AAV25995	Mistletoe lectin B
7	1403	98.9	264	20	AAV25990	Mistletoe lectin B
8	1403	98.9	264	20	AAV25996	Mistletoe lectin B
9	1379	97.2	264	20	AAV25987	Mistletoe lectin B

10	1379	97.2	265	20	AAV25993	Mistletoe lectin B
11	1339.5	94.5	263	20	AAV25985	Mistletoe lectin B
12	1339.5	94.5	264	20	AAV25991	Mistletoe lectin B
13	1339.5	94.5	531	20	AAV25979	Mistletoe lectin I
14	1339.5	94.5	532	20	AAV25982	Mistletoe lectin I
15	1333.5	94.0	263	19	AAV25982	Mistletoe lectin I
16	1333.5	94.0	264	19	AAV25982	Mistletoe lectin I
17	1333.5	94.0	267	19	AAV25982	Mistletoe lectin I
18	1333.5	94.0	267	19	AAV25982	Mistletoe lectin I
19	1333.5	94.0	564	18	AAV25982	Mistletoe lectin I
20	1333.5	94.0	564	18	AAV25982	Mistletoe lectin I
21	1290	91.0	264	20	AAV25978	Mistletoe lectin B
22	1290	91.0	264	20	AAV25978	Mistletoe lectin B
23	1290	91.0	264	20	AAV25975	Mistletoe lectin B
24	1290	91.0	533	20	AAV25970	Mistletoe lectin B
25	1290	91.0	533	20	AAV25973	Mistletoe lectin B
26	1290	91.0	533	20	AAV25976	Mistletoe lectin B
27	1290	91.0	533	20	AAV25977	Mistletoe lectin B
28	1290	91.0	533	20	AAV25978	Mistletoe lectin B
29	1290	91.0	533	20	AAV25979	Mistletoe lectin B
30	1058.5	74.5	551	23	AAV25950	Mistletoe lectin B
31	1005	70.9	286	22	AAV25993	Mistletoe lectin B
32	909.5	64.1	565	6	AAV25986	Mistletoe lectin B
33	909.5	64.1	565	22	AAV25980	Mistletoe lectin B
34	907.5	64.0	574	8	AAV25984	Mistletoe lectin B
35	907.5	64.0	574	10	AAV25985	Mistletoe lectin B
36	907.5	64.0	574	18	AAV25987	Mistletoe lectin B
37	907.5	64.0	576	20	AAV25989	Mistletoe lectin B
38	907.5	64.0	576	20	AAV25992	Mistletoe lectin B
39	907.5	64.0	576	22	AAV25993	Mistletoe lectin B
40	907.5	64.0	576	22	AAV25994	Mistletoe lectin B
41	907.5	64.0	576	22	AAV25995	Mistletoe lectin B
42	902.5	63.6	565	7	AAV25980	Mistletoe lectin B
43	901.5	63.4	282	10	AAV25980	Mistletoe lectin B
44	898.5	62.9	282	10	AAV25986	Mistletoe lectin B
45	891.5	62.9	576	8	AAV25986	Mistletoe lectin B

ALIGNMENTS

RESULT 1	AAV25986	standard; Protein; 264 AA.
ID	AAV25986	
AC	AAV25986	
XX	18-OCT-1999 (first entry)	
DT	Mistletoe lectin B1 protein fragment.	
DE		
XX	Mistletoe lectin, antitumour; immunostimulant; A-chain; MAb; immunit	
KM	induces 28S subunit; non-cytotoxic; antitumour; immunostimulant; B	
KM	chain; cytotoxicity; antigen; isoenzym; lectin B1.	
KW	Vaccum album.	
XX		
XX	DE19804210-A1.	
PN		
PD	12-AUG-1999.	
XX		
PF	03-FEB-1998; 98DE-1004210.	
XX		
XX	03-FEB-1998; 98DE-1004210.	
PA	(BLOS-) BIOSYN ARZNMNITTEL GMBH.	
XX		
PI	Morris P, Stiefel T, Voelker W, Wolters P;	
XX	WPI, 1999-45335/38.	
DR	N-PDB: AA209110.	
XX		

PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

XX Claim 9, Fig 8b; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B1 protein.

XX Sequence 264 AA;

XX Query Match 100.0%; Score 1418; DB 20; Length 264;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-131;
 XX Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVAVIGRNGKGVVDVDDPHDGNQIQLPKSKNDPNQMLTTRKDGTRIS 60
 DB 1 DDVTCASAEPTVAVIGRNGKGVVDVDDPHDGNQIQLPKSKNDPNQMLTTRKDGTRIS 60
 QY 61 NSGCLTFTGTAAGVYVAFPCNTAVRERATVQIMDNGTIIIPRSNLYLAASGIGKRTLT 120
 DB 61 NSGCLTFTGTAAGVYVAFPCNTAVRERATVQIMDNGTIIIPRSNLYLAASGIGKRTLT 120
 QY 121 VQTLDDYTLGGWLAGNDTAPREVTIYGFDDCHESNGSVWETCDSSOROKGKALYGD 180
 DB 121 VQTLDDYTLGGWLAGNDTAPREVTIYGFDDCHESNGSVWETCDSSOROKGKALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNBSAIIINLKGALMDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNBSAIIINLKGALMDVQA 240
 QY 241 NPKLRRIITYPATCKGNQMLPVF 264
 DB 241 NPKLRRIITYPATCKGNQMLPVF 264

RESULT 2
 AAY25992
 ID AAY25992 standard; Protein; 265 AA.
 AC AAY25992;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B1 variant protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B1.

XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) EIOGYN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelster W, Walters P.
 XX WtJ; 1999-44535/38.
 DR N-FSDB; AA609116.

XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 14b; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B1 protein.

XX Sequence 265 AA;

XX Query Match 100.0%; Score 1418; DB 20; Length 265;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-131;
 XX Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVAVIGRNGKGVVDVDDPHDGNQIQLPKSKNDPNQMLTTRKDGTRIS 60
 DB 1 DDVTCASAEPTVAVIGRNGKGVVDVDDPHDGNQIQLPKSKNDPNQMLTTRKDGTRIS 60
 QY 61 NSGCLTFTGTAAGVYVAFPCNTAVRERATVQIMDNGTIIIPRSNLYLAASGIGKRTLT 120
 DB 61 NSGCLTFTGTAAGVYVAFPCNTAVRERATVQIMDNGTIIIPRSNLYLAASGIGKRTLT 120
 QY 121 VQTLDDYTLGGWLAGNDTAPREVTIYGFDDCHESNGSVWETCDSSOROKGKALYGD 180
 DB 121 VQTLDDYTLGGWLAGNDTAPREVTIYGFDDCHESNGSVWETCDSSOROKGKALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNBSAIIINLKGALMDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNBSAIIINLKGALMDVQA 240
 QY 241 NPKLRRIITYPATCKGNQMLPVF 264
 DB 241 NPKLRRIITYPATCKGNQMLPVF 264

RESULT 3
 AAY25988
 ID AAY25988 standard; Protein; 264 AA.
 AC AAY25988;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B3 protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B3.

XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX WPI: 1999-445325/38.
 XX N-PSDB: AA209112.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 10B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a mistletoe lectin B3 protein.
 XX Sequence 264 AA;
 XX
 XX Query Match 99.6%; Score 1412; DS 20; Length 264;
 XX Best Local Similarity 99.6%; Pred. No. 7.3e-131;
 XX Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 DDTVCASSEPTVRIYVGNKGRVDVDDPHDQNOIQWPSKSNDDPQWLTIKEDTIRS 60
 XX 1 DDTVCASSEPTVRIYVGNKGRVDVDDPHDQNOIQWPSKSNDDPQWLTIKEDTIRS 60
 XX 61 NSGCTITGYTGAQVYVIMPCNTVREATVQIWDNGTINFRSNVLAASGIGKTTLT 120
 XX 61 NSGCTITGYTGAQVYVIMPCNTVREATVQIWDNGTINFRSNVLAASGIGKTTLT 120
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX
 XX RESULT 4
 XX AAY25994
 XX ID AAY25994 standard; Protein; 265 AA.
 XX AC AAY25994;
 XX 18-OCT-1999 (first entry)
 XX DT
 XX DT Mistletoe lectin B3 variant protein fragment.
 XX KM Mistletoe, lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 XX KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX KM cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX
 XX Viscum album.

XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX WPI: 1999-445325/38.
 XX N-PSDB: AA209118.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 16B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B3 protein.
 XX Sequence 265 AA;
 XX
 XX Query Match 99.6%; Score 1412; DS 20; Length 265;
 XX Best Local Similarity 99.6%; Pred. No. 7.3e-131;
 XX Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 DDTVCASSEPTVRIYVGNKGRVDVDDPHDQNOIQWPSKSNDDPQWLTIKEDTIRS 60
 XX 1 DDTVCASSEPTVRIYVGNKGRVDVDDPHDQNOIQWPSKSNDDPQWLTIKEDTIRS 60
 XX 61 NSGCTITGYTGAQVYVIMPCNTVREATVQIWDNGTINFRSNVLAASGIGKTTLT 120
 XX 61 NSGCTITGYTGAQVYVIMPCNTVREATVQIWDNGTINFRSNVLAASGIGKTTLT 120
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 121 VQTLDTYLLGGMLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALVGD 180
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRVVFNSGALINKGLAMDVQA 240
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX 241 NPKLRRIITVPATGKQNMALPVP 264
 XX
 XX RESULT 5
 XX AAY25989
 XX ID AAY25989 standard; Protein; 264 AA.
 XX AC AAY25989;
 XX 18-OCT-1999 (first entry)
 XX DT
 XX DT Mistletoe lectin B4 protein fragment.
 XX KM Mistletoe, lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 XX KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-445335/38.
 XX DR N-PSDB; AA209113.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 11b; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancer), and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen production of the
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a mistletoe lectin B4 protein.
 XX
 XX Sequence 264 AA;
 XX
 XX Query Match 99.1%; Score 1405; DB 20; Length 264;
 XX Best Local Similarity 99.2%; Pred. No. 3.6e-130;
 XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 DDTVCSASEPTVAVIVGNKGVAVYRDDDPHGNQQLMPKSNNDPQQLATIKKIDGRTS 60
 XX 1 DDTVCSASEPTVAVIVGNKGVAVYRDDDPHGNQQLMPKSNNDPQQLATIKKIDGRTS 60
 XX
 XX 61 NGSCITVGTAGVYVMAIPDONTAVENATIMQNDGTTINRSNLYLAASSGIKKTTT 120
 XX 61 NGSCITVGTAGVYVMAIPDONTAVENATIMQNDGTTINRSNLYLAASSGIKKTTT 120
 XX
 XX 121 VQTLDTYLGGQMLANGDTAPREVTIYGFQDLCHESGSGSWVETCDSSQKQWALYGD 180
 XX 121 VQTLDTYLGGQMLANGDTAPREVTIYGFQDLCHESGSGSWVETCDSSQKQWALYGD 180
 XX
 XX 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWVETNEGAILNLKGPAMDVAQA 240
 XX 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWVETNEGAILNLKGPAMDVAQA 240
 XX
 XX 241 NPKLRRLIIVPATGKPNQWMLPVF 264
 XX 241 NPKLRRLIIVPATGKPNQWMLPVF 264
 XX
 XX RESULT 6
 XX AA255995
 XX ID AA255995 standard; Protein; 265 AA.
 XX AC AA255995;
 XX XX
 XX 18-OCT-1999 (first entry)

XX
 XX Mistletoe lectin B4 variant protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-445335/38.
 XX DR N-PSDB; AA209113.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 17b; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancer), and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen production of the
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B4 protein.
 XX
 XX Sequence 265 AA;
 XX
 XX Query Match 99.1%; Score 1405; DB 20; Length 265;
 XX Best Local Similarity 99.2%; Pred. No. 3.6e-130;
 XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 DDTVCSASEPTVAVIVGNKGVAVYRDDDPHGNQQLMPKSNNDPQQLATIKKIDGRTS 60
 XX 1 DDTVCSASEPTVAVIVGNKGVAVYRDDDPHGNQQLMPKSNNDPQQLATIKKIDGRTS 60
 XX
 XX 61 NGSCITVGTAGVYVMAIPDONTAVENATIMQNDGTTINRSNLYLAASSGIKKTTT 120
 XX 61 NGSCITVGTAGVYVMAIPDONTAVENATIMQNDGTTINRSNLYLAASSGIKKTTT 120
 XX
 XX 121 VQTLDTYLGGQMLANGDTAPREVTIYGFQDLCHESGSGSWVETCDSSQKQWALYGD 180
 XX 121 VQTLDTYLGGQMLANGDTAPREVTIYGFQDLCHESGSGSWVETCDSSQKQWALYGD 180
 XX
 XX 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWVETNEGAILNLKGPAMDVAQA 240
 XX 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWVETNEGAILNLKGPAMDVAQA 240
 XX
 XX 241 NPKLRRLIIVPATGKPNQWMLPVF 264
 XX 241 NPKLRRLIIVPATGKPNQWMLPVF 264
 XX
 XX RESULT 7
 XX AA255990

ID AAV25990 standard; Protein; 264 AA.
XX
AC AAV25990;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B5 protein fragment.
XX
KW Mistletoe; lectin; antitumor; immunostimulant; B-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
OS Viscum album.
XX
DE19804210-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX
PR 03-FEB-1998; 98DE-1004210.
XX
PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-445335/38.
XX
DR N-PSDB; AA209114.
XX
PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 12b; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC mistletoe lectins in heterologous systems, particularly in yeast
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B5 protein.
XX
SQ Sequence 264 AA;
XX
Query Match 98.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 98.9%; Pred. No. 5,6e-130;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 DDTGCSASBPFTVRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIKEDGTRIS 60
DB 1 DDTGCSASBPFTVRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIKEDGTRIS 60
QY 61 NSGCLTGYTAGYVYWIIPDCNFAVEKATIQIMNGNTIIPRSNLVLAASGKIKTTLT 120
DB 61 NSGCLTGYTAGYVYWIIPDCNFAVEKATIQIMNGNTIIPRSNLVLAASGKIKTTLT 120
QY 121 VQTLDDYTLGGWLAGNDIAPEEVTIYGRPDLCESNGSSWVWZTDSOGKMAIYGD 180
DB 121 VQTLDDYTLGGWLAGNDIAPEEVTIYGRPDLCESNGSSWVWZTDSOGKMAIYGD 180
QY 181 GSIRKONODCLTSGRDSVSTVINIVSCGASGSGRWFTFEGALINLKNGLAMVQA 240
DB 181 GSIRKONODCLTSGRDSVSTVINIVSCGASGSGRWFTFEGALINLKNGLAMVQA 240
QY 241 NPKLRRIITVPATGKPNQWMLPVE 264
DB 241 NPKLRRIITVPATGKPNQWMLPVE 264

Db 241 NPKLRRIITVPATGKPNQWMLPVE 264
XX
RESULT 8
XX AAV25996
ID AAV25996 standard; Protein; 265 AA.
XX
AC AAV25996;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B5 variant protein fragment.
XX
KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
OS Viscum album.
XX
DE19804210-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX
PR 03-FEB-1998; 98DE-1004210.
XX
PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-445335/38.
XX
DR N-PSDB; AA209120.
XX
PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 18b; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC mistletoe lectins in heterologous systems, particularly in yeast
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B5 protein.
XX
SQ Sequence 265 AA;
XX
Query Match 98.9%; Score 1403; DB 20; Length 265;
Best Local Similarity 98.9%; Pred. No. 5,7e-130;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 DDTGCSASBPFTVRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIKEDGTRIS 60
DB 1 DDTGCSASBPFTVRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIKEDGTRIS 60
QY 61 NSGCLTGYTAGYVYWIIPDCNFAVEKATIQIMNGNTIIPRSNLVLAASGKIKTTLT 120
DB 61 NSGCLTGYTAGYVYWIIPDCNFAVEKATIQIMNGNTIIPRSNLVLAASGKIKTTLT 120
QY 121 VQTLDDYTLGGWLAGNDIAPEEVTIYGRPDLCESNGSSWVWZTDSOGKMAIYGD 180
DB 121 VQTLDDYTLGGWLAGNDIAPEEVTIYGRPDLCESNGSSWVWZTDSOGKMAIYGD 180
QY 181 GSIRKONODCLTSGRDSVSTVINIVSCGASGSGRWFTFEGALINLKNGLAMVQA 240
DB 181 GSIRKONODCLTSGRDSVSTVINIVSCGASGSGRWFTFEGALINLKNGLAMVQA 240

Db 181 GSIRPRKQNDCLTSRSDSVSTVINISCSGASGSGRWFTNEGAILNKGLANDVAQA 240
 QY 241 NPKLRRIIYPATGKPNQMWLPVF 264
 Db 241 NPKLRRIIYPATGKPNQMWLPVF 264

RESULT 9

AAZ5987
 ID AAZ5987 standard; Protein; 284 AA.

AC AAZ5987;
 XX

DT 18-OCT-1999 (first entry)
 XX

DE Mistletoe lectin B2 protein fragment.
 XX

KX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 XX

KW ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
 XX

KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX

KV cancer; cytotoxicity; antigen; isoform; lectin B2.
 XX

OS Viscum album.
 XX

PN DE19804210-A1.
 XX

PD 12-AUG-1999.
 XX

PF 03-FEB-1998; 98DE-1004210.
 XX

PE 03-FEB-1998; 98DE-1004210.
 XX

PR (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PS Morris P, Stiefel T, Voelter W, Welters P;
 XX

PI WPI; 1999-445335/38.
 XX

PT N-PSDB; AA209111.
 XX

PS Preparation of mistletoe lectins in heterologous systems,
 XX

PT particularly for use as anticancer agents and immunostimulants
 XX

PS Claim 9; Fig 9b; 78pp; German.
 XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)

CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly

CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin and its individual chains and different derivatives

CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence

CC represents a fragment of a mistletoe lectin B2 protein.
 XX

Sequence 264 AA;
 SQ

Query Match 97.2%; Score 1379; DB 20; Length 264;
 Best Local Similarity 97.7%; Pred. No. 1.3e-127;

Matches 259; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDTVCASSEPTVRIYAGKGRVDVADPDHFGNQICLMPKSNNDPNQMLTKIKNDITRS 60
 Db 1 DDTVCASSEPTVRIYAGKGRVDVADPDHFGNQICLMPKSNNDPNQMLTKIKNDITRS 60

QY 61 NGSCLITTYGTAGVYVAFDQCNVAKEATWQIMNDGTLIPRSNLYLAASGKIKTTLT 120
 Db 61 NGSCLITTYGTAGVYVAFDQCNVAKEATWQIMNDGTLIPRSNLYLAASGKIKTTLT 120

QY 121 VQTLDVTLGGGMLAGNQTAPREVTITGPRDLCMEANSGSYWTETCDSSQKQKQKALYGD 180
 Db 121 VQTLDVTLGGGMLAGNQTAPREVTITGPRDLCMEANSGSYWTETCDSSQKQKQKALYGD 180
 QY 181 GSIRPRKQNDCLTSRSDSVSTVINISCSGASGSGRWFTNEGAILNKGLANDVAQA 240
 Db 181 GSIRPRKQNDCLTSRSDSVSTVINISCSGASGSGRWFTNEGAILNKGLANDVAQA 240
 QY 241 NPKLRRIIYPATGKPNQMWLPVF 264
 Db 241 NPKLRRIIYPATGKPNQMWLPVF 264

RESULT 10

AAZ5993
 ID AAZ5993 standard; Protein; 265 AA.

AC AAZ5993;
 XX

DT 18-OCT-1999 (first entry)
 XX

DE Mistletoe lectin B2 variant protein fragment.
 XX

KX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 XX

KW ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
 XX

KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX

KV cancer; cytotoxicity; antigen; isoform; lectin B2.
 XX

OS Viscum album.
 XX

PN DE19804210-A1.
 XX

PD 12-AUG-1999.
 XX

PF 03-FEB-1998; 98DE-1004210.
 XX

PE 03-FEB-1998; 98DE-1004210.
 XX

PR (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PS Morris P, Stiefel T, Voelter W, Welters P;
 XX

PI WPI; 1999-445335/38.
 XX

PT N-PSDB; AA209111.
 XX

PS Preparation of mistletoe lectins in heterologous systems,
 XX

PT particularly for use as anticancer agents and immunostimulants
 XX

PS Disclosure; Fig 15b; 78pp; German.
 XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)

CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly

CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin and its individual chains, in many different isoforms

CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence

CC represents a fragment of a variant mistletoe lectin B2 protein.
 XX

Query Match 97.2%; Score 1379; DB 20; Length 265;
 Best Local Similarity 97.7%; Pred. No. 1.3e-127;

Matches 259; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDTVCASSEPTVRIYAGKGRVDVADPDHFGNQICLMPKSNNDPNQMLTKIKNDITRS 60
 Db 1 DDTVCASSEPTVRIYAGKGRVDVADPDHFGNQICLMPKSNNDPNQMLTKIKNDITRS 60

QY 61 NSCLTGYGTAGYVWIFPCNTAVREATIQTWNGTIIINPSNLVLAASSGIGKTTLT 120
 DB 61 NSCLTGYGTAGYVWIFPCNTAVREATIQTWNGTIIINPSNLVLAASSGIGKTTLT 120
 QY 121 VQILDYTLGGWLAGNDTAPREVTIYGFEDLCWESNGSFWETCSQKQKALYGD 180
 DB 121 VQILDYTLGGWLAGNDTAPREVTIYGFEDLCWESNGSFWETCSQKQKALYGD 180
 QY 181 GSIRPKNODCLTGRDSVSTVINIVSCGASGSRWFTNEGALTLKRGGLANDVAAQ 240
 DB 181 GSIRPKNODCLTGRDSVSTVINIVSCGASGSRWFTNEGALTLKRGGLANDVAAQ 240
 QY 241 NPKLRITIIYPAKNGKQNMWLPVF 264
 DB 241 NPKLRITIIYPAKNGKQNMWLPVF 264

RESULT 11
 AA25985
 AA25985 standard; Protein; 263 AA.
 AC AA25985;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B protein fragment.
 XX
 KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B.
 OS Viscum album.
 XX
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX PA Morris F, Stiefel T, Voelter W, Walters P;
 XX WPI; 1999-445335/38.
 XX DR N-PSDB; AA209109.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9; Fig 7B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.
 XX
 XX Sequence 263 AA;
 XX
 XX Query Match 94.5%; Score 1339.5; DA 20; Length 263;
 XX Best Local Similarity 95.8%; Prod. No. 18-123;

Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 1 DVVTCASBPVAVIVGNNGKAVDVDDDFDNGNQIQIAPSKSNNDPNQIWTIKROGTTT8 60
 DB 1 DVVTCASBPVAVIVGNNGKAVDVDDDFDNGNQIQIAPSKSNNDPNQIWTIKROGTTT8 60
 QY 61 NSCLTGYGTAGYVWIFPCNTAVREATIQTWNGTIIINPSNLVLAASSGIGKTTLT 120
 DB 61 NSCLTGYGTAGYVWIFPCNTAVREATIQTWNGTIIINPSNLVLAASSGIGKTTLT 120
 QY 121 VQILDYTLGGWLAGNDTAPREVTIYGFEDLCWESNGSFWETCSQKQKALYGD 180
 DB 121 VQILDYTLGGWLAGNDTAPREVTIYGFEDLCWESNGSFWETCSQKQKALYGD 180
 QY 181 GSIRPKNODCLTGRDSVSTVINIVSCGASGSRWFTNEGALTLKRGGLANDVAAQ 240
 DB 181 GSIRPKNODCLTGRDSVSTVINIVSCGASGSRWFTNEGALTLKRGGLANDVAAQ 240
 QY 241 NPKLRITIIYPAKNGKQNMWLPVF 263
 DB 241 NPKLRITIIYPAKNGKQNMWLPVF 263

RESULT 12
 AA25991
 AA25991 standard; Protein; 264 AA.
 AC AA25991;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B variant protein fragment.
 XX
 KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B.
 OS Viscum album.
 XX
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX PA Morris F, Stiefel T, Voelter W, Walters P;
 XX WPI; 1999-445335/38.
 XX DR N-PSDB; AA209115.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 13B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.

XX Sequence 264 AA;
SQ Query Match 94.5%; Score 1339.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 1e-123;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDVTGASBPVVAIVGNKMKRVDDPDRGNOIOLMPKSNNDPNOLMTIKROGTRIS 60
DB 1 DDVTGASBPVVAIVGNKMKRVDDPDRGNOIOLMPKSNNDPNOLMTIKROGTRIS 60

QY 61 NSCLTYYGTAGVYVWIPDCNTAVREKTIWQWNGTIIIPRSNLVLAASSGKGTLLT 120
DB 61 NSCLTYYGTAGVYVWIPDCNTAVREKTIWQWNGTIIIPRSNLVLAASSGKGTLLT 120

QY 121 VQTLDTLGGGMLAGNDTAPREVITVGFRLCMESNGSWVATCDSSQKQKMAVGD 180
DB 121 VQTLDTLGGGMLAGNDTAPREVITVGFRLCMESNGSWVATCDSSQKQKMAVGD 180

QY 181 GSIRPKONODCLTGRDSVSVINIVSCGASGSGQWVFTMGALINLKGGLADVQA 240
DB 181 GSIRPKONODCLTGRDSVSVINIVSCGASGSGQWVFTMGALINLKGGLADVQA 240

QY 241 NPKLRRIIIVPATGKPNQWMLPV 263
DB 241 NPKLRRIIIVPATGKPNQWMLPV 262

RESULT 13
AAV25979
ID AAV25979 standard; Protein; 531 AA.
XX AAV25979;
XX 18-OCT-1999 (first entry)
XX Mistletoe lectin I protein fragment.
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin I.
XX Viscum album.
XX DEL9804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX MPI; 1999-445335/38.
XX N-PSDB; AAZ09103.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 7, Fig 1b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a mistletoe lectin I protein fragment.
XX Sequence 531 AA;
SQ Query Match 94.5%; Score 1339.5; DB 20; Length 531;
Best Local Similarity 95.8%; Pred. No. 2e-123;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDVTGASBPVVAIVGNKMKRVDDPDRGNOIOLMPKSNNDPNOLMTIKROGTRIS 60
DB 269 DDVTGASBPVVAIVGNKMKRVDDPDRGNOIOLMPKSNNDPNOLMTIKROGTRIS 328

QY 61 NSCLTYYGTAGVYVWIPDCNTAVREKTIWQWNGTIIIPRSNLVLAASSGKGTLLT 120
DB 329 NSCLTYYGTAGVYVWIPDCNTAVREKTIWQWNGTIIIPRSNLVLAASSGKGTLLT 388

QY 121 VQTLDTLGGGMLAGNDTAPREVITVGFRLCMESNGSWVATCDSSQKQKMAVGD 180
DB 389 VQTLDTLGGGMLAGNDTAPREVITVGFRLCMESNGSWVATCDSSQKQKMAVGD 447

QY 181 GSIRPKONODCLTGRDSVSVINIVSCGASGSGQWVFTMGALINLKGGLADVQA 240
DB 448 GSIRPKONODCLTGRDSVSVINIVSCGASGSGQWVFTMGALINLKGGLADVQA 507

QY 241 NPKLRRIIIVPATGKPNQWMLPV 263
DB 508 NPKLRRIIIVPATGKPNQWMLPV 530

RESULT 14
AAV25982
ID AAV25982 standard; Protein; 532 AA.
XX AAV25982;
XX 18-OCT-1999 (first entry)
XX Mistletoe lectin I (variant) protein fragment.
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin I.
XX Viscum album.
XX DEL9804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX MPI; 1999-445335/38.
XX N-PSDB; AAZ09106.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 4b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (usually injected, particularly or viral). The method allows production of
 CC mistletoe lectin B, which is used in the treatment of cancer
 CC and on a large scale, at any time of the year. Recombinant
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 CC
 SQ Sequence 532 AA;

Query Match 94.5%; Score 1339.5; DB 20; Length 532;
 Best Local Similarity 95.8%; Pred. No. 2-be-123;

Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDVTCASBPPTVRIYGNMCMVDVRDDPFDNQIQIAMPKSNNDPQIWTIKRDTGIS 60
 DB 269 DDVTCASBPPTVRIYGNMCMVDVRDDPFDNQIQIAMPKSNNDPQIWTIKRDTGIS 328
 QY 61 NSCLITTYGTAGVYVNIPOCNVAREATTIQTQIMDEGTINPRSNVLAASSGIGITLT 120
 DB 329 NSCLITTYGTAGVYVNIPOCNVAREATTIQTQIMDEGTINPRSNVLAASSGIGITLT 388
 QY 121 VQTLDDYTLGGQMLAGNDTAPREVTIYGFRLCQESNGSNGSVWETCVSSQNGQ-RNALYGD 180
 DB 389 VQTLDDYTLGGQMLAGNDTAPREVTIYGFRLCQESNGSNGSVWETCVSSQNGQ-RNALYGD 447
 QY 181 GSIRPKNODCLTSGSDSVTVINIVSCASGSGQWFTNEGAILNLKXGLAMDVAQA 240
 DB 448 GSIRPKNODCLTSGSDSVTVINIVSCASGSGQWFTNEGAILNLKXGLAMDVAQA 507
 QY 241 NPKLRRIIIPATGKNQMLPEV 263
 DB 508 NPKLRRIIIPATGKNQMLPEV 530

RESULT 15

AA64662
 ID AA64662 standard; Protein; 263 AA.

AC AA64662;

DT 23-OCT-1998 (first entry)

DE Mistletoe rMLB variant protein.

XX Lectin B-chain; mistletoe; rMLB; fusion protein; effector; cytotoxic;
 KW intracellular; processing module; protease recognition; targeting module;
 KM internalisation; treatment; disorder; cell proliferation; activation;
 KM autoimmune disease; allergy; tumour; ricin; translocation.
 XX
 XX Viscum album.
 XX
 XX

FT Key Location/Qualifiers
 FT Protein 1..263
 FT /note= "partial protein"

XX MO829540-A2.

XX PD 09-JUL-1998.

XX 02-JAN-1998; 98WO-EP00009.

XX 02-JAN-1997; 97EP-0100012.

XX (BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.

XX Eck U, Schmidt A, Zinke H;

XX WFI; 1998-388122/33.

DR N-PSDB; AAV51344.

XX Nucleic acid encoding fusion protein containing mistletoe lectin A
 FT chain - useful for treatment of proliferative and autoimmune
 FT diseases, allergies and tumours
 XX
 XX Disclosure: Fig 1b'; 115pp; German.

CC This sequence represents a variant mistletoe lectin B-chain. rMLB. This
 CC sequence can be used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC covalently bonded to the processing module, able to bind specifically to
 CC the surface of a cell so as to mediate internalisation of the fusion
 CC protein. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated activation of cells, especially
 CC autoimmune disease, allergy and tumours. The proteins can be administered
 CC e.g. by injection or topically but especially by intravenous injection.
 CC e.g. by 300 mg/kg/day, or for ex vivo use at 1 pg to 500 ng/ml.
 CC Biotic fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the ML A-chain from the
 CC endoplasmic reticulum to the cytoplasm.
 XX

Sequence 263 AA;

Query Match 94.0%; Score 133.5; DB 19; Length 263;
 Best Local Similarity 95.4%; Pred. No. 4-be-123;

Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDVTCASBPPTVRIYGNMCMVDVRDDPFDNQIQIAMPKSNNDPQIWTIKRDTGIS 60
 DB 1 DDVTCASBPPTVRIYGNMCMVDVRDDPFDNQIQIAMPKSNNDPQIWTIKRDTGIS 60
 QY 61 NSCLITTYGTAGVYVNIPOCNVAREATTIQTQIMDEGTINPRSNVLAASSGIGITLT 120
 DB 61 NSCLITTYGTAGVYVNIPOCNVAREATTIQTQIMDEGTINPRSNVLAASSGIGITLT 120
 QY 121 VQTLDDYTLGGQMLAGNDTAPREVTIYGFRLCQESNGSNGSVWETCVSSQNGQ-RNALYGD 179
 DB 121 VQTLDDYTLGGQMLAGNDTAPREVTIYGFRLCQESNGSNGSVWETCVSSQNGQ-RNALYGD 179
 QY 181 GSIRPKNODCLTSGSDSVTVINIVSCASGSGQWFTNEGAILNLKXGLAMDVAQA 240
 DB 180 GSIRPKNODCLTSGSDSVTVINIVSCASGSGQWFTNEGAILNLKXGLAMDVAQA 239
 QY 241 NPKLRRIIIPATGKNQMLPEV 263
 DB 240 NPKLRRIIIPATGKNQMLPEV 262

Search completed: December 11, 2003, 14:07:43
 Job time : 26.0864 secs

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Qy 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 180
Db 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 179
Qy 181 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 240
Db 180 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 239
Qy 241 NPKLRITIIYPATGKPKQWMLFV 263
Db 240 NPKLRITIIYPATGKPKQWMLFV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/093470644
Sequence 10, US093470644
GENERAL INFORMATION:
APPLICANT: Eck, Jürgen
APPLICANT: Schmidt, Arno
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: ECT/EP98/00009
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: BE 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 94.0%; Score 133.5; DB 9; Length 267;
Best Local Similarity 95.4%; Pred. No. 6.9e-128;
Matches 251; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 DDVTCASEPTVIVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 60
Db 1 DDVTCASEPTVIVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 60
Qy 61 NNSCLTYGTAGVWIFPCNIVAEATIMQIWDGTTINPRSNLYLAASGIGTTLT 120
Db 61 NNSCLTYGTAGVWIFPCNIVAEATIMQIWDGTTINPRSNLYLAASGIGTTLT 120
Qy 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 180
Db 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 179
Qy 181 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 240
Db 180 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 239
Qy 241 NPKLRITIIYPATGKPKQWMLFV 263
Db 240 NPKLRITIIYPATGKPKQWMLFV 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Miliard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wainemacher, Robert W

Qy 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 180
Db 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 179
Qy 181 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 240
Db 180 GSIRPKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 239
Qy 241 NPKLRITIIYPATGKPKQWMLFV 263
Db 240 NPKLRITIIYPATGKPKQWMLFV 262

Query Match 64.0%; Score 907.5; DB 12; Length 576;
Best Local Similarity 63.8%; Pred. No. 6.5e-84;
Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;
Qy 5 GSASEPTVIVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 64
Db 318 GMPPELVIVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 377
Qy 65 LTTGYGTAGVWIFPCNIVAEATIMQIWDGTTINPRSNLYLAASGIGTTLT 124
Db 378 LTTGYGTAGVWIFPCNIVAEATIMQIWDGTTINPRSNLYLAASGIGTTLT 437
Qy 125 DYTLDYTLGGWLAGNDTAPREVTYIGFRDLCSNCSQSWVETCDSSQKQKALYGD 184
Db 438 IYASQWLPNTNTOFPYTYIGVGLCLQANSQWLEDC-SSKKEQWALYADGSI 496
Qy 185 PKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 244
Db 497 PKONODCLTSGSDSVSTVINIVSCGASGSGORWFTNKGALINLKNGLADVAQA 556
Qy 245 RRTIYPATGKPKQWMLFV 264
Db 557 KQIILYPLHDPQWMLFV 576

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Publication No. US2003092109A1
GENERAL INFORMATION:
APPLICANT: Orlowski, Irwin J.
APPLICANT: Krieger, Robert P.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom
FILE REFERENCE: US-07124
CURRENT APPLICATION NUMBER: US/10/137,077
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/354,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent In version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Ricinus communis
US-10-137-077-17

Query Match 13.1%; Score 186; DB 15; Length 44;
Best Local Similarity 77.3%; Pred. No. 9.7e-12;
Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 12 VRIYVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 55
Db 1 VRIYVGNKGRVYDDEDFHGNQIQLPKSKNDPNQWTIKRGTIRS 44

RESULT 5
US-10-074-527-5
Sequence 5, Application US/10074527

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Page 3

1 Publication No. US20020144246A1
 2 GENERAL INFORMATION:
 3 APPLICANT: Olandt, Peter J.
 4 APPLICANT: Meyers, Rachel E.
 5 APPLICANT: Salifu, Katherine A.
 6 APPLICANT: Millman, Adam
 7 TITLE OF INVENTION: Uses thereof
 8 FILE REFERENCE: MP12001-018P(RC11M)
 9 CURRENT APPLICATION NUMBER: US/10/074,527
 10 CURRENT FILING DATE: 2002-02-13
 11 PRIOR APPLICATION NUMBER: 60/269202
 12 PRIORITY FILING DATE: 2001-02-15
 13 INVENTOR: SEO ID NO: 9
 14 SOFTWARE: Patsseq for Windows Version 4.0
 15 SEO ID NO 5
 16 LENGTH: 145
 17 TYPE: PAT
 18 ORGANISM: Artificial Sequence
 19 FEATURE:
 20 OTHER INFORMATION: consensus
 21 IS-10-074-527-5

[illegible]

	Quality	Match	Similarity	Score	155	157	Length	430
QY	10.28%	1.28%	Freq. No. 3	18	17			
Db	Matches	47	Conservative	15	Matches	63	Models	10
								Gaps
								5
QY	1	DP	-VTCASAPFTRVVRKMRVMDVDDHSDNDIOLPMSNSPNQDMLTIXKDI	158				
Db	284	DYMTHTGSSCARITOLMGKCVAGASSANAPVDA	-DNGTAKRQRTVASTDTL	341				
	59	RSNSGCL	-TVYGTAGVYPMFDQDNVAVRATDQDINGTILNPSR	-LVLAASGSI	114			

Db 342 ~~ATAGCGCAGCTGTTGTAAGTCTGATGCGGAAAGG~~-~~ATTTAAGGCTVTPGATGACGCTGATGNSA~~ 399
Qy 115 ~~KGTLLTVOYDLYTLGGQWLAG~~ 135
||| :
400 ~~NGTRGATMGCGAAGAGKMGK~~ 420
Db

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1 RESULT 7
2 US-10-156-761-9724
3 Sequence 9724, Application US/10156761
4 Publication No. US2003019018A1
5 INFORMATION CONTAINS:
6 APPLICANT: OHTA, SATOSHI
7 APPLICANT: IZEDA, HARUO
8 APPLICANT: ISHIKAWA, JUN
9 APPLICANT: HORIKAWA, HIROSHI
10 APPLICANT: SHIBA, TADAYOSHI
11 APPLICANT: SAKAKI, YOSHIYUKI
12 APPLICANT: HATTORI, MASAHIRA
13 TITLE OF INVENTION: NOVEL POLYMEROLEFIDES
14 FILE REFERENCE: 249-362
15 CURRENT APPLICATION NUMBER: US/10/156,761
16 PENDING PENDING DATE: 2002-05-28
17 PRIOR APPLICATION NUMBER: JP 2001-204089
18 PRIOR FILING DATE: 2001-07-30
19 PRIOR APPLICATION NUMBER: JP 2001-272697
20 PRIOR FILING DATE: 2001-06-02
21 NUMBER OF SEQ ID NOS: 15109
22 SEQ ID NO 9724
23 LENGTH: 658
24 TYPE: PRT
25 ORGANISM: Streptomyces avermitilis
26 US-10-156-761-9724

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Query Match      9.8%; Score 138.5; DB 15; Length 658;
Best Local Similarity 12.1%; Pred. No. 2.8e+05;
Matches         17; Mismatches 57; Indels 19; Gaps 7

Qy 11 THR-1YGRKRV-----DYADDFHGNQGLTPSKSNDEPQGLT-IRKGTGT 59
Db 523 ITRPEIPIKMAVLTQKSGKSGCADIINNTITNGTQALM--DCKGDFPQISYTKSEKLV 560
Qy 60 SNKSGLTLY--GYAGYGVWIPPCVAVKELTIQIMQNGSTIINPNSNVLAA--SSGIK 115
Db 581 YGNKCLDANIGTNTGTNTGVIVVMDCKGNQK--WNINSDFITVYNQGLDAYNNAATN 638
Qy 116 GTTTLVQGLDLYTLTGQGV 132
Db 639 GTSLVMSGCTGNQK 655

RESULT 8
US-10-156-761-8170
; Sequence 8170, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; CITE REFERENCE: 249-742
; CITE REFERENCE: 249-742
; CURRENT FILING DATE: 2003-05-15
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8170

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; LENGTH: 536
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match      9.4%; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 66-05;
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

Cy 14 YGARNR-VPRDDPFDHNGQATMSKSNNDPQATIKKQCTISNC--SCITTV--68
Db 409 LVGASNNKCLDAYNQTAFGRKLEIMDC--GANNQVITIRAGSLRLVGTGCLADYN 465
Cy 69 GTAGAVYVVFECNTAVREATIWMQINDGIIINPSRLV-----AASGKGTTLVQ 122
Db 466 GTTSGKYVLYTCNGANCK--NSINPQVTVGTGSLCLDVTGSDQKSGVNGTALIEW 523
Cy 123 TLDTYLTGQGLWLG 135
Db 524 TCNGANQOWRLG 536

RESULT 9
US-10-137-077-18
; Sequence 18, Application US/10137077
; Publication No. US20030092109A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Irwin J.
; APPLICANT: Winter, Harry C.
; APPLICANT: Kruger, Robert P.
; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
; FILE REFERENCE: US-0714
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,596
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/254,322
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-137-077-18

Query Match      9.4%; Score 133; DB 15; Length 41;
Best Local Similarity 56.1%; Pred. No. 2.3e-06;
Matches 23; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Cy 224 GAILNKNGLADYVQANPKRRIITVPATGKPNQMLFVP 264
Db 1 GTILNYSGLVIDVPASDPSLRKQIILVLDGDPNQIMLELP 41

RESULT 10
US-09-973-457-5
; Sequence 5, Application US/09973457
; Patent No. US20020164746A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
; FILE REFERENCE: 10448-099001
; CURRENT FILING DATE: US/09/973,457
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/258,849
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 5
; LENGTH: 135
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match      9.1%; Score 129; DB 10; Length 135;
Best Local Similarity 28.1%; Pred. No. 3e-05;
Matches 41; Conservative 19; Mismatches 38; Indels 48; Gaps 9;

Cy 145 IYGRDLCHESNGSASWETCDSPQVCK--WALY-----DCSIRPKQ 187
Db 7 IGRNTSLDYN-----NSESQDNFQVMDCHGSGNQMLKLTYNESGALR--I 56
Cy 188 NDDCLTSGRDSVTVINIVSCG--ASGSQVFTNBSGAILNLKN-----GLADY 237
Db 57 NBDCLT-----VNGTVLVSQDGTGRKNDQVWVNDGTRFRKSKKGVDSGLCDV 111
Cy 238 AQANPKRRIITVPATGK--PNQML 261
Db 112 KQGN---KVQLWTCNSDAPNQKI 133

RESULT 11
US-10-074-527-6
; Sequence 6, Application US/10074527
; Publication No. US20020142426A1
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Galvin, Katherine A.
; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
; FILE REFERENCE: US-0714
; CURRENT FILING DATE: 2002-02-12
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/10/074,527
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match      9.1%; Score 129; DB 14; Length 135;
Best Local Similarity 28.1%; Pred. No. 3e-05;
Matches 41; Conservative 19; Mismatches 38; Indels 48; Gaps 9;

Cy 145 IYGRDLCHESNGSASWETCDSPQVCK--WALY-----DCSIRPKQ 187
Db 7 IGRNTSLDYN-----NSESQDNFQVMDCHGSGNQMLKLTYNESGALR--I 56
Cy 188 NDDCLTSGRDSVTVINIVSCG--ASGSQVFTNBSGAILNLKN-----GLADY 237
Db 57 NBDCLT-----VNGTVLVSQDGTGRKNDQVWVNDGTRFRKSKKGVDSGLCDV 111
Cy 238 AQANPKRRIITVPATGK--PNQML 261
Db 112 KQGN---KVQLWTCNSDAPNQKI 133

RESULT 12
US-10-156-761-10246
; Sequence 10246, Application US/10156761
; Patent No. US2003013018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
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Page 5

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIMA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: KAWANO, YOSHITAKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO: 10246
SEQ ID NO: 10247
SEQ ID NO: 10248
SEQ ID NO: 10249
SEQ ID NO: 10250
ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

Query Match 8.9% Score 126; DB 15; Length 647;
Best Local Similarity 26.3%; Pred. No. 0.00051;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

Qy 9 EPTVIRGNGRVVDVDDDDHQQIQIWPSSKNDPQQLMTIRKDETRNSGCL--T 66
Db 520 DQSGFVELAGKIDVASSSSANNAVGLY--DNGSTAGKMTVADSVGLKCIDVT 577
Qy 67 TGYTRGVYMTFDCNTAREATITQIWDNGTIIIPRSNVLVLAASGKQTLITVQTLDY 126
Db 578 SASADAGKICQIDCN-----GTAQKMSYN-----ASTGVYNTADKCIDV 620
Qy 127 TLGGWLAGNDTAPREVITYGFDLQMSGSGVWETCDSSQKQKQWAL 177
Db 621 T-----GNSSA-----NGRAAQIWSCTGAAGQ-KWEL 646

RESULT 13

US-09-770-621-4

Sequence 4, Application US/09770621

Patent No. US2001002481SA1

GENERAL INFORMATION:

APPLICANT: M nyl, Arja

APPLICANT: Vehmanper m, Richard

APPLICANT: Fagerster m, Richard

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Laitinen, Tarja

TITLE OF INVENTION: Production and Secretion of Proteins of

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W. Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,621

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/590,563

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

COMPUTER: IBM PC compatible

CLASSIFICATION:
Prior Application Data:
Application Number: US 08/282,001
Filing Date: 29-JUL-1994
Classification:
Attorney/Agent Information:
Name: Bugalsky, Lawrence B.
Registration Number: 35,086
Address: 202-371-2600
Telephone: 202-371-2600
Telefax: 202-371-2600
Information for SEQ ID NO: 4:
Sequence Characteristics:
Length: 492 amino acids
Type: amino acid
Topology: linear
Molecule Type: protein
US-09-770-621-4

Query Match 8.8% Score 124.5; DB 9; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00051;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

Qy 23 DVRDDPHGNGQCLMPK--KSNNDPQQLMTIRKDETR--SNGSCLTYG-- 70
Db 168 DVVNAEAFDNGSRGDSNLTORTND---MIEAETRAQGPBALCYNDVITENNA 223
Qy 71 --DAGYVNI-----EDCNTRVEXTIWMQNDGTIIIPRSNVLVLAASGKQTL 119
Db 224 AKQAVNHWDFRSGVPLDC---VGRQSHFNSGNSVNPFRITLQGFAL-GVDV 276
Qy 120 TQGLDYLTLGGWLAGNDTAPREVITYGFDLQMSGSGVWETCDSSQKQKQWAL 177
Db 277 EYTELDD-----ENAPQIYASVIRCLAVDRCTGIWGVHSDSMYSNPIL 326
Qy 133 MESN-----GGSYVW-----ET 164
Db 327 FNNKNKQAVYAVDALNMGSDGSGPSPVPPGGGSGQIRGVASNCIDVNGNT 386
Qy 165 CDSGQ-----KNGKRALYDGSIFPKQNDQCLTSGRDSVSTVINTVSGSAGS 215
Db 387 ADQTVQGLDCHSGSNQ-QMTTSSGSHFNG--KCLDQSSGSAVAVQITRQWGA-N 442
Qy 216 QKWTNTEGAILNLRKGLAND-VQGNPRLTIRIITPRQKQW 260
Db 443 QKWEIRADGTIVWGSLCDAVGGGTGNGRRLQIYSGWGNQW 488

RESULT 14

US-09-770-621-7

Sequence 7, Application US/09770621

Patent No. US2001002481SA1

GENERAL INFORMATION:

APPLICANT: M nyl, Arja

APPLICANT: Vehmanper m, Richard

APPLICANT: Fagerster m, Richard

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Laitinen, Tarja

TITLE OF INVENTION: Production and Secretion of Proteins of

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W. Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 31-OCT-1994
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 5,086,503
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
STRANDEDNESS: NO. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
THICKNESS/SEGMENT: AM50
US-09-770-621-7

Query Match      8.8%; Score 124.5; DB 9; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVREDDPHDNGQIOLMPS---KSNNDPNQMLTIKEDGTR---SNASCLTYGY-----70
DB 168 DVVNAEPEDNSGRCDNSLQRTGND---MIEVAFRTAQGDSFALKCYNDYINEMNA 223
QY 71 --TAGYVYMI-----FDCNTAVRENTIWIQINDGIIIPNSMLVLAASGIKTTL 119
DB 224 AKQAVYVYVNDPKSRGVPIDC-----VGFQSHNSGNPYNPFTLLQGFAL-GVDV 276
QY 120 TVQCLDTYLGQMLAGNDAPR-----VTYGRPD-----LC 152
DB 277 EYTELDI-----ENAPQTYASYIRDLAVDRCTGITYWGVDSDEMSYQNPPL 126
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDNKKNKQAVYAVLDALNESDGDGSPNPVSPPGSSQJRGVANSRCIDVPNGNT 386
QY 165 CDSQ-----KQCKMALYGDSIIPKQNDQCLTSGRDSVSTYINITYCSASGS 215
DB 387 ADGTIVQVLDHSGSNQ-QWYTSSEPRIFGN-KILDGSSSNQAVQVYCSWGGA-N 442
QY 216 QWVFTNEGALINLKNGLAMD-VACANPKLRRIIYYPATGKPNQW 260
DB 443 QKWEIRADGTIVQVSGICLDVAGGTGNGTRLOLYSCWGNQKX 488
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RESULT 15
US-0-286-993-4
Sequence 4; Application US/10286993
Publication No. US20030146653A1
GENERAL INFORMATION:
APPLICANT: Mantyla, Arja
APPLICANT: Paltoelmo, Marja
APPLICANT: Lantto, Raija

```
APPLICANT: Pagersstrom, Richard
APPLICANT: Lantto, Raija
APPLICANT: Suomenen, Rikko
APPLICANT: Vehmaampere, Jari
TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
FILE REFERENCE: 1716.034004
CURRENT FILING DATE: 28-02-08-93
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/FI97/00037
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 492
TYPE: PRT
ORGANISM: Actinotadura flexuosa
US-10-286-993-4

Query Match      8.8%; Score 124.5; DB 12; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

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DB 168 DVVNAEPEDNSGRCDNSLQRTGND---MIEVAFRTAQGDSFALKCYNDYINEMNA 223
QY 71 --TAGYVYMI-----FDCNTAVRENTIWIQINDGIIIPNSMLVLAASGIKTTL 119
DB 224 AKQAVYVYVNDPKSRGVPIDC-----VGFQSHNSGNPYNPFTLLQGFAL-GVDV 276
QY 120 TVQCLDTYLGQMLAGNDAPR-----VTYGRPD-----LC 152
DB 277 EYTELDI-----ENAPQTYASYIRDLAVDRCTGITYWGVDSDEMSYQNPPL 126
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDNKKNKQAVYAVLDALNESDGDGSPNPVSPPGSSQJRGVANSRCIDVPNGNT 386
QY 165 CDSQ-----KQCKMALYGDSIIPKQNDQCLTSGRDSVSTYINITYCSASGS 215
DB 387 ADGTIVQVLDHSGSNQ-QWYTSSEPRIFGN-KILDGSSSNQAVQVYCSWGGA-N 442
QY 216 QWVFTNEGALINLKNGLAMD-VACANPKLRRIIYYPATGKPNQW 260
DB 443 QKWEIRADGTIVQVSGICLDVAGGTGNGTRLOLYSCWGNQKX 488
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Job time : 18.0129 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:55:54 ; Search time 130.432 Seconds

1841.713 Million cell updates/sec

Title: US-09-601-667C-7

Sequence: 1 DVVTCASAEPTVRIVGRNGM.....RRIITYPATGKPNQMTLPVP 264

Scoring table: BLOSUM62

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 s

Database : Pending Patents_AA Main:*

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3:	/csm2_6/p/odata/1/paa/US07 COMB. pep.*
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25:	/csm2_6/p/odata/1/paa/US10 COMB. pep.*
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27:	/csm2_6/p/odata/1/paa/US10.2 COMB. pep.*
28:	/csm2_6/p/odata/1/paa/US10.3 COMB. pep.*
29:	/csm2_6/p/odata/1/paa/US10.4 COMB. pep.*
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31:	/csm2_6/p/odata/1/paa/US10.6 COMB. pep.*
32:	/csm2_6/p/odata/1/paa/US10.7 COMB. pep.*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1418	100.0	264	20	US-09-601-667B-7	Sequence 7, Appli...

[illegible]

ALIGNMENTS

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1 RESULT 1
2 US-09-601-667B-7
3     APPLICATION US/09601667B
4     GENERAL INFORMATION
5     APPLICANT: Morrice, Peter
6     APPLICANT: Stiefel, Thomas
7     APPLICANT: Voelger, Wolfgang
8     APPLICANT: Welzer, Peter/Jeanne
9     INVENTOR: Jeanne Welzer/Michael Stiefel
10    FILE REFERENCE: 29641/76636
11    CURRENT FILING DATE: 2000-10-06
12    CURRENT APPLICATION NUMBER: US/09/601,667B
13    PRIOR FILING DATE: 1999-02-03
14    PRIOR APPLICATION NUMBER: PCT/EP99/00696
15    PRIOR FILING DATE: 1998-04-21
16    PRIOR FILING DATE: 1998-09-03
17    NUMBER OF SEQ ID NOS: 41
18    SEQ ID NO 7
19
20    LENGTH: 264
21
22    TYPE: PRT
23    ORGANISM: Artificial Sequence
24    FUNCTION:
25
26    OTHER INFORMATION: micleaoe lectin 1 (match)
27 US-09-601-667B-7

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us-09-601-667c-7.ram

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Query Match
Best Local Similarity 99.6%; Score 1412; DB 20; Length 264;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
DB 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
QY 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
QY 241 NPFLKRIITIPATGKPNQWMLPVF 264
DB 241 NPFLKRIITIPATGKPNQWMLPVF 264
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RESULT 5
US-09-601-667c-9
; Sequence 9, Application US/09601667C
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welte, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; PRIOR FILING DATE: 2000-10-06/0696
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: D 398 04 210.8
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 9
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: mistletoe lectin B3 (match)
US-09-601-667c-5
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Query Match
Best Local Similarity 99.6%; Score 1412; DB 20; Length 264;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
DB 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
QY 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
QY 241 NPFLKRIITIPATGKPNQWMLPVF 264
DB 241 NPFLKRIITIPATGKPNQWMLPVF 264
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RESULT 6
US-09-791-537-111176
; Sequence 10, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 111176
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Viscum album
US-09-791-537-111176
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Query Match
Best Local Similarity 99.3%; Score 1407.5; DB 22; Length 265;
Matches 264; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
DB 1 DVTCSASEPTVAVGKNGKRVVDDPHDNGQIQLPKSKNDPQQLATIKKGGTTS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKKTITL 120
QY 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTPAREVTIYGFEDLCNESNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGALINLKGLANDVQA 240
QY 241 NPFLKRIITIPATGKPNQWMLPVF 264
DB 241 NPFLKRIITIPATGKPNQWMLPVF 265
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RESULT 7
US-09-601-667b-10
; Sequence 10, Application US/09601667B
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welte, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667B
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 10
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: mistletoe lectin B4 (match)
US-09-601-667b-10
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Query Match 99.1%; Score 1405; DB 20; Length 264;

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Page 4

Best Local Similarity 99.2%; Pred. No. 1.9e-140;
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Qy 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Db 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Db 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Qy 241 NPKLRRIIIPATGKPNQWMLPVF 264
Db 241 NPKLRRIIIPATGKPNQWMLPVF 264

RESULT 8
US-09-601-667c-10
; Sequence 10, Application US/09601667C
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 10
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin B4 (match)
US-09-601-667c-10

Query Match 99.1%; Score 1405; DB 20; Length 264;
Best Local Similarity 99.2%; Pred. No. 1.9e-140;
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Qy 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Db 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Db 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Qy 241 NPKLRRIIIPATGKPNQWMLPVF 264
Db 241 NPKLRRIIIPATGKPNQWMLPVF 264

RESULT 9
US-09-601-667b-11
; Sequence 11, Application US/09601667B
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636 US/09/601,667B
; CURRENT APPLICATION NUMBER: US/09/601,667B
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 11
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin B5 (match)
US-09-601-667b-11

Query Match 99.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 98.9%; Pred. No. 3e-140;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMTIKKIDGTRIS 60
Qy 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Db 61 NSCLTGYGTAGYVYMI FDCNVAAREATTIWOJNDNGTIIIPRSNLYLAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Db 121 VQTLDTYLAGQWLAGNDTAPREVITYGFRDLQMSNGSVWETCDSSQKQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTIVIVSGSASQSQWVFTNEGAILNLKGPAMDVAQA 240
Qy 241 NPKLRRIIIPATGKPNQWMLPVF 264
Db 241 NPKLRRIIIPATGKPNQWMLPVF 264

RESULT 10
US-09-601-667c-11
; Sequence 11, Application US/09601667C
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 11
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: mismatch locin B2 (match)
US-09-601-667c-11

Query Match 98.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 98.9%; Pred. No. 3a-140; 2; Mismatches 261; Conservative 1; Indels 0; Gaps 0;

QY 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
DB 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
QY 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
DB 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240
QY 241 NPKLRRIIIPATKRPKNQMLPVF 264
DB 241 NPKLRRIIIPATKRPKNQMLPVF 264

RESULT 11

US-09-601-667b-8
Sequence 8, Application US/09601667b

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667b
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 8

LENGTH: 264
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: mismatch locin B2 (match)
US-09-601-667b-8

Query Match 97.2%; Score 1379; DB 20; Length 264;
Best Local Similarity 97.7%; Pred. No. 1.1e-137;

Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
DB 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
QY 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
DB 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240

QY 241 NPKLRRIIIPATKRPKNQMLPVF 264
DB 241 NPKLRRIIIPATKRPKNQMLPVF 264

RESULT 12

US-09-601-667c-8
Sequence 8, Application US/09601667c

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667c
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 8

LENGTH: 264
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: mismatch locin B2 (match)
US-09-601-667c-8

Query Match 97.2%; Score 1379; DB 20; Length 264;
Best Local Similarity 97.7%; Pred. No. 1.1e-137;

Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
DB 1 DVTCSASBPYRIYKNGKGVDDDDPDHNOIQIAPSKSNNDPQWLTKIKDGTIRS 60
QY 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
DB 61 NSCLTYGYTAGYVWIFDCNTAVREKATIQIWMNGTIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQKQGMALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNKGAILNKSLAMVDVAQA 240
QY 241 NPKLRRIIIPATKRPKNQMLPVF 264
DB 241 NPKLRRIIIPATKRPKNQMLPVF 264

RESULT 13

US-09-601-667b-6
Sequence 6, Application US/09601667b

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667b
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 6

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LENGTH: 263
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: mismatch locin B
US-09-601-667b-6

Query Match 94.5%; Score 1339.5; DB 20; Length 263;
Best Local Similarity 95.8%; Pred. No. 1.8e-133;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

OY 1 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 60
DB 1 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 60
OY 61 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 120
DB 61 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 120
OY 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 180
DB 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 180
OY 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 179
DB 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 179
OY 181 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 240
DB 181 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 239
OY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 14
US-09-601-667c-6
Sequence 6, Application US/09601667C
GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
APPLICANT: Welters, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601.667C
PRIORITY FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: mismatch locin B
US-09-601-667c-6

Query Match 94.5%; Score 1339.5; DB 20; Length 263;
Best Local Similarity 95.8%; Pred. No. 1.8e-133;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

OY 1 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 60
DB 1 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 60
OY 61 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 120
DB 61 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 120
OY 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 180
DB 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 179

OY 181 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 240
DB 180 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 239
OY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 15
US-09-601-667b-4
Sequence 4, Application US/09601667B
GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
APPLICANT: Welters, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601.667B
PRIORITY FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 4
LENGTH: 531
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: MLI match
US-09-601-667b-4

Query Match 94.5%; Score 1339.5; DB 20; Length 531;
Best Local Similarity 95.8%; Pred. No. 4.9e-133;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

OY 1 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 60
DB 269 DDVTCASBPVRIYVGNKGVYVDDPDHGNQIQIMPSSKNDPQWLTKIKDGTIRS 328
OY 61 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 120
DB 329 NSGCLTYGTAGYVWIFDCNTAVREKTIWQIMNGTIIIPRSNLYLAASGIGKTLT 388
OY 121 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 180
DB 389 VQTLDTYLGQWLAGNDTAPREVITVIGFRLCWSNGSVWETCSQKQKXALYGD 447
OY 181 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 240
DB 448 GSIRPKONDOCLTGRDSVSTVINIVSCGASGQWFTNKGALINLNGKGLANDVQA 507
OY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 508 NPKLRRIIYPATGKPNQMLPV 530

Search completed: December 11, 2003, 14:44:21
Job time : 130.432 secs

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RESULT 2
US-08-776-059-33
Sequence 33, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-33

Query Match 94.0%; Score 1333.5; DB 3; Length 264;
Best Local Similarity 95.4%; Pred. No. 6.4e-131;
Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDTGASAPPTVIVGNKGVVDDDFDNGDQIOLWPSKSNNDPNQMTIKKDTTTS 60
DB 2 DDTGASAPPTVIVGNKGVVDDDFDNGDQIOLWPSKSNNDPNQMTIKKDTTTS 61
QY 61 NSGCLTYGTAAGYVWTFPCNTAVERATITQINDGTITIPRSVTLAASGIGKTLT 120
DB 62 NSGCLTYGTAAGYVWTFPCNTAVERATITQINDGTITIPRSVTLAASGIGKTLT 121
QY 121 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCEWSNGSVWETCDSSQKQKALYGD 180
DB 122 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCEWSNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRPKQNDGCTISGRDSVSTVNIIVSGSAGSQGWFTNEGAILNKNGLANDVQA 240
DB 181 GSIRPKQNDGCTISGRDSVSTVNIIVSGSAGSQGWFTNEGAILNKNGLANDVQA 240
QY 241 NPKLRRIIYPATGKPKQWMLPV 263
DB 241 NPKLRRIIYPATGKPKQWMLPV 263

RESULT 3
US-08-776-059-35
Sequence 35, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

US-08-776-059-35
Query Match 94.0%; Score 1333.5; DB 3; Length 564;
Best Local Similarity 95.4%; Pred. No. 1.9e-130;
Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDTGASAPPTVIVGNKGVVDDDFDNGDQIOLWPSKSNNDPNQMTIKKDTTTS 60
DB 302 DDTGASAPPTVIVGNKGVVDDDFDNGDQIOLWPSKSNNDPNQMTIKKDTTTS 361
QY 61 NSGCLTYGTAAGYVWTFPCNTAVERATITQINDGTITIPRSVTLAASGIGKTLT 120
DB 362 NSGCLTYGTAAGYVWTFPCNTAVERATITQINDGTITIPRSVTLAASGIGKTLT 421
QY 121 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCEWSNGSVWETCDSSQKQKALYGD 180
DB 422 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCEWSNGSVWETCDSSQKQKALYGD 480
QY 181 GSIRPKQNDGCTISGRDSVSTVNIIVSGSAGSQGWFTNEGAILNKNGLANDVQA 240
DB 481 GSIRPKQNDGCTISGRDSVSTVNIIVSGSAGSQGWFTNEGAILNKNGLANDVQA 540
QY 241 NPKLRRIIYPATGKPKQWMLPV 263
DB 541 NPKLRRIIYPATGKPKQWMLPV 563

RESULT 4
US-08-378-761a-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378.761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: C302
AUTHOR: BORUCKI, ANDREA T
INVENTOR: BORUCKI, ANDREA T
REGISTRATION NUMBER: 31651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRADNESS: single
NOISE: linear
MEDIUM TYPE: protein
US-08-378-761a-77

Query Match 55.3%; Score 783.5; DB 1; Length 540;
Best Local Similarity 56.2%; Pred. No. 3.9e-73;
Matches 146; Conservative 41; Mismatches 72; Indels 1; Gaps 1;

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QY 5 CSASEPTVATVGNKMEYVARDDDPHDNGQIQIOLMPKSNNDPNQIATIKEDGTTIRNSGC 64
DB 282 CMDEPTVATVGNKGLCVDTVGEEFPDGNPIQLMPCKSNNTDNLKRDSTIRNSGKC 341
QY 65 LITVGYTAGVYVIMFDGNTAREATTIWOIMDNGTIINPSNLVLAASGIGKTLTVQTL 124
DB 342 LITKSSPRQGVYVINCSTATVGTATKQIMNNTIINPSGLVLAATSGNSGKTLTVQTN 401
QY 125 DYLGGQMLAGNDTAPREVITYGPAIDCMHNSGSGVWTCOSQKQXALYGGSGIR 184
DB 402 IYAVSQGMLPTNNTPFVITIVGLYKCLQNSGKWLDDC-TSEKAEQOMLYADGSIR 460
QY 185 PRQNDQCLTSRDSVSTVINIVSGSGASGQWVFTNESAIIINKGLAMDYAQAPEL 244
DB 461 POQRNDCLTTDANKIGTVKXLSGCPASGQWVFTNDSITLNLVGLVYDVRSDPSL 520
QY 245 RLIIYPAKGNQOMLPVF 264
DB 521 KQIIVHPFHNANQIWLEPLF 540

RESULT 5

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5646026
Patent No. 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match 55.3%, Score 783.5, DB 1, Length 540,
Best Local Similarity 56.2%, Pred. No. 3,9e-73,
Matches 146, Conservative 41, Mismatches 72, Indels 1, Gaps 1,

QY 5 CSASEPTVATVGNKMEYVARDDDPHDNGQIQIOLMPKSNNDPNQIATIKEDGTTIRNSGC 64
DB 282 CMDEPTVATVGNKGLCVDTVGEEFPDGNPIQLMPCKSNNTDNLKRDSTIRNSGKC 341
QY 65 LITVGYTAGVYVIMFDGNTAREATTIWOIMDNGTIINPSNLVLAASGIGKTLTVQTL 124
DB 342 LITKSSPRQGVYVINCSTATVGTATKQIMNNTIINPSGLVLAATSGNSGKTLTVQTN 401
QY 125 DYLGGQMLAGNDTAPREVITYGPAIDCMHNSGSGVWTCOSQKQXALYGGSGIR 184
DB 402 IYAVSQGMLPTNNTPFVITIVGLYKCLQNSGKWLDDC-TSEKAEQOMLYADGSIR 460
QY 185 PRQNDQCLTSRDSVSTVINIVSGSGASGQWVFTNESAIIINKGLAMDYAQAPEL 244
DB 461 POQRNDCLTTDANKIGTVKXLSGCPASGQWVFTNDSITLNLVGLVYDVRSDPSL 520
QY 245 RLIIYPAKGNQOMLPVF 264
DB 521 KQIIVHPFHNANQIWLEPLF 540

RESULT 6

US-09-512-342-14
Sequence 14, Application US/09512342
Patent No. 6388068
GENERAL INFORMATION:
APPLICANT: SATOH, SHINGO
APPLICANT: MASUDA, SUSUMU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-512-342-14
Query Match 12.9%, Score 182.5, DB 4, Length 293,
Best Local Similarity 28.1%, Pred No 7,1e-11,
Matches 63, Conservative 31, Mismatches 91, Indels 39, Gaps 10,
QY 14 IYGNKMEYVARDDDPHDNGQIQIOLMPKSNNDPNQIATIKEDGTTIRNSGKC 59
DB 41 LVGSDCLTEHNSP-----WYKPAIGINFPRLSCCEKQOTQIIVYDQTTIRN 89
QY 60 SNKCLT--VYTAGVYVIMFDGNTAREATTIWOIMDNGTIINPSNLVLAASGIGK 116
DB 90 NKRCILAEVFGVIL--RAVSSCGKXSPNKWKTKNDGTLAVDSRWLIGDLY-- 145
QY 117 TLTGVLDTLTCQMLAGNDTAPREVITYGPAIDCMHNSGSGVWTCOSQKQXALYGGSGIR 174
DB 146 --VTLGSKTTPSOMYEVYESLNMWANIEMANLCLGSTDSSHGANGCINTDKQK 202
QY 175 WATGSGSIRPQNDQCLTSRDSVSTVINIVSGSGASGQWVFTNESAIIINKGLAMDYAQAPEL 218
DB 203 WATYADGRTQIHQVHNNANCLTSPDQFRRV--VYKCEKDXPQQRW 244

RESULT 7

US-09-159-106-15
Sequence 15, Application US/09159106
Patent No. 6284503
GENERAL INFORMATION:
APPLICANT: FERRER, PAN
APPLICANT: DIERS, IVAN
APPLICANT: HALKIER, TORBEN
APPLICANT: HEDSGAARD, LISBERGH
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
US-09-159-106-15

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Page 4

FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOURCE: ResSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 132
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

Query Match
Best Local Similarity 36.3%; Pred. No. 1.5e-06;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

OY 18 NCKRYVDDPHENQGLMPSKSNNDPNQATIKEDTIRNSGCTTT--GITAGVY 75
DB 14 NCKCYVPRADPTDNPVQVITGSGN--AAQWYRSGDGVYSLKEDVYDSDTRRAA 71
OY 76 VMFPCNTAVREATINQW--DNQF--IIPRSLVLAASG---KGTTLVQTLDTTL 128
DB 72 VQVWTCN-----GTGQKMAVDAGSKALNRPQSGCLDAPGAPAPRDQGRLTQVTCNGIT 126
OY 129 GQGW 132
DB 127 AQGW 130

RESULT 8
US-09-159-106-11
Sequence 11, Application US/09/159.106
Patent No. 6284509
GENERAL INFORMATION:
APPLICANT: Ferrier, Pau
APPLICANT: Dietz, Ivan
APPLICANT: Halkier, Torben
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOURCE: ResSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 435
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match
Best Local Similarity 36.3%; Pred. No. 8.9e-06;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

OY 18 NCKRYVDDPHENQGLMPSKSNNDPNQATIKEDTIRNSGCTTT--GITAGVY 75
DB 317 NCKCYVPRADPTDNPVQVITGSGN--AAQWYRSGDGVYSLKEDVYDSDTRRAA 374
OY 76 VMFPCNTAVREATINQW--DNQF--IIPRSLVLAASG---KGTTLVQTLDTTL 128
DB 375 VQVWTCN-----GTGQKMAVDAGSKALNRPQSGCLDAPGAPAPRDQGRLTQVTCNGIT 429

OY 129 GQGW 132
DB 430 AQGW 433

RESULT 9
US-08-468-812-4
Sequence 4, Application US/08/468.812
Patent No. 593835
GENERAL INFORMATION:
APPLICANT: M. Ruy, Jari
APPLICANT: M. Ruy, Jari
APPLICANT: Paget, m. Richard
APPLICANT: Lantto, Raija
APPLICANT: Pajohelmo, Marja
APPLICANT: Suominen, Pirko
APPLICANT: Lantinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: REGISTER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT RELEASE: Release #1.0, Version #1.30
CURRENT RELEASE: Release #1.0, Version #1.30
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US/08/468.812
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-OCT-1994
TITLE OF INVENTION: 435
TITLE OF INVENTION: 435
NAME: Bogalsky, Larry B.
REFERENCE/DOCKET NUMBER: 35,086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
KEYWORDS: 432 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-812-4

Query Match
Best Local Similarity 8.8%; Score 124.5; DB 2; Length 492;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

OY 23 DYRDDPHDNGQGLMPS--KSNQPNQATIKEDGTF--SNQSTITTYG----- 70
DB 168 DYVRAEDELNSGKSCDSNLTGSD--NIEVAFRIAGQDPSKALGVNDVNIEMNA 223
OY 71 --TAGYVNT-----PDQNTAVREATINQW--DNQF--IIPRSLVLAASGCTTT 119
DB 224 ATOQAVYNNVADPKRSQVPIDC-----VGPQSHNSGSPNVPNFTTLQGFAL--GVGV 276

QY 120 TWTGTLTYLGGGMLAGNDTPRE-----VTIYGRD-----LC 152
DB 277 EYTHLDI-----ENKRPQYASVIRDCIANDRCITGIWGVNDSMSYQNPFL 326
QY 153 MESN-----GGSTWV-----ET 164
DB 327 FNNGNKQAYAVYALNLSGSDGGSNPPVSPPGGSGQIRGVASNRCDIVPNGNT 386
QY 165 CDSGQ-----KNQCKMALYGDGSIIRPKQNDQCTGSRDVSVTYINIVSCGASGS 215
DB 387 ADGTQVQLYDCHSGSNQ-QWTYSSGFRIRPN-KCLDAGSSNGAVVQYVSCWGA-N 442
QY 216 QRWYTFNEGALINLKNGLAND-VQAMPKLRRIIYIPATKPNQW 260
DB 443 QKMLRADGTTIVGVSGLCLDVGSGTGNGTRLDJSCWGNQK 488

RESULT 10

US-08-468-812-7
Sequence 7, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vennaemper, Jari
APPLICANT: M nyl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Paloheimo, Ralf
APPLICANT: Suontinen, Pirkko
APPLICANT: Lahninen, Taina
APPLICANT: Kistio, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: US 08/332,412
PRIORITY APPLICATION NUMBER: 130CT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340002
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STANDARDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50

US-08-468-812-7
Query Match 8.88; Score 124.5; DB 2; Length 492;
Best Local Similarity 20.88; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
QY 23 DYRDEDFDNDQCLMPS---KSNDPYQMLTKDGTG---SNGSLTGY-----70
DB 168 DIVVAEAFEDVSGRCDSNLCRTGND---WIEVAFTRQGDPSAKCYNDVNIEMMA 223
QY 71 --TAGYVYMI-----FDCNVAFRANTIQINDGTTIPPSRLVLAASGKQKTL 119
DB 224 AKTYAVYMWDFKSRGVPIDC-----VGFSHNSGNPNPFRFTLQGFAL-GVDV 276
QY 120 TWTGTLTYLGGGMLAGNDTPRE-----VTIYGRD-----LC 152
DB 277 EYTHLDI-----ENKRPQYASVIRDCIANDRCITGIWGVNDSMSYQNPFL 326
QY 153 MESN-----GGSTWV-----ET 164
DB 327 FNNGNKQAYAVYALNLSGSDGGSNPPVSPPGGSGQIRGVASNRCDIVPNGNT 386
QY 165 CDSGQ-----KNQCKMALYGDGSIIRPKQNDQCTGSRDVSVTYINIVSCGASGS 215
DB 387 ADGTQVQLYDCHSGSNQ-QWTYSSGFRIRPN-KCLDAGSSNGAVVQYVSCWGA-N 442
QY 216 QRWYTFNEGALINLKNGLAND-VQAMPKLRRIIYIPATKPNQW 260
DB 443 QKMLRADGTTIVGVSGLCLDVGSGTGNGTRLDJSCWGNQK 488

RESULT 11

US-08-590-563-4
Sequence 4, Application US/08590563
Patent No. 6100114
GENERAL INFORMATION:
APPLICANT: Vennaemper, Jari
APPLICANT: M nyl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Paloheimo, Ralf
APPLICANT: Suontinen, Pirkko
APPLICANT: Lahninen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536

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Page 6

ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-590-563-4

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

Db 23 DVPDDPHDGNQIOLMPS--KSNNDPNQIWTIKDGTIR---SNGSLTITGYG-----70
Db 168 DVNAPEDFGNSGRCDNQLRTND---WIEVAFRTNQGDSFKALINDIWIENNA 223
QY 71 --TAGYVWI-----FDCTAVREATIQIWDNGETIINPNSNVLVAASSGIRGTL 119
Db 224 AKTOAVYNNVADPKSRGVPIDC-----VGFQSHNSGNSPVNPNFTTLOQFAL-GVDV 276
QY 120 TVQTLDTYLGQWMLANDVAPRE-----VTIYGFSD-----LC 152
Db 277 EYTELDI-----ENAPQYASVIRCLADVRCITGVWGRBDSMSYQNFLL 326
QY 153 MESN-----GGSVWV-----ET 164
Db 327 FPNNGKQKQAYVLDALNEDSGDGPSPNPVSPPGSSGQIRGVASNCTIDVPMNT 386
QY 165 CDSGQ-----KQSKALYDGSIRPNKQDQCLTSGDVSATVINIYCCGASG 215
Db 387 ADQTVQVLDYCHSGSNQ-QWTTYSSEFRIRPN--KCLDAGSSNSGAVQIYSCWGA-N 442
QY 216 QRWVPTNEGALINIKKGLAND-VQANPKIRIITIVATGKPNQW 260
Db 443 QKWLADQTVVQSGCLDAVGGGTGNGTGLQYSCWGNQKX 488

RESULT 12
US-08-590-563-7
Sequence 7, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M. Nyl, A. Aja
APPLICANT: Vehmanner, Jari
APPLICANT: Fagerström, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Raija
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
POSITION IN GENOME:
MOLECULE TYPE: peptide
CHROMOSOME/SEGMENT: AM50
US-08-590-563-7

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

Db 23 DVPDDPHDGNQIOLMPS--KSNNDPNQIWTIKDGTIR---SNGSLTITGYG-----70
Db 168 DVNAPEDFGNSGRCDNQLRTND---WIEVAFRTNQGDSFKALINDIWIENNA 223
QY 71 --TAGYVWI-----FDCTAVREATIQIWDNGETIINPNSNVLVAASSGIRGTL 119
Db 224 AKTOAVYNNVADPKSRGVPIDC-----VGFQSHNSGNSPVNPNFTTLOQFAL-GVDV 276
QY 120 TVQTLDTYLGQWMLANDVAPRE-----VTIYGFSD-----LC 152
Db 277 EYTELDI-----ENAPQYASVIRCLADVRCITGVWGRBDSMSYQNFLL 326
QY 153 MESN-----GGSVWV-----ET 164
Db 327 FPNNGKQKQAYVLDALNEDSGDGPSPNPVSPPGSSGQIRGVASNCTIDVPMNT 386
QY 165 CDSGQ-----KQSKALYDGSIRPNKQDQCLTSGDVSATVINIYCCGASG 215
Db 387 ADQTVQVLDYCHSGSNQ-QWTTYSSEFRIRPN--KCLDAGSSNSGAVQIYSCWGA-N 442
QY 216 QRWVPTNEGALINIKKGLAND-VQANPKIRIITIVATGKPNQW 260
Db 443 QKWLADQTVVQSGCLDAVGGGTGNGTGLQYSCWGNQKX 488

RESULT 13
US-09-770-621-4
Sequence 4, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M. Nyl, A. Aja
APPLICANT: Vehmanner, Jari
APPLICANT: Fagerström, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Raija
TITLE OF INVENTION: Production and Secretion of Proteins of

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us-09-601-667c-7.ra1

Page 7

NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1050,0340003
FILING DATE: 202-371-2540
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4
Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
Db 23 DYPDDPHDQGLWPS--KSNNDPQMLTKIRDTIR--SNQSLTGY-----70
168 DVNAFEDNSGRCDNSLQRTND---WISVAFRTAQDPSAKLCYNDVNIEMNA 223
OY 71 --TAGTYVNI-----FDGNTAVRATVQIDNGTIIIPRSNLVLAASGKGTLL 119
OY 224 AKTQAVYNNVDPKSRGVPIDC-----VGFQSHNSGNPNVPRFTLLQGFAL-GVDV 276
Db 120 TVQTLDTYTLGGWLAGNDTAPRE-----VTIYGFDD-----LC 152
Db 277 EYVELDI-----ENAPQAVSYIRDLAVDRCTGIYVGVDSWSRYONPL 326
OY 153 MESN-----GGSVW-----ET 164
Db 327 FDNNGNKQATYVLDALNBSDDGGSPNPSPFGSSGQIGVANSRCDIVEMNT 386
OY 165 CASSQ-----XGCKNALYGGGSIIRPKNOGDCLTSGRPSYVINYSCSAGS 215
Db 387 ADGTQVQDYCHSGSNQ-QWYTSGGSFIRPGV-KCDAGSSNGAVQVQIYSWGA-N 442
OY 216 QWVFTNEGAILNFKGLAND-VQANPKRIIRIIIPATGPKPQW 260
443 QKVELRADGTIVGVSGLCIDAVGGGTGNGTGLQIYSCMGANNQW 488

RESULT 14
US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M etyl, Arja
APPLICANT: Peterson, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Taina
TITLE OF INVENTION: Production and secretion of proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1050,0340003
FILING DATE: 202-371-2540
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM60
US-09-770-621-7
Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
Db 23 DYPDDPHDQGLWPS--KSNNDPQMLTKIRDTIR--SNQSLTGY-----70
168 DVNAFEDNSGRCDNSLQRTND---WISVAFRTAQDPSAKLCYNDVNIEMNA 223
OY 71 --TAGTYVNI-----FDGNTAVRATVQIDNGTIIIPRSNLVLAASGKGTLL 119
OY 224 AKTQAVYNNVDPKSRGVPIDC-----VGFQSHNSGNPNVPRFTLLQGFAL-GVDV 276
Db 120 TVQTLDTYTLGGWLAGNDTAPRE-----VTIYGFDD-----LC 152

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Page 8

Db 277 EVELDI-----ENAPQYVAVIRDCIAYDSCTGIVYVNDSDMSYQNFLL 326
QY 153 MSN-----GGSVWV-----ST 164
Db 327 FNNNGKQAYVADALNBSDDGSPNPVSPPEGSSGQIRVASNCDIVPNKNT 386
QY 165 CDSG-----KQCKALYDPSIRFKQKQOCLISGRDSVSTVITNVCCGSSS 215
Db 387 ADGTQVLYDCHSGSNQ-CWTYTSSEPHFGN-KCLDSSSSNNAVQIYSNGSR-N 442
QY 216 QWVFTNCGAILNKLKGLAND-VQANPELRITIIYPATKPNQW 260
Db 443 QWELRADETIVQVSGCLDVGSGTGNTRLOIYSCWGNQKX 498

RESULT 15
US-08-468-812-5
Sequence 5, Application US/08468812

GENERAL INFORMATION:
APPLICANT: Vahmanper, Jari

APPLICANT: M. Uyl, Aija
APPLICANT: Ragerstr m, Richard

APPLICANT: Lanto, Raita
APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja

APPLICANT: Kietto, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods

TITLE OF INVENTION: 25
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/MS-DOS

SOFTWARE: Pathsoft Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/468, 812

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/332,412

APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 1050,0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:

CHROMOSOME/SEGMENT: AM50
US-08-468-812-5

Query Match 6.6%; Score 122.5; DB 2; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.00026;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
Db 22 VDVRRDDPDHGNQCLMPKSNNDPNVQWLTIRKQGTIRSNQS-CLTGYGYTGYVWF 80
QY 379 IDVPKNTADGTQVLYDCHSGS--NQWTYTSSEPHFGN-KCLDSSSSNNAVQIYS 436
Db 81 CNTARAKTINQINDGTIRPSNULVLAASSGKRTLTWQ 122
QY 437 CWGANQK-WELRADETIVQVSGCLDVGSGTGNTRLO 476

Search completed: December 11, 2003, 14:11:33
Job time : 10.1403 secs

A:Molecule type: protein
A:Residues: 1-285 <SOL>
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: glycoprotein
F:61.95.136/Binding site: carbohydrate (asn) (covalent) #catus experimental

Query Match	96.8%;	Score 1368.5;	DB 2;	Length 265;
Best Local Similarity	97.4%;	Pred. No. 1e-109;		
Matches 258; Conservative	2;	Mismatches 4;	Indels 1;	Gaps 1;

1 DVI L C A S S E F I V R I V G R S G M R V D V K D D D H D G N Q I Q L M P S K S N N D P N Q L W T I K R D S T I R S 60
 1 D V T C A S E P E T R I V G R N G M R V D V K D D D H D G N Q I Q L M P S K S N N D P N Q L W T I K R D S T I R S 60

D6 61 NSCSLTYYGYAGAYVNI FDCNTAVREAI IWQIDNCSII INRPSNVLVAASGIGKTLT 120

Db 121 VQTLDTLQCGWLAGNDTALPREVTLTYGFRDLCMBSNGGSVWVRICDSSQKQKRALYED 180

DU 161G51RPNOMDQCLHISGRDSVIVINIVSSGASGSQRMVFTNEGRIENLJNGLANDVAGA 240
 QY 241 NPKLRRIITYPATGRPNOM-LPVF 264

RESULT 3

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
CDate: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext change 16-Jul-1999

A; Title: Genomic cloning and characterization of a ricin gene from *Ricinus communis*
A; Reference number: A24041; MIMD:86067214; DMTD:299973
A; Author(s): Halling, A.C.; Murray, E.B.; Ladin, B.F.; Houston, L.L.; Wevers,
Sinning, R.; Halling, A.C.; Murray, E.B.; Ladin, B.F.; Houston, L.L.; Wevers,
Nucleic Acids Res. 13, 8019-8033, 1985

A;Molecule type: DNA
A;Residues: 1-576 <HAL>
A;Cross-references: GB:X03179; NID:g21082; PTDN:CAA26939.1; PTD:g21083

A:Title: The lectin gene family of *Rhizus communis*: cloning of a functional rRNA gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513

A:Cross-references: EMBL:X52908; NID:g21084; PIDD:CAA37095.1; PID:g21085
 R:Jamb, F.I.; Roberts, L.M.; Lord, J.M.
 SUR: J. Biochem 148 265-270 1985

A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA

A: Title: Isolation and sequences of peptic peptides, and the complete sequence
R: Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
FIDN:CA426250.41 FIDP:G21078

A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>
 !:Note: This paper cites the others in the series sequentially.
 A:Molecule type: protein
 A:Accession: P03572

FEBS Lett. 191, 121-124, 1985

A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', 386-576 <AB>
R:Funatsu, G. J., Kimura, M., Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374

A:Accession: A03374
A:Molecule type: Protein
A:Residues: 315-333, 'NH', 337-342, 'NH', 345-352, 354-383, 'ES', 386-399, 'T', 401, 'D', 403, 'E',
527, 'E', 529-554, 'W', 566, 'H', 567-570, 'I', 573-574, 'P', <TN>
A:Note: This paper, one of a series, summarizes the experimental details for the deter-
minations. W. R. Kilm, J. R. Koehnert, J. D.

A:file: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action of the toxin
A:Reference number: A4237; PMID:15152005; PMID:1881983
A:Contents: annotation; active site
R:Rutember, E.; Robertus, J.D.
P:Proteins 10, 260-269, 1991
A:file: Structure of ricin B-chain at 2.5 angstrom resolution.

A:contents: annotation; X-ray crystallography, 2.5 angstroms
R:Katzur, B.J.; Collins, E.U.; Robertus, J.D.
Proteins 10, 251-259, 1991
A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; PMID:15152004; PDB:1A81861
A:contents: annotation; X-ray crystallography, 2.5 angstroms

C:Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit and the cell of the A chain. B chains are also responsible for cell agglutination (lectin).
C:Comment: This protein is cytotoxic and very poisonous to animals.
C:Superfamily: ricin, rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosylase; C
I:1-35/Domain: signal sequence #status predicted C
P:binding; lectin; PM binding; see

P-46-239/Domains: RNA N-glycosylase experimental <ch>
P-415-576/Product: rich D chain B Ascaris experimental <ch>
P-331-313-314-414-417-485-462-467-501-550-543-576/Comment: repeats
P-445-409-443-444-binding site: carboxydrane (Ano) (revertant) Ascaris experimental
P-415-158-243-244/Binding site: substrate (Tyr, Tyr, Glu, Asn) Ascaris experimental
P-212/Active site: Glu Ascaris experimental

Query Match	63.4%	Score 896.5;	DB 1;	Length 576;
Blast Local Similarity	63.5%	Pred. No. 7.le-69;		
E:336.318.330.333	377.294.465.478	S04-S52/Diisulfide bond; Serpin experimental		
F:336.318.330.333	Binding site: N-acetylglycosaminidase (Asp, Gln, Asn)	Status experimental		
F:548.569	Binding site: N-acetylgalactosamine (Asp, Asn)	Status experimental		

	Accession	Protein	Length	Score	E-value
Qy	5	CSALPFWIVAGSGRRIVLDDPHDSNOLQWSSGSSNNDDQLMTIRTNENPNSGC	64	1.0	0.000000
Db	318	CHDPEPFAIVIGSNGICVDVIRGFRHNGVALQALPCKSSNTDALQMLTKLRNTIRNSKXC	377	1.0	0.000000
Qy	65	LTFTGAGGVYVPIPCNIVVBEATITQIMONGTIIINRSNIVLAASQISGTTITLVQTL	124	1.0	0.000000

Db 378 LTTTISPSQYVWIDCHNADTKRQKQWNGKGLINSHSLVLAATKISNGTLLVIVGN 437

Qy 125 DVTLAGQAGNDTPAREVLIYGRDLCEMSNGSWYFCSSQKQKQKALAYGSGIT 184

Db 438 IAVAGQMLPTNTQPFVTTIVGLYGLCLANGQGMIEDC-SSEKAEQQAALYADGSR 496

[illegible]

RESULT 4

A>Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A:Reference number: A39761; PMID:91201339; PMID:2016300
A:Accession: A39761; Nucleotide sequence not shown
A:Molecule type: DNA
A:Residues: 18; 2-251 <EXT>
A:Cross-references: GB:X54872
R:Name: residues 1-8 were derived from the synthesized primer
R:Kimura, M.; Sumizawa, T.; Funatsu, G.
Bioset: Biochem J. Biochem. 57, 166-169, 1993
A>Title: The complete amino acid sequences of the B-chains of Abrin-A and Abrin-B, toxic proteins from *Rhinoceros spheniscus*.
A:Contig: VCL358; PMID:51695023; PMID:7763422
A:Accession: JCI3396
A:Molecule type: protein
A:Residues: 261-347; /T, 349-351; /N, 353-357; /L, 359-528 <XIN>
A:Experimental source: seed
R:Iversen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A:Description: Direct molecular cloning of two distinct abrin A-chains.
A:Reference number: S14471
A:Accession: X14471
A:Molecule type: DNA
A:Residue type: rDNA
A:Accession: MEI_2-251 <EVZ>
A:Cross-references: EMBL:X54873; NID:g16090; PIDD:CAJ3655.1; PID:g16091
R:Chen, Y.L.; Chow, L.P.; Tsungchi, A.; Lin, U.Y.
FEBS Lett. 309, 115-118, 1992
A>Title: The complete primary structure of abrin-A B chain.
A:Reference number: S24133; PMID:92371656; PMID:1505674
A:Accession: S24133
A:Molecule type: protein
A:Residues: 282-297; /Y, 299-426; /L, 428-466; /P, 468-482; /L, 484-528 <CHE>
R:Lill, S.H.; Chow, L.P.; Chen, Y.C.; Liaw, Y.C.; Chen, C.K.; Lin, U.Y.
Eur. J. Biochem. 240, 564-569, 1996
A>Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; PMID:97008945; PMID:8856055
A:Accession: S74110
A:Molecule type: protein
A:Residues: 159-109; /S151-172 <LIN>
A:Experimental source: seed
A:Accession: S7411
A:Molecule type: protein
A:Residues: 262-276; /X, 278-280; /329-348; /369-388; /399-418 <LIN>
A:Experimental source: seed
C:Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits protein synthesis on the cell surface. The A and B chains are linked by a single disulfide bond.
C:Superfamily: Ricin, RNase-N-glycosidase homology
C:Subfamily: Ricin, RNase-N-glycosidase homology
P:1-551/Product: abrin-a chain A #status experimental <RC>
F:7-246/Domains: RNA-N-glycosidase homology <RG>
F:7-246/Domains: RNA-N-glycosidase homology <RG>
F:261-528/Product: abrin-a chain B #status experimental <RC>
F:261-528/Domains: pyrrolidone carboxylic acid (Gln) #status experimental
F:261-528/Domains: pyrrolidone carboxylic acid (Gln) #status experimental
F:74,113-196/Binding site: substrate (TY, TYR, GLU, ASN) #status predicted
F:74,113-196/Binding site: substrate predicted
F:164,157-167/Binding site: GluArg #status predicted
F:164,157-167/Binding site: GluArg #status predicted
F:288,312/Binding site: carbohydrate (Asn) [covalent] #status predicted
F:288,312/Binding site: carbohydrate (Asn) [covalent] #status predicted
F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.6%; Score 758; DB 1; Length 528;
Best Local Similarity 54.4%; Pred. No. 4.5e-57;
Matches 147; Conservative 42; Mismatches 75; Indels 2; Gaps 2;

OY 5 CSAS RTCTATVTSSESTVDPPDDPHQNOALWFSKSNDRPOLATKEDNTIRNSGS 63
DB 265 GSRRPEPTLRICGHDDMDVUDVNDGNHGRNLIMHKDQRLFNEMOGLSLSDITRNKX 328
OY 64 CLTTGTAGTVGVYVVIDPDNAAYEARLTITNDGNGIIINPSNVLAASGGIKETTLVTG 123
DB 329 CLTTGTAGTGVYVVIDPDNSTAVANVAEIVINDGIIINPSNVLAASSSGMGKTLVTG 388

Dy		114	LYTLGGWLGKNDPAPEVETIYGRDLTMSNGQSIVVEPTDSQSGNKGAKALYDDSDSI	183
Oy		369	NELIMRGWRGTGNSTSPVTYSISGDILOMAGSVMALMDCDNSKKED-CMALYTDSISI	447
Dy		184	RPNQNDQCLTVGSADSVTYVINYSGSGASGSGRKYFTNEITALINKSLANDYQAANPK	243
Oy		448	REVDINMLNLSIKDHKSGLITLICKSNMNAQRVAFINDGSIKSLDVRMDYKSDPS	507
Dy		244	LRRIITYPATKXNQNMWLPVF	264
Oy		508	LKQILMFYTKGNMQWLTWF	528
<hr/>				
RESULT 7				
abrin.b precursor - Indian jilofice (fragment)				
N:contamin: rRNA N-glycosylase (EC 3.2.2.22)				
C:Species: Abrus precatorius (Indian jilofice)				
C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999				
C:Accession: S32430/JC1399				
R:Hing, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.				
J. Mol. Biol. 229, 263-267, 1993				
A>Title: Primary structure of three distinct isoenzymes determined by cDNA sequencing.				
A:Reference number: S32429; WUID:93123798; PMID:8421333				
A:Accession: S32430				
A:Molecule type: rRNA-				
A:Cross-references: GB:98345; NID:9166236; PION:AAB3625.1; PID:g166297				
R:Kimura, M.; Sumitawa, T.; Furutani, G				
Biosci. Biotechnol. Biochem. 57, 166-169, 1993				
A>Title: The complete amino acid sequences of the B-chains of Abirin-a and Abirin-b,				
A:Reference number: JC1398; WUID:93169023; PMID:7763422				
A:Accession: JC1399				
A:Molecule type: protein				
A:Residue: 260-281, 'P', 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-4				
C:Experimental source: Arabidopsis thaliana L-glycosylase homology				
C:Keywords: disulfide bond applications glycoprotein; glycosylase; hydrolase; lectin;				
F:7-245/Product: abrin.b chain A #status predicted <ANCH>				
F:7-245/Domian: rRNA-N-Glycosylase homology <RNG>				
F:260-537/Product: abrin.b chain B #status predicted <BEH>				
F:282-334,335-365,366-406,413-448,448-491,494-527/Region: all -residue repeats				
F:/Modified site: pyrroldione carbonylto acid (Gln) #status predicted				
F:4,113,199,195/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted				
F:160,380,400/Binding site: carboxylate (Asp) (covalent) #status predicted				
F:163,360/Active site: Gln, Arg, Histatys predicted				
F:280,281,325-343,416-429,435-472/Pisulide bonds: #status predicted				
F:280,281,325-343,416-429,435-472/Pisulide bonds: #status predicted				
F:499,530/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted				
<hr/>				
Query Match 52.6% Score 744; DB 2; Length 527;				
Beat Local Similarity 53.6% Pred. No. 7, 2e-56;				
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;				
<hr/>				
Oy		5	GSAH-EFTTRIVRSQGVVDDEDPHDNOIQUMPSNNPDNLTKDKNTIRNSGS	63
Dy		268	GSSRIEYTRIGSNQKCCVYDDOCHNKMTIAMCKDLSENLDTLASIKTSINSK	327
Oy		64	CLTYTGATGYWMIPDONTAAERETINDNGCTINPSMWLAASGKRTPLAYOT	123
Dy		328	CLTBGVAGNYWICYDTGSAVAEFYWEIMDNGTIHPESALVLVSRESSMGGITVQT	387
Oy		124	LYTLGGWLGKNDPAPEVETIYGRDLTMSNGQSIVVEPTDSQSGNKGAKALYDDSDSI	183
Dy		368	NELIMRGWRGTGNSTSPVTYSISGDILOMAGSVMALMDCDNSKKED-CMALYTDSISI	446
Oy		184	RPNQNDQCLTVGSADSVTYVINYSGSGASGSGRKYFTNEITALINKSLANDYQAANPK	243
Dy		447	REVDINMLNLSIKDHKSGLITLICKSNMNAQRVAFINDGSIKSLDVRMDYKSDPS	506
Oy		244	LRRIITYPATKXNQNMWLPVF	264
Dy		507	LKQILMFYTKGNMQWLTWF	527

RESULT 8
A:Cross-references: Indian licorice
A:Residues: 1-562 <IND>
A:Reference number: S16022
A:Accession: S16022
A:Title: Preprobrin: genomic cloning, characterization and the expression of the A-chain
A:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
A:Comment: Brin consists of an A chain which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
F/35-285/Product: abrin-c chain A #status predicted <RNG>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <RNG>
F/317-359/380-400, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats
F/359-428/Binding site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/198-201/Active site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/234-287, 395-435, 436/Binding site: Arg #status predicted (Asn) (covalent) #status predicted
F/281-303, 320-339, 353-380, 451-464, 480-507/Disulfide bonds: #status predicted
F/322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.6%; Score 744; DB 2; Length 562;
Best Local Similarity 53.6%; Pred. No. 7, 8e-56;
Matches 140; Conservative 42; Mismatches 77; Indels 2; Gaps 2;

QY 5 CSAS-EPTVAIVGSGKRVYDDDFDHQCIQLMPKSKNDPNQJMTIRKNTIRNSGS 63
DB 303 CSRSREPTVIGSDKQCVYDDDFDHQKQRLKMKCHRLKQKLENOQMTLSKDKTRNSK 362
QY 64 CLTVGYAGVYVWFPGQAVREATITNINDGNTINPRSNLYLAASGIGKTLTYGT 123
DB 363 CLTSEYAPGVYVWIDCTSAVAERATVWIDGNTINPRSNLYLAASGIGKTLTYGT 422
QY 124 LDVTLGQGLAGNDPAFREVITVGFDDLOHESNQSVWETGDSQKQKMAALYGGSI 183
DB 423 NSEILMRQKMTNTNTPPVTSISGYSDDLQKQKQSNVWALADCDNKKKQ-QVALVTGSI 481
QY 184 RKQNDQCLTVGRDSVSTVNTVSCASGSGRWFFTEYATILNKSGLADVAQANPK 243
DB 482 RSVQNTNCLTSKDKQSGPTVWASQSNWASQWLFKNDGSIYSLYDQWVDVSGSDPS 541
QY 244 LRRIITVPATGKQKQWLPVF 264
DB 542 LREIILHPHKKQKQIMLTF 562

RESULT 9
A:Cross-references: Indian licorice (fragment)
A:Residues: 1-570 <IND>
A:Reference number: S34408
A:Accession: S34408
A:Title: Primary structure of three distinct isoforms determined by cDNA sequencing.
A:Keywords: RNA N-glycosidase homology <RNG>
A:Comment: Brin consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
F/200-253, 361, 401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted
F/238-263, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F/500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.5%; Score 743; DB 2; Length 528;
Best Local Similarity 53.6%; Pred. No. 8, 7e-56;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;

QY 5 CSAS-EPTVAIVGSGKRVYDDDFDHQCIQLMPKSKNDPNQJMTIRKNTIRNSGS 63
DB 269 CSRSREPTVIGSDKQCVYDDDFDHQKQRLKMKCHRLKQKLENOQMTLSKDKTRNSK 328
QY 64 CLTVGYAGVYVWFPGQAVREATITNINDGNTINPRSNLYLAASGIGKTLTYGT 123
DB 329 CLTSEYAPGVYVWIDCTSAVAERATVWIDGNTINPRSNLYLAASGIGKTLTYGT 386
QY 124 LDVTLGQGLAGNDPAFREVITVGFDDLOHESNQSVWETGDSQKQKMAALYGGSI 183
DB 389 NSEILMRQKMTNTNTPPVTSISGYSDDLQKQKQSNVWALADCDNKKKQ-QVALVTGSI 447
QY 184 RKQNDQCLTVGRDSVSTVNTVSCASGSGRWFFTEYATILNKSGLADVAQANPK 243
DB 448 RSVQNTNCLTSKDKQSGPTVWASQSNWASQWLFKNDGSIYSLYDQWVDVSGSDPS 507
QY 244 LRRIITVPATGKQKQWLPVF 264
DB 508 LKQIILHPHKKQKQIMLTF 528

RESULT 10
A:Cross-references: European elder
A:Residues: 1-570 <IND>
A:Reference number: S62627
A:Accession: S62627
A:Title: The Neulac(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Keywords: RNA N-glycosidase homology <RNG>
A:Comment: Brin consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
F/200-253, 361, 401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted
F/238-263, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F/500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 36.6%; Score 517; DB 2; Length 570;
Best Local Similarity 44.4%; Pred. No. 2, 1e-36;

A:Cross-references: GB:M98346
R.Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-169, 'C', 171-320, 'V', 322-528 <RU2>
A:Cross-references: GB:M98346
A:Comment: Brin consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
F/1-251/Product: abrin-d chain A #status predicted <RNG>
F/7-246/Domain: RNA N-glycosidase homology <RNG>
F/261-528/Product: abrin-d chain B #status predicted <RNG>
F/283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/164, 167/Active site: Glu, Arg #status predicted
F/200, 253, 361, 401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted
F/238-263, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F/500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.5%; Score 743; DB 2; Length 528;
Best Local Similarity 53.6%; Pred. No. 8, 7e-56;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;

QY 5 CSAS-EPTVAIVGSGKRVYDDDFDHQCIQLMPKSKNDPNQJMTIRKNTIRNSGS 63
DB 269 CSRSREPTVIGSDKQCVYDDDFDHQKQRLKMKCHRLKQKLENOQMTLSKDKTRNSK 328
QY 64 CLTVGYAGVYVWFPGQAVREATITNINDGNTINPRSNLYLAASGIGKTLTYGT 123
DB 329 CLTSEYAPGVYVWIDCTSAVAERATVWIDGNTINPRSNLYLAASGIGKTLTYGT 386
QY 124 LDVTLGQGLAGNDPAFREVITVGFDDLOHESNQSVWETGDSQKQKMAALYGGSI 183
DB 389 NSEILMRQKMTNTNTPPVTSISGYSDDLQKQKQSNVWALADCDNKKKQ-QVALVTGSI 447
QY 184 RKQNDQCLTVGRDSVSTVNTVSCASGSGRWFFTEYATILNKSGLADVAQANPK 243
DB 448 RSVQNTNCLTSKDKQSGPTVWASQSNWASQWLFKNDGSIYSLYDQWVDVSGSDPS 507
QY 244 LRRIITVPATGKQKQWLPVF 264
DB 508 LKQIILHPHKKQKQIMLTF 528

RESULT 10
A:Cross-references: European elder
A:Residues: 1-570 <IND>
A:Reference number: S62627
A:Accession: S62627
A:Title: The Neulac(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Keywords: RNA N-glycosidase homology <RNG>
A:Comment: Brin consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglytamic acid
F/200-253, 361, 401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted
F/238-263, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F/500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 36.6%; Score 517; DB 2; Length 570;
Best Local Similarity 44.4%; Pred. No. 2, 1e-36;

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	Matches	115; Conservative	32; Mismatches	100; Indels	12; Gaps	6;
QY	5	CSASEPTVIVGSGARVDEDDPFHDCNOLOLMPSSKNNPDLOTTKXNDKNTISNSG	C	64		
Db	316	CSVEVETRIISGMDGLADVGRGVYIDGNPOLAR--CANEQCNLWTFPRIDGTIMVIGKC		373		
QY	65	LTFTGYAGVYNNIPDCNPAVEKTIWQMDNTINERSNIVLAASGIGKTLIVQTL		124		
Db	374	LT--HASSVWNTDNCNPPKATKAVSTIDTINPSSGLVTLPOAAGSLALSTEN		428		
QY	125	DVLTGGWAGNTPAPRSTVYIGRLCSMN--QSGVSTVCSQSGCKGKALYDGS		142		
Db	429	HAARQGWTVG-DVLEPLVETVYGRKQCLGRNSNNPVLMDCTVLRVQD--RMVLYDDET		486		
QY	183	IFRPNQDDCLTVGRDSVSTVINIVSCGASGSGQWFENETALILSGLDLVDAQAP		242		
Db	487	IKVNSNRSLCYTSBDEHSDDLVLKICRG--SGNQEVFTNTGISPNKALIMDAQDV		545		
QY	243	KLRRIIVPATGKPNQML	261			
Db	546	SKRKILVLPFGNPQOMI	564			

RESULT 11
JC7535
Chitinase [EC 3.2.1.14] 35 - Streptomyces thermoviolaceus
C:Species: Streptomyces thermoviolaceus
C>Date: 30-Jun-2001 #sequence_rev:30-Jun-2001 #ext_change 30-Jun-2001
C/Accession: JC7535
R:/Synbio: H.; Okamoto, T.; Hatanu, N.; Miyano, K.; Watanabe, T.; Mitsutomi, N.; Inoue
Biosci.: Biotechnol. Biochem. 64, 2445-2453, 2000
A>Title: Family 18 chitinases from Streptomyces thermoviolaceus CPC-520: Molecular cloning
A/Reference number: JC7535; PMID:21036907; PMID:1193414
A/Accession: JC7535
A/Molecule type: DNA
A/Residues: 1-377 #TSU-
A/Cross-references: DDBJ:25016942
C:Experimental source: strain CPC-520
C:Comment: This enzyme, a member of the family 18 chitinases, is involved in chitin degradation
in a chitinase-binding domain that is important in the efficient hydrolysis of insoluble chitin.
C/GeneID: 3155
A/Name: Ch155
A/Keywords: glycosidase; hydrolase

	Query Match	Best Local Similarity	20.9%	Score 129.5%	DB 2:	Length 377:
	Matches	Conservative	62	Mismatches 112:	Indels 89:	Gaps 16
Qy	7	ASPTVYVSGMAYRDPDHPHNGQGLMPSKSNPNQMLKNDTNSNSGCT	66			
Ds	33	AAHATSGITDELGCKLDVAGADAGAGAPVQIYDNGEN--AQQMTVSDDTILAKCLD	90			
Qy	67	TYEYVA--GVYVMTFCDTANATRAITVQIMDNGIINPNSHVLAA--SGIKETVLVQ	122			
Ds	91	VDSKSTADAKVQLMCTGGANMK--VYVAHADIYVNPAAKCLVLTDRSNANFTVQIV	148			
Qy	123	TLDTYLTGQGLA-----NQDAPEAVTI-----YQFADQCHNSQSGVW	162			
Ds	149	TCGGSGNQKNAFATGGASTAPSGVASEAQFQWFPNRPYVYQGLVQLAKPQGA	208			
Qy	163	ETDSSGQKQ-----GKALYDGD	181			
Ds	190	NPDQDTTQKGAHAFIAVNHGEGQLYVETELANITPYIDMGSGICGCAQAGQAGG	268			
Qy	192	SIRPQMOQCLTGVDSVSTVINSQSGA--S--SGRVTEYVALINSGCL	233			
Ds	269	FILQSNV-----NTKAGAGIAYGLDINNPVLVENDPALA--WKGGI	308			

```

RESULT 12
JS0589
endc-1,4-beta-xylosylase (EC 3.2.1.8) A precursor - Streptomyces lividans
N:Alternate names: xylosylase A

```

```
C|Species: Streptomyces lividans  
C|Name: 10-Mar-1994 #sequence_revision 22-Nov-1996 #ext_change 26-Feb-1999  
C|Accession: J050589; P80238  
R|ShareKey: F., Roy, C.; Yaguchi, M., Morosoli, R.; Kluepfel, D.  
Gene ID: 75-82_1991_CytB  
A|Title: Sequence of three genes specifying xylanases in Streptomyces lividans.  
A|Accession: J050589; N0219207433; PMID:1749521  
A|Molecule type: DNA  
A|Residues: 1-477 <SHA>  
A|Cross-references: GB:M64551  
A|Accession: P80238 protein  
A|Residues: 42-92 <SM2>  
C|Genetics:  
A|Gene: xlnA  
A|Description:  
A|Function: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylans  
A|Pathway: xylan degradation  
C|Superfamily: Streptococcus endo-1,4-beta-xylanase A; Streptococcus endo-1,4-beta-xylanase B; Bacillus subtilis endo-1,4-beta-xylanase; polysaccharide degradation  
F1:1|Domain: signal sequence stratum predicted SFG  
F2:2-477|Product: endo-1,4-beta-xylanase A Petrus experimental <NMT>  
F7:1-431|Domain: Streptococcus endo-1,4-beta-xylanase A homology <SVX>  
F7:169,277|Active site: glu #status predicted
```

```

Query Match      8.7%; Score 122.5; DB 1; Length 477;
Best Local Similarity 29.9%; Pred. No. 0.01;
Matches 40; Conservative 19; Mismatches 62; Indels 13; Gaps 6

QY 7 AASP-----TAAIVGSGCMVVDVRDDFDHGNQIOLAMSSKNDNDQTLTKIRNTIRSN 61
Db 346 SSSEPPDGGQIKRQG--FSCCLADVPASTSDGLOLMCHSGST--NQAADADAGELRY 402
QY 62 G--SCATTGYTAYGYVMFF--PQRTALAFETATINDGHTIINPSMUTVLA--SSSGIKRT 118
Db 403 GKXCLDAATSTNSKQIYSCWGEENQK--WRLNSDSVGVQSGCLCLAVGNCTANGTL 460
QY 119 LTVGTLDYTLAQGN 132
Db 461 IDLYTCSNNSQNR 474

```

```

RESULT 13
T34603
xylanase A - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence:revision 05-Nov-1999 #text:change 28-Jul-2000
C:Accession: T34603
R:Wu, P. Y., Harris, D., Parkhill, J., Barrett, B. G., Rajadaram, M. A.
submitted to the SDBL Data Library, January 1998
A:Reference number: Z21548
A:Accession number: Z21548
A:Status:preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-283 <EMR>
A:Cross-references: EMBL:AJ021539; FIDN:CAAL66.1;
A:Experimental source: strain AJ(2)
C:Genetics:
A:Gene: xlmA; SCOE0B:SC10A5.36c
C:Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylan
1-247;Domain: Streptomyces endo-1,4-beta-xylanase A homology <STX>

```

```

Best Match      8.5%: Score 119.5; Bf 2; Length 383;
Query Local Similarity 29.98%: Pval. 0.0; 0.014; 63; Indels 13; Gaps 6
Matches 40; Conservative 18; Mismatches 63;
QY 7 ASP-----TRVYGSMSSEVDEDDRDNDNGOGLMSKNDNDNOLWTFIRPONTIRSN 61
252 SSPPADGGQIKRGV--SRCLDVPASTSTDFGLQGLMSHST--NQGAANDADGELRY 308
D5 62 G-SCTTGYTAGVYMMIPFQNTAPRATIRINDGCTINPNSVYLA--SSGKGTG 118
QY 62 G-SCTTGYTAGVYMMIPFQNTAPRATIRINDGCTINPNSVYLA--SSGKGTG 118

```

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Db 309 GPKLDAAGTNGSKVQVYSCNGDNGK--WRINDSDVVGVSGLCLDANVGATNGTL 366
QY 119 LTVQTLDTLTGQGM 132
Db 367 IOLVTCNGSGNQRM 380

RESULT 14

33543
33544
33545
D:Sample hydrolytic protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T35943
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, N.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: 221551
A:Accession: T35943
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1744
A:Residues: 1744
A:Cross-references: EMBL:AL035206; FIDN:CA22765.1; GSPDB:GN00070; SCOPDB:SC9B5.23c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SC9B5.23c

Query Match

Best local similarity 27.4%; Score 113; DB 2; Length 464;

Matches

37; Conservative 28; Mismatches 52; Indels 18; Gaps 8;

QY

139 APPRY---TLYGF-RDCRSGNSQSYV---VENCDSGNOGQRMALYGGSTREKCH 188

Db

332 APEPVARGTITIGMANRCEV-NQHWMDGAPLQINDCTGSGNQMDPRPDGTH---S 387

QY

189 QDQCL--TVGRDSYTVINIVSGSGSGSQSGQSWETFEATILNLSGLANDYA-QANPELR 245

Db

388 LGLCLDALTWGTWGTWVGVAVCSG-NPAQOFLIAGPRDLVWVANKCYDVDEKTNCA 446

QY

246 RITITPATSGENQGM 260

Db

447 RLDGMECSGNQGM 461

RESULT 15

A39094
glucan endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - Oerskovia xanthineolytica

C:Species: Oerskovia xanthineolytica
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999

C:Accession: A39094
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, N.A.
submitted to the EMBL Data Library, January 1999

A:Reference number: 221551
A:Accession: A39094
A:Status: preliminary

A:Residues: 1-548 <SHS>
A:Cross-references: GB:M60826; GB:M38734; NID:g150444; PTDN:AA25520.1; PTD:g150445

A:Molecule type: DNA
A:Keywords: glycosidase; hydrolase

Query Match
Best local similarity 31.7%; Score 108; DB 2; Length 548;

Matches 39; Conservative 18; Mismatches 52; Indels 14; Gaps 6;

Query

16 SGKRVYRDDDEHNGQIQLPKSNNDPMQMTIKENTISNSCL--TYYGTAGY 75

Db

430 STCLDVPWADPTVNGVQL--ATCSGNAQQWTRGTDTGVALKCLDVASSTNDGTA 487

QY

76 VAIIDCN-TVREATITWQMDNGT--IINRSNIVLAASGL--KPTLTIVQTLDTLTG 129

Db

488 VITITNGTGAQNT---YDSKITALNPSGKCLDQSGAPLADQKQVQWTCQTERA 543

QY

130 QGM 132

Db 544 QRM 546
Search completed: December 11, 2003, 13:55:44
Job time: 9.20622 secs

GenCore version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 4.53677 Seconds
(without alignments)

2736.539 Million cell updates/sec

Title: US-09-601-667C-8

RefSeq score: 1414

Sequence: 1 DDTYCSASEPTVRIYVNSGM.....RRIITYPARGKNQWLPVF 264

Scoring table: Biosum62

Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1379	97.5	264	1 MIB_VITNL
2	896.5	63.4	596	1 RICI_RICCO
3	764.5	54.1	564	1 AGGL_RICCO
4	758	52.6	528	1 ABRA_ARPR
5	744	52.6	527	1 ABRC_ARPR
6	744	52.6	562	1 ABRC_ARPR
7	516.5	36.5	563	1 NIGB_SAMNI
8	122.5	8.7	477	1 XNVA_STRLI
9	108	7.6	348	1 E11B_ARPS
10	108	7.6	348	1 E11B_ARPS
11	107.95	7.6	348	1 E11B_ARPS
12	105	7.4	525	1 SPI_ESTR
13	104.5	7.4	475	1 ABPR_STRLI
14	91.5	6.5	1526	1 VY46_ANASP
15	90	6.4	1723	1 PM40_CHLPM
16	87.5	6.2	545	1 AGAL_ASPNG
17	87.5	6.2	827	1 YZ23_METVA
18	87.5	6.2	1258	1 YS00_ANASP
19	87	6.2	880	1 CADP_XANLA
20	86.5	6.1	1693	1 Y163_SNVY3
21	86	6.1	1943	1 D1P2_YRST
22	85	6.1	1483	1 T24_AANSP
23	85	6.0	1054	1 RPOC_XERPA
24	85	6.0	1054	1 RPOC_XERPA
25	84.5	6.0	231	1 F1GD_TROLI
26	84.5	6.0	288	1 V609_BPT4
27	84.5	6.0	1577	1 HLYA_PROMT
28	84	5.9	1265	1 RPOD_CVAP
29	84	5.9	4074	1 PKHD_HUMAN
30	82.5	5.8	471	1 VVHA_VIBUV
31	82.5	5.8	510	1 YDID_SCHPO
32	82	5.8	386	1 RGLM_ASPFO
33	82	5.8	617	1 V311_BPMO2

ALIGNMENTS

Result No.	Score	Query Length	DB ID	Description
1	1379	97.5	264	1 MIB_VITNL
2	896.5	63.4	596	1 RICI_RICCO
3	764.5	54.1	564	1 AGGL_RICCO
4	758	52.6	528	1 ABRA_ARPR
5	744	52.6	527	1 ABRC_ARPR
6	744	52.6	562	1 ABRC_ARPR
7	516.5	36.5	563	1 NIGB_SAMNI
8	122.5	8.7	477	1 XNVA_STRLI
9	108	7.6	348	1 E11B_ARPS
10	108	7.6	348	1 E11B_ARPS
11	107.95	7.6	348	1 E11B_ARPS
12	105	7.4	525	1 SPI_ESTR
13	104.5	7.4	475	1 ABPR_STRLI
14	91.5	6.5	1526	1 VY46_ANASP
15	90	6.4	1723	1 PM40_CHLPM
16	87.5	6.2	545	1 AGAL_ASPNG
17	87.5	6.2	827	1 YZ23_METVA
18	87.5	6.2	1258	1 YS00_ANASP
19	87	6.2	880	1 CADP_XANLA
20	86.5	6.1	1693	1 Y163_SNVY3
21	86	6.1	1943	1 D1P2_YRST
22	85	6.1	1483	1 T24_AANSP
23	85	6.0	1054	1 RPOC_XERPA
24	85	6.0	1054	1 RPOC_XERPA
25	84.5	6.0	231	1 F1GD_TROLI
26	84.5	6.0	288	1 V609_BPT4
27	84.5	6.0	1577	1 HLYA_PROMT
28	84	5.9	1265	1 RPOD_CVAP
29	84	5.9	4074	1 PKHD_HUMAN
30	82.5	5.8	471	1 VVHA_VIBUV
31	82.5	5.8	510	1 YDID_SCHPO
32	82	5.8	386	1 RGLM_ASPFO
33	82	5.8	617	1 V311_BPMO2

FT	VARIANT	231	231	N	-	S	OR	T	
FT	VARIANT	231	231	N	-	SG	OR	T	
FT	VARIANT	231	231	N	-	SG	OR	T	
FT	VARIANT	231	231	N	-	SG	OR	T	
SO	SEQUENCE	264	AA	23981	MM	7DDCG32CCCF55A4	CRC64		
Query Match	Similarity	97.54	Score 1379	DB 1	Length 264				
Base Local	Similarity	97.78	Score 1422	DB 1	Length 264				
Matches	258	Conservative	2	Mismatches	2	Indels	0	Gaps	0
QY	1	DVDTGSASBEPTLRVYSGSASGVYRDDPHDDNQOLQMSKSSNNDDPOLWTKRENTNIS	60						
Db	1	DVDTGSASBEPTLRVYSGSASGVYRDDPHDDNQOLQMSKSSNNDDPOLWTKRENTNIS	60						
QY	61	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
Db	61	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
QY	121	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
Db	121	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
QY	121	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
Db	121	NSGCLTGYTGAGYVAILPDQNTARENTIWOIMDNELINERSNIVLAASGINKGTLT	120						
QY	181	GSIRGRNQDQOLTVSGDSVETVIVINVS CGSASGSGRWFTNEVAILMLSGSLANDVQA	240						
Db	181	GSIRGRNQDQOLTVSGDSVETVIVINVS CGSASGSGRWFTNEVAILMLSGSLANDVQA	240						
QY	241	NPPLKRIIIVPTAKRPMQLPVF	264						
Db	241	NPPLKRIIIVPTAKRPMQLPVF	264						

[illegible]

DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DR Rich precursor (Continfs: Rctin A chain (tRNA N-glycosidase)
DS EC 3.2.2.22; Rctin B chain).
OS Ricinus communis (Castor bean).
OS Bakaraeae: Viridiplantae; Streptophyta; Embryophyta; Tracheophytes;
OC eudicotyledons; Malvaceae; Euphorbiales; Euphorbiaceae; Ricinus.
OX NR_1_TxId=3386;.
RX
RY SEQUENCE FROM N.A.
RP MEDLINE=86067214; PubMed=2699712;
RA Halling K.F., Halling A.C., Murray S.E., Ladin B.P., Houston L.T.,
RZ Weaver R.P.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
RR communis".
RL Nucleic Acids Res. 13:8013-8033(1985).
RN
RU SEQUENCE FROM N.A.
RV MEDLINE=92163016; PubMed=1371405;
RW Tregear T.W., Roberts L.M.;
RX "The lectin gene family of Ricinus communis: cloning of a functional
RY ricin gene and three lectin pseudogenes".
RL Plant Mol. Biol. 18:515-525(1992).
RN [3]
RP SEQUENCE OF 12-576 FROM N.A.
RV MEDLINE=85179479; PubMed=8838723;
RW Lamb A., Roberts L.M., Lord J.M.;
RX Nucleotide sequence of cloned cDNA coding for preproricin".
RY J. Biochem. 146:1265-270(1985).
RN [4]
RP SEQUENCE OF 36-302.
RV Yoshitake S., Funatsu M.;
RX "Isolation and sequences of peptide sequences, and the complete
RY sequence of the chain of ricin-D".
RL Agric. Biol. Chem. 42:1267-1274(1978).
RN [5]
RP SEQUENCE OF 315-576.

RA Punatier G., Kimura M., Punatier M.;
 RA "Primary structure of Ala chain of ricin D.";
 RT *Agric. Biol. Chem.* 43:1221-1224(1979).
 RL [6].
 RN CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
 RX MEDLINE=30344223; PubMed=1568517;
 RX "Primary structure of the N-glycan chains of ricin A-chain";
 RT *J. Biol. Chem.* 262:5398-5403(1987).
 RL [9].
 RN REVIEW.
 RX MEDLINE=21480122; PubMed=11595634;
 RX Olsnes S., Kozlov J.V.;
 RL *Toxicol.* 39:1732-1728(2001).
 RN [10].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=87165993; PubMed=5583897.
 RX Montfort M., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B.,
 RA Rumberg E., Xiong N.H., Hamlin R., Robertus J.D.;
 RT "The three-dimensional structure of ricin at 2.8 Å";
 RL *J. Biol. Chem.* 262:5398-5403(1987).
 RN [9].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=91552004; PubMed=1691681;
 RX Katzin B.J., Collins B.O., Robertus J.D.;
 RL *Proteins* 10:251-259(1992).
 RN [10].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RX MEDLINE=91552005; PubMed=1691682;
 RX Rumberg E., Robertus J.D.;
 RT "Structure of ricin B-chain at 2.5-Å resolution.";
 RL *Proteins* 10:260-269(1992).
 RN [11].
 RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=50582010; PubMed=9901307;
 RX Pasapiri R.A., Tucker A.D., Thatcher D.R., Deryshvite D.J.;
 RT "X-ray structure of recombinant ricin A-chain at 1.8-Å resolution";
 RL *J. Mol. Biol.* 244:410-420(1998).
 RN [12].
 RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HTS-215.
 RX MEDLINE=96374222; PubMed=9705133;
 RX Day P.J., Ernst S.R., Pankel A.E., Monzingo A.F., Pascal J.M.,
 RA Molina-Synth M.C., Robertus J.D.;
 RT "Structure and activity of an active site substitution of ricin A
 RL [13].
 RX "Structure-based identification of a ricin inhibitor";
 RL *J. Mol. Biol.* 266:1043-1049(1997).
 RN [14].
 RX MEDLINE=91165632; PubMed=1267657;
 RX Kin Y., Robertus J.D.;
 RT "Analyses of several key active site residues of ricin A chain by
 RL *Protein Eng.* 5:775-779(1992).
 RN [15].
 RX -1- FUNCTION. Ricin is highly toxic to animal cells and to a less
 RX extent to plant cells. The A chain is responsible for inhibiting
 RX protein synthesis through the catalytic inactivation of 60S
 RX ribosomal subunits. It acts as a glycosylase that removes a
 RX RNA adenosine residue from an exposed loop of 28S ribosomal
 RX RNA. This modification inhibits the binding of eukaryotic
 RX factors. The modified ribosomes are unstable and support protein
 RX synthesis. The A chain can inactivate a few thousand ribosomes
 RX per minute, thus inactivating them faster than the cell can make
 RX new ones. A single A chain molecule can therefore kill an animal

CC cell. The B chain binds to cell receptors and facilitates the
CC entry into the cell of the A chain; B chains are also responsible
CC for cell agglutination (lectin activity). It binds to beta-D-
CC galactopyranoside moieties.
CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: Disulfide-linked dimer of A and B chains.
CC -1- DOMAIN: The B chain is composed of two domains, each domain
CC consists of 3 homologous subdomains (alpha, beta, gamma).
CC -1- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
CC DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 31 of February 2003;
CC WWW=http://www.ezraasy.org/spotlight/articles/spot1031.html".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X03179; CA26939.1; -;
DR EMBL: X52908; CA37095.1; -;
DR EMBL: X02388; CA26230.1; -;
DR EMBL: A12892; CA01058.1; -;
DR PIR: A24041; RLCSD.
DR PDB: 2Aa1; 3i-DAN-94.
DR PDB: 1Ae9; 3i-DAN-94.
DR PDB: 1FmP; 3i-OCT-93.
DR PDB: 1If8; 14-DAN-98.
DR PDB: 1If7; 14-DAN-98.
DR PDB: 1IfU; 14-DAN-98.
DR PDB: 1RtC; 3i-OCT-93.
DR PDB: 1Oe8; 16-DUN-97.
DR PDB: 1ObT; 16-DUN-97.
DR PDB: 1BR5; 02-SEP-98.
DR PDB: 1BR6; 02-SEP-98.
DR PDB: 1113; 16-DAN-02.
DR PDB: 1114; 16-DAN-02.
DR PDB: 1115; 16-DAN-02.
DR GlycoSuiteDB: P02879; -;
DR InterPro: IPR001772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2

FT DISURFD 377 394
FT DISURFD 465 478
FT DISURFD 504 521
FT CARBOHYD 45 45
FT CARBOHYD 271 271
FT CARBOHYD 409 409
FT CARBOHYD 449 449
FT CONFLICT 76 76
FT CONFLICT 551 551
FT STRAND 43 47
FT TURN 49 50
Query Match 63.4%; Score 896.5; DB 1; Length 576;
Best Local Similarity 63.5%; Pred. No. 4,8e-70;
Matches 165; Conservative 53; Mismatches 61; Indels 1; Gaps 1;
QY 5 CSASEPVRIVRSRRVYRDDPHDNOIQLPKSKNDPNQMTWKEDNTRSGSC 64
DB 318 CMDEPIYRVARNGLOVDYDGRFNNHAIQMPCKSTDAQMLTKEDNTRSGSC 377
QY 65 LITGTPAGVYVIFDONTAVRENTIWIQNDGIIINPESHVLAASSGKSTLTWQTL 124
DB 378 LITGYSRGVYVIMDNTAATRAIRNGIITINPSSVLVAATSGSTLTWQTN 437
QY 125 DYTGGWLAGNDTAPREVTIYGFQDQWESQSVAVETCSSQDQNGWALYGDGSR 184
DB 438 IYVSGWELPTWNPQPEVTIYVGLQDQANSQWIEDC-SSEKMQQWALYADGSR 496
QY 188 EKNDQGLTVGRDSYTVIMVICSQSGSRQVTFNENYAIINLSLMTVYQANFTL 244
DB 497 PQQRNGLTSDSNIRETVYKILSGPSSGQRMKFRNDGIIINLYSGVLVYRASPSTL 556
QY 245 RLIIYPAKGNQMLPVF 264
DB 557 KQIIIVPMDNQMLPVF 576
RESULT 3
AGEL RICOO STANDARD; PRT; 564 AA.
AC P06750;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-
DE glycosidase) (EC 3.2.2.22); Agglutinin B chain).
OS Ricinus communis (castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eutoside I; Malpighiales; Euphorbiaceae; Ricinus.
NCBI_TaxID=3988;
EN [1]

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rtf

Page 4

[illegible]

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DB   146 IYASGCMFNNRQCFVTTIVGLGMCIGIANSKRWLEDC-YSKSGEOMALVADSR 494
OY   185 PRONDDCLTVGRDSVFVNIVYSCSAGCSQRWTFTEVALINIKSLMDVYAQNPL 244
DB   145 FQNDNCDLTDNIDKMGVLEAF 264
CY   245 RRIYPAKCKGNMDELF 264
DB   545 KOTIVHFGMLNDIMLELF 564

RESUT 4
ABRA ABPR STANORD; PRT; 528 AA.
ID ABRA ABPR STANORD; PRT; 528 AA.
PI10: P2889;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB AbPrin-a precursor [Contains: AbPrin-A chain (tRNA N-glycosidase)]
DB AbPrin-B precursor [Contains: AbPrin-B chain (tRNA N-glycosidase)]
DB AbPrin-C precursor [Contains: AbPrin-C chain (tRNA N-glycosidase)]
OC Bacteriophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoids 1; Fabales; Fabaceae; Papilionoideae; Abruseae; Abrus;
NCBI_TaxId=3816;
RN (1)
RN SEQUENCE FROM N.A. Pubmed=9421113;
RN MEDLINE=91201123; PubMed=2016300;
RN Hann C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
RN "Primary structure of three distinct isoforms determined by cDNA
RN sequencing. Conservation and significance.";
RN J. Mol. Biol. 229:263-267(1993).
RN (2)
RN SEQUENCE OF 1-251.
RN TISSUE=seed.
RN "Abprin-a, a protein from the seeds of Abrus precatorius".
RN Agric. Biol. Chem. 57:1095-1097(1986).
RN (3)
RN SEQUENCE OF 1-251 FROM N.A.
RN TISSUE=leaf.
RN MEDLINE=91201123; PubMed=2016300;
RN Hann C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
RN "Direct molecular cloning and expression of two distinct abrin
RN A-chains";
RN J. Biol. Chem. 266:16848-16852(1991).
RN (4)
RN SEQUENCE OF 262-528.
RN MEDLINE=9231165; PubMed=1505674;
RN Chen Y.-D., Chou L.-P., Tseng H.-A., Lin J.-Y.;
RN "Isolation and characterization of complementary DNA clones encoding
RN the direct molecular cloning and expression of two distinct abrin
RN A-chains";
RN FEBS Lett. 309:115-116(1992).
RN (5)
RN X-RAY CRYSTALLOGRAPHY (2.14 ANGSTOMS);
RN MEDLINE=9533188; PubMed=7608980;
RN Tahirov T.H., Li T.-H., Liaw Y.-C., Chen Y.-D., Lin J.-Y.;
RN "Crystal structure of abrin-a at 2.14 A.";
RN J. Mol. Biol. 250:355-367(1995).
RN -1- SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
RN SUBUNIT BY REMOVING ADENINE FROM POSITION 4,124 OF 28 S RNA.
RN ABRIN-A IS MORE TOXIC THAN RICIN.
CC -1- FUNCTION: THE B INDICES OF ABRIN TO THE CELL MEMBRANE THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PERMEABLE ENDOCYTOSIS.
CC -1- STABILITY: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- SPECIFIC DETECTION OF THE 28S rRNA.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL TYPE 2 RIP SUBFAMILY.
CC INACTIVATING PROTEIN FAMILY.

```

DB 146 IYASGCMFNNRQCFVTTIVGLGMCIGIANSKRWLEDC-YSKSGKQCMALVADSR 494

DB 145 PRONDDCLTVGRDSVFVNIYVSCSASGSGRWTFTEVALINIKSLMDVYQANPL 244

DB 145 FQNDNDCLTVGRDSVFVNIYVSCSASGSGRWTFTEVALINIKSLMDVYQANPL 544

Cy 245 RRIYVPAKCGKMGVLEVF 264

DB 545 KQIVHFPGMLNDIMLELF 564

SEQUIT 4

ID ABRA ABPR STANORD; PRT; 528 AA.

PI110: P28589;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Abtin-a precursor [Contains: Abtin-a chain (tRNA N-glycosidase)]

DB Abtin-a chain (tRNA N-glycosidase)

DB Abtin-a chain (tRNA N-glycosidase)

CC Bacteria: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

CC eucoids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrys;

NCBI_TaxID=3816;

RN (1)

RN SEQUENCE FROM N.A.

RN MEDLINE=91201323; PubMed=48421313;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 229:263-267 (1993).

RT [2]

RN SEQUENCE OF 1-251.

RN TISSUE=seed.

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 229:263-267 (1993).

RT [3]

RN SEQUENCE OF 1-251 FROM N.A.

RN TISSUE=leaf.

RN MEDLINE=91201323; PubMed=2016300;

RN "Direct molecular cloning and expression of two distinct abtin A-chains.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [4]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [5]

RN X-RAY CRYSTALLOGRAPHY (2.14 ANGSTOMS).

RN MEDLINE=95331183; PubMed=7608980;

RN Tahirov T.H., Li T.-H., Liaw Y.-C., Chen Y.-D., Lin J.-Y.;

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [6]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [7]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [8]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [9]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [10]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [11]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [12]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [13]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [14]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [15]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [16]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of abtin-a at 2.14 A.";

RN J. Mol. Biol. 250:385-391 (1995).

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Biol. Chem. 266:16848-16852 (1991).

RN [17]

RN SEQUENCE OF 262-528.

RN MEDLINE=92371656; PubMed=1505674;

RN "The complete amino acid sequence of the A chain of abtin-a, a toxic protein from the seeds of *Abrys precatorius*.";

RT J. Mol. Biol. 250:385-391 (1995).

RN "Crystal structure of

CC -----1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -----
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CC -----
DR EMBL; M98344; AAA32624.1; ALT INIT.
DR EMBL; X54872; -; NOT_ANNOTATED_CDS.
DR PIR; S32429; T2LSN.
DR PDB; 1ABR; 07-FEB-95.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00161; Ricin_B_lectin; 6.
DR PRINTS; PR00356; SHIGARICIN.
DR SMART; SM00458; RICIN_2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; 3D-structure; Pyroglutamate carboxylic acid.
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FT PEPTIDE 252 261
FT DOMAIN 262 261
FT DOWN 263 490
FT REPEAT 283 325
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FT REPEAT 369 401
FT REPEAT 414 449
FT REPEAT 453 492
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FT DISULFID 326 345
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FT STRAND 497 501

Query Match 53.6%; Score 758; DB 1; Length 528;
Best Local Similarity 54.4%; Pred. No. 4, 1e-58;
Matches 142; Conservative 42; Mismatches 75; Indels 2; Gaps 2;
CY 5 CSAS-EPTVIRVSGKRVAVDADDFHDCNQIQWESKNNPDQMTIKDNTIRSGS 63

DB 269 CSSEYPTVIRIGRQKCVVDYDGNHNGNRIIMKCKLEEMQATLKSKDITRANK 328
QY 64 CLTGYAGYVWIMFDCTNAREATVQIWDGTLINPESNLVLAASGIGKTLTVOT 123
DB 329 CLTGYAGYVWIMFDCTNAREATVQIWDGTLINPESNLVLAASGIGKTLTVOT 388
QY 124 LPTLQGMALNDTAPREVTYGRDLCMESQSVWETQSSQKQKALYGGSI 183
DB 389 NEYLMQGMRTGNNSPVTISQSDLOMQSGSNWADCDNKQD QNALTDGSI 447
QY 184 RPKNOQDCLTVGRDSVSTVIVYSCGASGQSWFTNEVAILNKSGLAMVQANX 243
DB 448 RSVQNNCLTSKDKHQSITLLMGCSNMAQSWFVFNQSGISYLDMDVMDVGSDB 507
QY 244 LRRTIIPATGKPNQMWLPVF 264
DB 508 LKQIILPPTGKPNQMWLPVF 528

RESULT 5

ABRB_ABRP STANDARD: PRT: 527 AA.

AC 006077: P81374;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abxin-b precursor [Contains: Abxin-b A chain (RNA N-glycosidase)
DE (EC 3.2.2.22); Abxin-b B chain)
OS Abxin precursor (human Abxin-b) (Crab's eye);
OS Abxin precursor (human Abxin-b) (Crab's eye);
OC Spermatophyta: Magnoliopsida: Euphorbiaceae: Euphorbia
OC Euphorbia: Euphorbia
OX NCBI_TaxID=3816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9332798; PubMed=842233;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isobutins determined by cDNA
RT sequencing. Conservation and significance.";
RN [2]
RN Mol. Biol. 229:263-267 (1993).
RP SEQUENCE OF 260-527.
RC Tissue=seed;
RX MEDLINE=9316903; PubMed=7763422;
RA Kimura M., Sumitani T., Funatsu G.;
RT "The complete amino acid sequences of the B-chains of abxin-a and
RT abxin-b, toxic proteins from the seeds of Abux precursor.";
RL Biochim. Biophys. Acta 571:166-169 (1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- SIMILARITY: THIS TOXIC PROTEIN RESEMBLES THE RIBOSOME-
CC INHIBITING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -----
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DR EMBL: M98345; AAA13625.1;
DR PIR: S12430; S32430.
DR HSSP: P11440; 1ABR.
DR Interpro: IPR000772; Ricin_B_lectin.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00356; SHIGARICIN.
DR SMART: SM00583; RICIN_2; LECTIN; 2.
DR PROSITE: PS00221; SHIGARICIN; 1.
KW Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lactin; Pyridoxone carboxylic acid.
FT CHAIN 1 260
FT PEPTIDE 251 260
FT CHAIN 1 260
FT DOMAIN 272 399
FT DOMAIN 402 526
FT REPEAT 282 324
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FT REPEAT 361 413
FT REPEAT 414 448
FT REPEAT 452 491
FT ACT SITE 163 163
FT DISULFID 246 268
FT DISULFID 285 304
FT DISULFID 328 345
FT DISULFID 416 429
FT DISULFID 455 472
FT MOD RES 1 1
FT CARBOHYD 110 110
FT CARBOHYD 360 360
FT CARBOHYD 400 400
FT CONFLICT 282 282
FT CONFLICT 291 291
FT CONFLICT 350 351
FT CONFLICT 378 378
FT CONFLICT 426 426
FT CONFLICT 428 428
FT CONFLICT 432 432
FT CONFLICT 434 434
FT CONFLICT 481 481
FT CONFLICT 491 491
FT CONFLICT 502 502
FT CONFLICT 509 509
FT CONFLICT 513 513
FT CONFLICT 516 516
FT SEQUENCE 527 AA; 59114 MW; 3253A940CE49A CRC64;
Query Match 52.6%; Score 744; DB 1; Length 527;
Best Local Similarity 53.6%; Freq. No. 6; 7e-57;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;
QY 5 CSSEYPTVIRIGRQKCVVDYDGNHNGNRIIMKCKLEEMQATLKSKDITRANK 327
DB 268 CSSEYPTVIRIGRQKCVVDYDGNHNGNRIIMKCKLEEMQATLKSKDITRANK 327
QY 64 CLTGYAGYVWIMFDCTNAREATVQIWDGTLINPESNLVLAASGIGKTLTVOT 123
DB 328 CLTGYAGYVWIMFDCTNAREATVQIWDGTLINPESNLVLAASGIGKTLTVOT 387
QY 124 LPTLQGMALNDTAPREVTYGRDLCMESQSVWETQSSQKQKALYGGSI 183
DB 389 NEYLMQGMRTGNNSPVTISQSDLOMQSGSNWADCDNKQD QNALTDGSI 446
QY 184 RPKNOQDCLTVGRDSVSTVIVYSCGASGQSWFTNEVAILNKSGLAMVQANX 243
DB 447 RSVQNNCLTSKDKHQSITLLMGCSNMAQSWFVFNQSGISYLDMDVMDVGSDB 506
QY 244 LRRTIIPATGKPNQMWLPVF 264

	RESULT 6	STANDARD;	PRT;	562 AA.
Db	507 LKAITHHYHGKPGKQIMTLWF 527			
AC	128550			
AD	128550			
AE	128550			
AF	128550			
AG	128550			
AH	128550			
AI	128550			
AJ	128550			
AK	128550			
AL	128550			
AM	128550			
AN	128550			
AO	128550			
AP	128550			
AQ	128550			
AR	128550			
AS	128550			
AT	128550			
AV	128550			
AW	128550			
AX	128550			
AY	128550			
AZ	128550			
BA	128550			
BB	128550			
BC	128550			
BD	128550			
BE	128550			
BF	128550			
BG	128550			
BH	128550			
BI	128550			
BJ	128550			
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BM	128550			
BN	128550			
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BP	128550			
BQ	128550			
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BS	128550			
BT	128550			
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BV	128550			
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BX	128550			
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BZ	128550			
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CK	128550			
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CM	128550			
CN	128550			
CO	128550			
CP	128550			
CQ	128550			
CR	128550			
CS	128550			
CT	128550			
CU	128550			
CV	128550			
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CX	128550			
CY	128550			
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CC	128550			
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CF	128550			
CG	128550			
CH	128550			
CI	128550			
CJ	128550			
CK	128550			
CL	128550			
CM	128550			
CN	128550			
CO	128550			
CP	128550			
CQ	128550			
CR	128550			
CS	128550			
CT	128550			
CU	128550			
CV	128550			
CW	128550			
CX	128550			
CY	128550			
CA	128550			
CB	128550			
CC	128550			
CD	128550			
CE	128550			
CF	128550			
CG	128550			
CH	128550			
CI	128550			
CJ	128550			
CK	128550			
CL	128550			
CM	128550			
CN	128550			
CO	128550			

[illegible]

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rsp

Page 8

CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE
CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
CC ENDOCYTOSIS.
CC
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S RRNA.
CC -I- SIMILARITY: IN THE N-TERMINAL SEQUENCE; BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIB SUBFAMILY.
CC
CC -I- SIMILARITY: Contains 2 richly B-type lectin domains.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@ebi.ac.uk).

DR	SMO01_471226	122294475.1	-	
DR	PIR_537382	537382	Ricin_B_lectin	
DR	InterPro: IPR0010732		Ricin_B_lectin	
DR	InterPro: IPR001574		RIP	
DR	Pfam: PF00652		Ricin_B_lectin; 6	
DR	Pfam: PF00661		RIP; 1	
DR	PRINTS: PR003967		SHIGACININ	
DR	SMART: SMO0458		RICIN; 2	
DR	PROSITE: PS00275		SHIGA_RICIN; 1	
DR	PROSITE: PS02031		RICIN_B_LECTIN; 2	
KW	Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;			
KM	Glycoprotein; Lectin; Signal			
FT	SIGNAL	1	25	
FT	CHAIN	288	563	
FT	CHAIN	288	563	NIGERIN B A CHAIN
FT	DOMAIN	305	431	NIGERIN B CHAIN
FT	DOMAIN	434	559	RICIN B-TYPE LECTIN 1.
FT	REPEAT	316	356	RICIN B-TYPE LECTIN 2.
FT	REPEAT	357	397	1-ALPHA.
FT	REPEAT	400	432	1-BETA.
FT	REPEAT	445	482	1-GAMMA.
FT	REPEAT	546	554	2-ALPHA.
FT	REPEAT	567	554	2-BETA.
FT	REPEAT	557	554	2-GAMMA.
FT	ACT_SITE	158	168	BY SIMILARITY.
FT	ACT_SITE	219	332	INVERSELY BY SIMILARITY.
FT	DISULFID	219	332	BY SIMILARITY.
FT	DISULFID	360	377	BY SIMILARITY.
FT	DISULFID	448	463	BY SIMILARITY.
FT	DISULFID	489	506	BY SIMILARITY.
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. .)
FT	CARBOHYD	368	368	N-LINKED (GLCNAC. .)
FT	CARBOHYD	376	376	N-LINKED (GLCNAC. .)
FT	CARBOHYD	483	483	N-LINKED (GLCNAC. .)
FT	CARBOHYD	537	537	N-LINKED (GLCNAC. .)
FT	CONFLICT	39	39	(POTENTIAL).
QO	SEQUENCE	563 AA;	62300 MW;	K -> V (IN REP. 2)
				P250CBR24521B14 CRG64;

Query Match 36.5%; Score 516.5; DB 1; Length 563;

Matches 108; Conservative 43; Mismatches 106; Indels 7; Gaps 5;

QY 1 DDVTCSASEPTVR-IVGRSGMRVDVRRDDFDHGNQIQLMPSKSNNDPNQLWTIKRDNTIR 59

Db 298 DGETCTLRISFTRNIVGRDGLCVDRNGYDTDGTPLQLWPCGTOR--NQRWTFDSDDTIR 355

QY 60 SNGSCLTTYGYTAGVYVMI FDCNTAVREATIWIQIWDNGTIINPRSNLVLAASSGIKGTTL 119

Db 356 SMGKCMTANGLNNGSNIVIFNCSTAENAIKWEVPIDGSIINPSSGLVMTAPRAASRTIL 415

120 TVQTLDBYTLGGWLAGNDTAPREVITYGFRDLCMESN--QGSVWVEITCDSSQKNQKMWAL 177

DB 416 LLEBDNIXAASQGWTVTNNVKPIVASIVGYKEMCLQSNGENNGVMMEDCEATSLQ-QWAL 474

QY	178	YGGISGIPFQMOQDCLITGGDSSTVYINIVSGSAGSGSRQWFTWEXALINIKSGIANDV	237
DB	475	YGRIRIVNSFRGLCVLTNNYNSKLLIILNCGQPL-SGRWFNSDSGATWPKSRHWVD	533
QY	238	AAQANFKLPELIIIIIPANGSEPMQML	261
DB	534	RASNSVLEIRLIIIPANGSEPMQNV	557
RESULT 8			
XYNA_STRL1			
ID	XYNA_STRL1	STANDARD:	PRT: 477 AA.
AC	P26514: P96464:		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)		
DS	(1,4-beta-D-xylan xylanohydrolase A).		
EN	KLDA		

CC CC
OC Streptomyces lividans L., Actinobacteridae; Actinomycetales;
OC Streptomyces lividans L., Actinomycetales; Streptomycetaceae;
CC Streptomyces lividans L., Actinomycetales; Streptomycetaceae;
CN NCBI_TextID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yanuch M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylosylases in Streptomyces
lividans;"
RL Gene 107:75-82(1991).
RN [2]
RL REVISIONS TO 20 AND 140-141.
RX STRAIN=66 / 1326;
RA Shareck F. / 1326;
RL Submitted (JUL-1998) to the EMBL/GenBank/CDDB databases.
[3]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-240.
RX MEDLINE=9434223; PubMed=806593;
RA Devereuda U., Swenson L.V., Green R., Wei Y.Y., Shareck F.,
RA Kluepfel D., Devereuda Z.S.;
RT "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans
xylosylase A, a member of the F family of beta-D-1,4-D-glycosylases";
RJ J. Biol. Chem. 266:20811-20814(1991); PubMed=1743521;
CC -1- FUNCTION: Enrichment of the major carbon source, xylan, seems to act
CC sequentially on the substrate to yield xylobiose and xylose
CC as carbon sources
CC
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: Contains 1 rich B-type lectin domain.

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CC-----
CC-----
DE-----
DEBT - MCAEET - ACCOCCOE ?

DR JS0589; JS0589.
PIR;
PFB: 1YAC. 31 MAY 05

DR PDB; 1E0V; 25-MAY-01.
 DR PDB; 1E0V; 25-MAY-01
 DR PDB; 1E0V; 25-MAY-01

DR PDB; 1KNL; 19-JUN-02.
DE PDB; 1KYM; 19-JUN-02

DR PDB; 1MC9; 11-SEP-02.
DB Tuto-Pro; TEP001000; Clues budwe 10

```
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00031; Glyco_hydro_10; 1.
DR SMART: SM00452; Ricin_B_lectin; 3.
DR SMART: SM00452; Ricin_B_lectin; 1.
DR SMART: SM00452; Ricin_B_lectin; 1.
DR PROSITE: PS00531; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00531; Ricin_B_lectin; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; Lactin;
KV 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
FT ACT_SITE 169 169 PROTON PUMP.
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 5162 MW; 5147FE37EDC69CC CRC64;

Query Match
Best Local Similarity 29.9%; Pred. No. 0.0033.
Matches 40; Conservative 19; Mismatches 62; Indels 13; Gaps 6;

OY 7 ASBP-----TVIVGSGKRVADDDPHGNGQLMPKSNNDPQWLTKIKNDITRN 61
DB 346 SSEPDPDQGIKGVG-SGRCLDVPDASTDQTLQMDCHSGT--NQQMAIDAGELRY 402
OY 62 G-SCITTYGAGTWMIPDQNAVEATWQIMDNGITINRSNLVLA--SSGIXGT 118
DB 403 GPKLDMAQTSNSKQISGCGDQK--WKLNDQSVGVOSGLDVAVGTNGTL 460
OY 119 LTVQTLDTYLGQW 132
DB 461 IDLYTCSNSQW 474

RESULT 9
E13B_ARTSP STANDARD; PRT; 548 AA.
ID E13B_ARTSP
RT 15-JUL-1998 (Rel. 36, Created)
DT 15-OCT-2001 (Rel. 36, Last sequence update)
DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-
DE glucan endohydrolase) ((1->3)-beta-glucanase).
GN GUCI.
OS Arabidopsis sp. (strain YCWD3).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Micrococcales; Micrococcaceae; Arthrobacter.
OX NCBI_TaxId=167;
RA Sequence from N.A.
RP Walmsley C, Hasenack H, Tanaka H, Doi A, Doi Y,
RA Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
RL FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
CC SIMILARITY).
CC CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC SUBCELLULAR LOCATION: Periplasmic (by similarity).
CC SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
CC SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the European Bioinformatics
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
DR EMBL: D33668; BAB04892.1; -
DR EMBL: D33668; BAB04892.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 3.

DR SMART: SM00458; Ricin; 1.
DR PROSITE: PS00531; Ricin_B_lectin; 1.
KW Hydrolyase; Glycosidase; Signal; Periplasmic; Cell wall; Lactin.
KV 3D-structure.
FT SIGNAL 1 36
FT CHAIN 37 548 POTENTIAL.
FT DOMAIN 422 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
SQ SEQUENCE 548 AA; 58164 MW; B05654315705896 CRC64;

Query Match
Best Local Similarity 31.7%; Pred. No. 0.07.
Matches 39; Conservative 18; Mismatches 52; Indels 14; Gaps 6;

OY 18 SGRKRVDDPHGNGQLMPKSNNDPQWLTKIKNDITRNSGCL--TVGYTAGY 75
DB 430 STCLDVPADPTTQVQV--ATCSNLAQDQWRTGTGTRALCKLDVASGADGTA 487
OY 76 WMIPDQNAVEATWQIMDNGT--IMPNSNLVLAASGCI--KPTLVYQTLDTYLG 129
DB 488 WMITGAGTQAKMT--TQSTALANPQSGKCLDQSAFLHDQKVLMTQNGTA 543
OY 130 QGW 132
DB 544 QGW 546

RESULT 10
E13B_OERXA STANDARD; PRT; 548 AA.
ID E13B_OERXA
RT 02-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-
DE glucan endohydrolase) ((1->3)-beta-glucanase).
OS Oerskovia xanthineolytica.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Micrococcales; Promicromonosporaceae; Cellulomicrobium.
OX NCBI_TaxId=1710;
RA Sequence from N.A. AND SEQUENCE OF 37-63.
RP Shen S-H, Christel B, Sliemers S, Sliemers S, Sliemers S,
RA "Primary sequence of the glucanase gene from Oerskovia
RT xanthineolytica. Expression and purification of the enzyme from
RT Escherichia coli."
RT J. Biol. Chem. 266:1058-1063 (1991).
RL J. Biol. Chem. 266:1058-1063 (1991).
CC FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
CC CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC SUBCELLULAR LOCATION: Periplasmic.
CC SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
CC SIMILARITY: Contains 1 ricin B-type lectin domain.
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CC or send an email to license@sib-sib.ch).
DR EMBL: A36082; J0503570.1; -
DR EMBL: A36082; J0503570.1; -
DR HSBP: P02879; 2241.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 3.
DR SMART: SM00458; Ricin; 1.
DR PROSITE: PS00531; Ricin_B_lectin; 1.
KW Hydrolyase; Glycosidase; Signal; Periplasmic; Cell wall; Lactin.
KV 3D-structure.
FT SIGNAL 1 36
FT CHAIN 37 548 POTENTIAL.
FT DOMAIN 422 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
SQ SEQUENCE 548 AA; 58164 MW; B05654315705896 CRC64;

Query Match
Best Local Similarity 31.7%; Pred. No. 0.07.
Matches 39; Conservative 18; Mismatches 52; Indels 14; Gaps 6;
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us-09-601-667c-8.rspt

Page 1

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OW protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 ; Search time 20.3487 Seconds
3347.915 Million cell updates/sec

Title: US-09-601-667C-8

Perfect score: 1414
Sequence: 1 DDVTCASAEPTVAIVGRSGM.....RRITTPATKDNQWLPVF 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Display first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organella:*
9: sp_plant:*
10: sp_protist:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match	Length	DB ID	Description
1	1283.5	90.8	531	10	Q8RXH6
2	1092.5	77.3	263	10	Q8LXQ2
3	1077.5	76.2	565	10	Q8W433
4	1058.5	74.9	263	10	Q8LXQ1
5	988.5	63.2	266	10	Q8LXQ3
6	988.5	61.0	263	10	Q8LXQ4
7	863	59.3	580	10	Q94BW4
8	832	58.8	580	10	Q94BW3
9	800.5	56.6	549	10	Q94BW2
10	800.5	56.6	549	10	Q94BW1
11	790.5	52.3	528	10	Q86076
12	739.5	52.3	382	10	Q8S443
13	662.3	51.8	547	10	Q8M659
14	662.3	51.8	547	10	Q8M658
15	662.3	51.8	547	10	Q8M657
16	566.5	47.1	592	10	Q8W267

17	554.5	39.2	316	10	Q8GTA5	Q8GTA5 sambucus nl
18	553.5	39.1	316	10	Q93WL1	Q93WL1 sambucus nl
19	552.5	39.1	316	10	Q94554	Q94554 sambucus nl
20	551	39.0	570	10	Q22415	Q22415 sambucus nl
21	544.5	38.5	564	10	Q94VW2	Q94VW2 sambucus nl
22	535.5	37.9	563	10	Q04357	Q04357 sambucus nl
23	526.5	37.2	563	10	Q8GTA2	Q8GTA2 sambucus nl
24	525.5	37.2	604	10	Q94W53	Q94W53 sambucus nl
25	523.5	37.1	604	10	Q94W54	Q94W54 sambucus nl
26	517	36.6	570	10	Q41358	Q41358 sambucus nl
27	516.5	36.5	563	10	Q94552	Q94552 sambucus nl
28	515.5	36.5	320	10	Q04356	Q04356 sambucus nl
29	509	36.0	603	10	Q94653	Q94653 polygonatum
30	503	35.6	566	10	Q04071	Q04071 sambucus nl
31	500	35.4	500	10	Q04072	Q04072 sambucus nl
32	488	34.5	507	10	Q8GTA6	Q8GTA6 sambucus nl
33	481	30.5	569	10	P93543	P93543 sambucus nl
34	479	12.7	293	10	Q95L49	Q95L49 sambucus nl
35	477	9.8	422	10	Q95L45	Q95L45 sambucus nl
36	477	8.2	415	2	Q8GTA3	Q8GTA3 sambucus nl
37	477	8.2	415	2	Q8GTA4	Q8GTA4 sambucus nl
38	477	8.2	415	2	Q8GTA5	Q8GTA5 sambucus nl
39	477	8.2	415	2	Q8GTA6	Q8GTA6 sambucus nl
40	477	8.2	415	2	Q8GTA7	Q8GTA7 sambucus nl
41	477	8.2	415	2	Q8GTA8	Q8GTA8 sambucus nl
42	477	8.2	415	2	Q8GTA9	Q8GTA9 sambucus nl
43	477	8.2	415	2	Q8GTA10	Q8GTA10 sambucus nl
44	477	8.2	415	2	Q8GTA11	Q8GTA11 sambucus nl
45	477	8.2	415	2	Q8GTA12	Q8GTA12 sambucus nl

ALIGNMENTS

RESULT 1
ID Q8RXH6 PRELIMINARY; PRT; 531 AA.
AC Q8RXH6;
DT 01-JUN-2002 (TRENKLE, 21, Created)
FT 12-DEC-2002 (TRENKLE, 21, Last sequence update)
DT 12-DEC-2002 (TRENKLE, 23, Last annotation update)
DE 12-DEC-2002 (TRENKLE, 23, Last annotation update)
OS Viscum album (European mistletoe).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
CX NCBI_TaxID=3972;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RA Parasitism N., Mista V., Srivastava A., Singh T.P.;
RT Chaining album (Indian) mRNA for Mistletoe lectin chain A isoform 1 and
BL Submitted (FEB-2002) to the EMBL/GenBank/DDB databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADenosine ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY081149; ALAB006.1; -;
DR InterPro; IPR000772; R1C1N_B.lectin.
DR InterPro; IPR001574; R1P.
DR Pfam; PF00652; R1C1N_B.lectin; 6.
DR Pfam; PF00652; R1P; 1.
DR PROSITE; PS00520; R1C1N_2.
DR PROSITE; PS00520; R1C1N_2.
KW Hydrolyase; Toxin.
FT CHAIN 1 249 LECTIN CHAIN A ISOFORM 1.
FT CHAIN 269 531 LECTIN B CHAIN.
SQ SEQUENCE 531 AA; 58802 MW; 18244BEEFEF5422 CRC64;
Best Match 90.8%; Score 1283.5; DB 10; Length 531;
Best Local Similarity 92.0%; Pred. No. 7.2e-106;

[illegible]

RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA	Do M.-S., Song S.K.,
RT	"CDNA cloning and album colocalization of the lectin genes of the Korean
RT	mistletoe (<i>Viscum album coloratum</i>)."
RN	Mol. Cells 12:215-220(2001).
[12]	
CC	SEQUENCE FROM N.A.
RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA	Do M.-S., Song S.K.,
RL	Submitted (May-2002) to the EMBL/GenBank/DDEx databases.
RL	EMBL; AF508917; AAM66935.1;
DR	InepPro; IPR000772; Ricin B.Lectin.
DR	Pfam; PF00652; Ricin B.Lectin; 5.
DR	SMART; SM0458; RICIN; 2.
DR	PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT	NON TER
FT	1
FT	266
SQ	SEQUENCE 266 AA; 29537 MW; 4A5147C37B94C73 CRC64;
Query Match	68.3%; Score 965; DB 10; Length 266;
Best local	Similarity 67.2%; Pctd No. 5e-78;
Matches 180;	Conservative 33; Mismatches 49; Indels 4; Gaps 2;
Dy	1 DVDTSSASPFVTRIVSRGKRVADVEDDPEHGNOILPMSKSNPRVOLMTRENDYTRS 60
Db	1 DVTCTTSPTFRVGRNGCLADPEEDYHDGSGLMPCKNSDPQMLTIRIDOTIRS 60
Dy	61 NSGCLTYGTAGVYMFDICNTAVREATIWOIMDNGTIMPSIDL--AASSGIKET 117
Db	61 NSGCLITIGTDSSYLIMIDDKNGSGMLTWQIKNGGILIPRSMMVLTGPSGKRITKG 120
Dy	118 TLTVQVLDTATGGMAINTNPAPRETATIGSPOLCKENSGCWATERCSSGSKRGKAL 177
Db	121 TPLTLQTGYSLGGQMANSNTARFATITVGRDHCKERSGAKVWGTCYSKKQRQ-RNAL 179
Dy	178 YCGSGISHPQNDDCTFYGDSTSYGVINIVSCSGASGSGSWPTINEVALIKSGGLANDV 237
Db	180 YCGSISHPRPQDCITSQGBDSRYVINFCTQS PRGSAWPTNKALKALINKRLAMDV 239
Dy	238 AQANETLRRIITTFITATNCERQMDPY 263
Db	240 ASNSPLRLIIPISTVGMFGMMLPV 265
RESULT 6	
ID	Q41174 PRELMINARY; FRT, 541 AA.
CD	O41174
DT	01-NOV-1996 (TrEMBL) 01, Created.
DT	01-NOV-1996 (TrEMBL) 01, Updated.
DT	01-MAR-2003 (TrEMBL) 23, Last annotation update)
DE	Prioridin A chain (EC 3.2.2.22) (RNA-N-glycosidase) (Fragment).
OS	Eukarya; eucaryotes (Castor bean).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophytes I; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosidia I; Malvales; Euphorbiales; Euphorbiaceae; Ricinus.
OX	NCB1_TaxID=3989;
OX	SEQUENCE FROM N.A.
AX	MEDLINE=9238877; PubMed=133311;
RX	Roberts L.M., Treese J.W., Lloyd J.M.;
RL	"Molecular cloning of ricin."
RL	Targeted Diagn. Ther. 7:81-97(1992).
CC	-1- CATALYTIC ACTIVITY: ENOXYHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC	EMBL; A40366; AAE22582.1;-.
DR	HSSP; P02879; IRK;
DR	InepPro; IPR001574; RIP
DR	InepPro; IPR001574; Ricin B.Lectin.
DR	Pfam; PF00652; Ricin B.Lectin; 6.

DR PFAM: PF00161; RIP; 1.
 DR SMART: SMO0458; RICIN; 2.
 DR PROSITE: P50231; RICIN_B_LECTIN; 2.
 DR PROSITE: P50275; SHIGA_RICIN; 1.
 DR PROSITE: P50338; SOMATOTROPIN_2; 1.
 KM Hydroxylase; Toxin.
 RI Nucleoside diphosphate kinase.
 SQ SEQUENCE 541 AA; 60281 MW; 28732CDPFI1239D5 CRC64;

Query Match 63.5%; Score 898.5; DB 10; Length 541;
 Best Local Similarity 63.5%; Pred. No. 1,4e-71;
 Matches 165; Conservative 34; Mismatches 60; Indels 1; Gaps 1;

QY 5 CSASEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 64
 DB 283 CMDEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 342
 QY 65 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 124
 DB 343 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 402
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNQTPFTTVIGVGLCLQNSGQVTEDC-SSKRAQGMALYQDSIR 461
 QY 185 PRONODCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNPYL 244
 DB 462 PQMRNDCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNPYL 521
 QY 245 LRLLITVPATGKPNQKMLPV 264
 DB 522 KQILLVPHRNLQIWLPLF 541

RESULT 7

Q41143 PRELIMINARY; FRT; 263 AA.

ID Q41143
 AC Q41143; PRELIMINARY; FRT; 263 AA.
 DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)
 GN RICIN B BETA CHAIN (Fragment).
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 NC NCBI:TaxID=3988.
 NX [1]
 RF SEQUENCE FROM N.A.
 RA Leadin B.F., Murray E.E., Halling A.C., Halling K.C., Tlalkaracine N.,
 RA Leadin B.F., Murray E.E., Halling A.C., Halling K.C., Tlalkaracine N.,
 RT "Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus
 RT communis agglutinin gene from the castor plant Ricinus communis.";
 RL Plant Mol. Biol. 9:287-295(1987).
 DR EMBL: M1631; AA06306.1; -.
 DR HSSP: P02879; 2M1.
 DR InterPro: IPR000772; Ricin_B_Lectin.
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR SMART: SMO0458; RICIN; 2.
 DR PROSITE: P50231; RICIN_B_LECTIN; 2.
 DR PROSITE: P50338; SOMATOTROPIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 263 AA; 29134 MW; AAB0PDDIDIE44 CRC64;

Query Match 61.0%; Score 863; DB 10; Length 263;
 Best Local Similarity 60.9%; Pred. No. 8.1e-69;
 Matches 159; Conservative 36; Mismatches 62; Indels 2; Gaps 2;

QY 5 CSASEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 64
 DB 283 CMDEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 342
 QY 65 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 124
 DB 343 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 402
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNQTPFTTVIGVGLCLQNSGQVTEDC-SSKRAQGMALYQDSIR 461
 QY 185 PRONODCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNPYL 244
 DB 462 PQMRNDCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNPYL 521
 QY 245 LRLLITVPATGKPNQKMLPV 264
 DB 522 KQILLVPHRNLQIWLPLF 541

DB 4 CMDEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 63
 QY 65 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 124
 DB 64 LTTTGATGATVYVMTFCNTAVREATTWQINDGTTINPSSNVLAAASGKIGTLLVQTL 123
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNQTPFTTVIGVGLCLQNSGQVTEDC-SSKRAQGMALYQDSIR 461
 QY 185 PRONODCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNP 243
 DB 462 PQMRNDCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQNP 521
 QY 245 LRLLITVPATGKPNQKMLPV 264
 DB 522 KQILLVPHRNLQIWLPLF 541

RESULT 8

Q41143 PRELIMINARY; FRT; 580 AA.

ID Q41143
 AC Q41143; PRELIMINARY; FRT; 580 AA.
 DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
 DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)
 DE Type 2 ribosome-inactivating protein in cinnaomoin II precursor
 (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinnaomoin campore (Campor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnaomoin.
 NC NCBI:TaxID=19429.
 RF SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnaomoin proteins and study of their expression
 RT patterns.";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SPECIFIC ADenosINE ON THE 28S RRNA.
 CC -1- SPECIFIC ADenosINE ON THE 28S RRNA.
 CC FME: S1070; AA06306.1; -.
 DR EMBL: M1631; AA06306.1; -.
 DR InterPro: IPR000772; Ricin_B_Lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR SMART: SMO0458; RICIN; 2.
 DR PROSITE: P50231; RICIN_B_LECTIN; 2.
 DR PROSITE: P50338; SOMATOTROPIN_2; 1.
 DR Hydroxylase; Signal; Toxin.
 FM SIGNAL 1
 FT NON TER 1
 SQ SEQUENCE 580 AA; 64265 MW; 37342892CCEDECBF CRC64;

Query Match 59.3%; Score 839; DB 10; Length 580;
 Best Local Similarity 61.0%; Pred. No. 3.1e-66;
 Matches 161; Conservative 34; Mismatches 67; Indels 2; Gaps 2;

QY 1 DYTLCQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 60
 DB 60 DYTLCQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 120
 QY 317 RBDPCDDEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 376
 DB 317 RBDPCDDEPTVAVIGSGKRVVDNDPFDQNOIQAMPSSKNDPNOQLTKRDNITSSNGSC 376
 QY 377 NGKCLTNGSGADYVWIDCRPVPAAISWOFANQITIPQSAIVLVAESGNPRTT 436
 DB 377 NGKCLTNGSGADYVWIDCRPVPAAISWOFANQITIPQSAIVLVAESGNPRTT 436
 QY 121 VQTLTATGQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 180
 DB 121 VQTLTATGQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 180
 QY 437 VQNTAVSRQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 495
 DB 437 VQNTAVSRQGMLAGNDPAPEVTVIGSRRLCMSSNGSVWVETDSSQKQKALYQDSIR 495
 QY 181 GSIRPRONODCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQ 239
 DB 181 GSIRPRONODCLTVGRDSVSTVINIVSCGASGSGQVFTNEVAILNLKSLAMVDAQ 239

[illegible]

Query Match 52.3%; Score 739.5; DB 10; Length 382;
Best Local Similarity 53.5%; Pred. No. 1,3e-57;
Matches 137; Conservative 41; Mismatches 77; Indels 1; Gaps 1;
OY EPTTRIVGSGRVDVDDPHDQNOIQWPSKSNDFPQWLTIRKNTIRNSGCLTTF 68
DB EPTTRIVGSGRVDVDDPHDQNOIQWPSKSNDFPQWLTIRKNTIRNSGCLTTF 128
OY GTTASGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTLDTL 128
DB GTTASGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTLDTL 187
OY GYDPSYVMVYDCTSAVPEATVETWIDGNTINPSNULVLAASGKGTTLVOTLDTL 247
DB GYDPSYVMVYDCTSAVPEATVETWIDGNTINPSNULVLAASGKGTTLVOTLDTL 247
OY 123 GQGLAGNDTAPREVITYGFRDLQMSNQSVAWETCDSSQKQGNALYDGSIRPKON 188
DB 248 RQMRKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIRPKON 306
OY 189 ODQCLTVGRDSVSTVINIVSGSGASGGRVFTNVAIINLKSGLADVAQAPFK 248
DB 307 TNNCLSKHGKSTIVKGSNMAQWVFKDSVSLYDQWVADVKSDBSLKQII 366
OY 249 IYPATGKGNQWMLPVF 264
DB 367 LMPYTGKGNQWMLPVF 382
RESULT 14
OY 09M653 PRELIMINARY; FRT; 547 AA.
AC 09M653; 2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Preproglutinin (EC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abtseae; Abrus.
OX NCBI_TaxId=3816;
RN 1) SEQUENCE FROM N.A.
RS MEDLINE=2010702; PubMed=1063690;
RA Liu C.T., Tsai C.C., Lin S.C., Wang L.I., Hsu M.J.,
RA Lin J.Y.;
RT "Primary Structure and Function Analysis of the Abrus precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
RT alpha-Helix H Impairs Protein Synthesis Inhibitory Activity.";
RL J. Biol. Chem. 275:1897-1901(2000)
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC EMBL: AF00251; EMBL: AF00251;
CC EMBL: AF00251; EMBL: AF00251;
CC HSSP: P1140; JABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00251; RICIN_B_LECTIN; 2.
DR PROSITE: PS00251; SHIGARICIN; 1.
SQ SEQUENCE 547 AA; 61248 MW; 355A325C2354A1BD CRC64;
Query Match 51.8%; Score 733; DB 10; Length 547;
Best Local Similarity 53.3%; Pred. No. 8e-57;
Matches 139; Conservative 39; Mismatches 81; Indels 2; Gaps 2;
OY 5 CSAS-EPTTRIVGSGRVDVDDPHDQNOIQWPSKSNDFPQWLTIRKNTIRNSG 63
DB 288 CSAS-EPTTRIVGSGRVDVDDPHDQNOIQWPSKSNDFPQWLTIRKNTIRNSG 347

OY 64 CLITGYTAGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTL 123
DB 348 CLITGYTAGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTL 407
OY 124 LDYTLGQGLAGNDTAPREVITYGFRDLQMSNQSVAWETCDSSQKQGNALYDGSIR 183
DB 408 NDRMRKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIR 466
OY 184 RPKMRKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIR 243
DB 467 RPKMRKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIR 526
OY 244 LRRITVATGKGNQWMLPVF 264
DB 527 LRRITVATGKGNQWMLPVF 547
RESULT 15
OY 09M258 PRELIMINARY; FRT; 573 AA.
AC 09M258;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2003 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein IRat (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
GN Lecitin.
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OX NCBI_TaxId=35976;
RN 1) SEQUENCE FROM N.A.
RS Van Damme E.J.M., Pauwels W.J.;
RT "Iris Iris hollandica var. Professor Blaauw plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC EMBL: AF00251; EMBL: AF00251;
CC EMBL: AF00251; EMBL: AF00251;
CC HSSP: P1140; JABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00251; RICIN_B_LECTIN; 2.
DR PROSITE: PS00251; SHIGARICIN; 1.
RN 1) SEQUENCE FROM N.A.
RS MEDLINE=2010702; PubMed=1063690;
RA Liu C.T., Tsai C.C., Lin S.C., Wang L.I., Hsu M.J.,
RA Lin J.Y.;
RT "Primary Structure and Function Analysis of the Abrus precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
RT alpha-Helix H Impairs Protein Synthesis Inhibitory Activity.";
RL J. Biol. Chem. 275:1897-1901(2000)
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC EMBL: AF00251; EMBL: AF00251;
CC EMBL: AF00251; EMBL: AF00251;
CC HSSP: P1140; JABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00251; RICIN_B_LECTIN; 2.
DR PROSITE: PS00251; SHIGARICIN; 1.
SQ SEQUENCE 573 AA; 63759 MW; 144A339AECDA5C CRC64;
Query Match 47.1%; Score 666.5; DB 10; Length 573;
Best Local Similarity 49.8%; Pred. No. 7.1e-51;
Matches 132; Conservative 38; Mismatches 92; Indels 3; Gaps 3;
OY 1 DPTVTSAPREVITYGFRDLQMSNQSVAWETCDSSQKQGNALYDGSIR 60
DB 311 DPTVTSAPREVITYGFRDLQMSNQSVAWETCDSSQKQGNALYDGSIR 120
OY 61 NSGCTGYTAGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTL 120
DB 371 NSGCTGYTAGYVMIPDONTAVREACTIQINDGNTINPSNULVLAASGKGTTLVOTL 429
OY 121 VOTLDTLQGLAGNDTAPREVITYGFRDLQMSN- QGAWETCDSSQKQGNALYDGSIR 179
DB 430 MUYHLHNSQCMPLPSNTRPFLPIIGLNCIQORDDQEDVGLTCDQNNNO KMYLYG 488
OY 180 DSGIRPKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIR 239
DB 489 DSGIRPKNDTSPPTVTSIAGYDLQMSNQSVAWETCDSSQKQGNALYDGSIR 548

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Page 8

Oy 240 ANPCLRRITYPATGKNQWMLPVF 264
Db 549 SDBLQOIIWSTGNQWMTTF 573
Search completed: December 11, 2003, 14:01:02
Job time : 21.3497 secs

PI Preparation of mistletoe lectins in heterologous systems,
PI particularly for use as anticancer agents and immunostimulants
XX
XX
PS Claim 9; Fig 9B; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B2 protein.
SQ Sequence 264 AA;
Query Match 100.0%; Score 144; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 5,9e-135; Indels 0; Gaps 0;
Matches 264; Conservative 0; Mismatches 0;
QY 1 DDTVCASSEPTVAVIGSGARVDVDDPHQNGIOIAPSKSNNDPQMLTKRNDTRIS 60
DB 1 DDTVCASSEPTVAVIGSGARVDVDDPHQNGIOIAPSKSNNDPQMLTKRNDTRIS 60
QY 61 NSCLTGYGTAGVYVWFPCNTAVRETIQIWDNGTIINPSSVLAAASGIKOTLT 120
DB 61 NSCLTGYGTAGVYVWFPCNTAVRETIQIWDNGTIINPSSVLAAASGIKOTLT 120
QY 121 VQTLDTLQGMAGNDTPAREVTIYGFEDLCWESNQSQVWETCDSSQXQGMALYGD 180
DB 121 VQTLDTLQGMAGNDTPAREVTIYGFEDLCWESNQSQVWETCDSSQXQGMALYGD 180
QY 181 GSIRPKNOQCLTVGRDSYSTVIVYSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
DB 181 GSIRPKNOQCLTVGRDSYSTVIVYSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
QY 241 NPKLRILIIYPATKRNQMLPVF 264
DB 241 NPKLRILIIYPATKRNQMLPVF 264
RESULT 2
AAV25993
ID AAV25993 standard; Protein; 265 AA.
XX
XX AAV25993;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B2 variant protein fragment.
DB
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B2.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOG-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P. Stiefel T. Voelter W. Wellers P;
XX
XX WPI; 1999-445335/38.
DR N-PSDB; AA209117.
XX
XX Preparation of mistletoe lectins in heterologous systems,
PI particularly for use as anticancer agents and immunostimulants
XX
XX
PS Disclosure; Fig 15B; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B2 protein.
SQ Sequence 265 AA;
Query Match 100.0%; Score 144; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 5,9e-135; Indels 0; Gaps 0;
Matches 264; Conservative 0; Mismatches 0;
QY 1 DDTVCASSEPTVAVIGSGARVDVDDPHQNGIOIAPSKSNNDPQMLTKRNDTRIS 60
DB 1 DDTVCASSEPTVAVIGSGARVDVDDPHQNGIOIAPSKSNNDPQMLTKRNDTRIS 60
QY 61 NSCLTGYGTAGVYVWFPCNTAVRETIQIWDNGTIINPSSVLAAASGIKOTLT 120
DB 61 NSCLTGYGTAGVYVWFPCNTAVRETIQIWDNGTIINPSSVLAAASGIKOTLT 120
QY 121 VQTLDTLQGMAGNDTPAREVTIYGFEDLCWESNQSQVWETCDSSQXQGMALYGD 180
DB 121 VQTLDTLQGMAGNDTPAREVTIYGFEDLCWESNQSQVWETCDSSQXQGMALYGD 180
QY 181 GSIRPKNOQCLTVGRDSYSTVIVYSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
DB 181 GSIRPKNOQCLTVGRDSYSTVIVYSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
QY 241 NPKLRILIIYPATKRNQMLPVF 264
DB 241 NPKLRILIIYPATKRNQMLPVF 264
RESULT 2
AAV25986
ID AAV25986 standard; Protein; 264 AA.
XX
XX AAV25986;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B1 protein fragment.
DB
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX

XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX MPI: 1999-44535/38.
XX N-PSDB; AA209110.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 8b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B1 protein.
XX Sequence 264 Aa;
XX
XX Query Match 97.5%; Score 1379; DB 20; Length 264;
XX Best Local Similarity 97.7%; Pred. No. 2,1e-131;
XX Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 DVTTCASSEPPTVAVIGSGMVDVDDDFDQNGQIQMFSSKNDPQGLMTIKEDMTIS 60
XX 1 DVTTCASSEPPTVAVIGSGMVDVDDDFDQNGQIQMFSSKNDPQGLMTIKEDMTIS 60
XX 51 NSGCLTGYTAGVYVMTFCNTAVREATIQIWDNGIINPESNLVLAASGKQTTLT 120
XX 61 NSGCLTGYTAGVYVMTFCNTAVREATIQIWDNGIINPESNLVLAASGKQTTLT 120
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 181 GSIRPKNOQDCLTSGDSVSTVINIVSCGASGSGRWVTFNEGAILNLKSLAMVQA 240
XX 181 GSIRPKNOQDCLTSGDSVSTVINIVSCGASGSGRWVTFNEGAILNLKSLAMVQA 240
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX
XX RESULT 4
XX AA25988
XX ID AA25988 standard; Protein; 264 Aa.
XX AA25988;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 protein fragment.
XX Mistletoe, lectin; antitumour; immunostimulant; A-chain; MA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B3.
XX
XX Viscum album.

XX DB19604210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX MPI: 1999-44535/38.
XX N-PSDB; AA209112.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 10b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B3 protein.
XX Sequence 264 Aa;
XX
XX Query Match 97.5%; Score 1379; DB 20; Length 264;
XX Best Local Similarity 97.7%; Pred. No. 2,1e-131;
XX Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 DVTTCASSEPPTVAVIGSGMVDVDDDFDQNGQIQMFSSKNDPQGLMTIKEDMTIS 60
XX 1 DVTTCASSEPPTVAVIGSGMVDVDDDFDQNGQIQMFSSKNDPQGLMTIKEDMTIS 60
XX 51 NSGCLTGYTAGVYVMTFCNTAVREATIQIWDNGIINPESNLVLAASGKQTTLT 120
XX 61 NSGCLTGYTAGVYVMTFCNTAVREATIQIWDNGIINPESNLVLAASGKQTTLT 120
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 121 VQTLDTYLGQMLAGNDTAPREVITYGPRDLCSNSQSGVWVEITDSSQNGKMAIYGD 180
XX 181 GSIRPKNOQDCLTSGDSVSTVINIVSCGASGSGRWVTFNEGAILNLKSLAMVQA 240
XX 181 GSIRPKNOQDCLTSGDSVSTVINIVSCGASGSGRWVTFNEGAILNLKSLAMVQA 240
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX
XX RESULT 5
XX AA25994
XX ID AA25994 standard; Protein; 265 Aa.
XX AA25994;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 variant protein fragment.
XX Mistletoe, lectin; antitumour; immunostimulant; A-chain; MA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX

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XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B3.
XX Viscum album.
XX DEL9804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209118.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 16B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX (humoral response to bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B3 protein.
SQ Sequence 265 AA;
Query Match 97.5%; Score 1379; DB 20; Length 265;
Best Local Similarity 97.7%; Pred. No. 2.1e-131;
Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DDTYCSASPTVAIVSGKRVYEDDDPHDQNLQWFSKSNDDPQMTYKNDUTRS 60
DB 1 DDTYCSASPTVAIVSGKRVYEDDDPHDQNLQWFSKSNDDPQMTYKNDUTRS 60
QY 61 NSGCLTYGTAGVYVIMFPCNTAVRATIMQINDGTTIMPSSNLVLAASSGKGTIT 120
DB 61 NSGCLTYGTAGVYVIMFPCNTAVRATIMQINDGTTIMPSSNLVLAASSGKGTIT 120
QY 121 VQTLTYLQGMALGNDTPAREVTYGFRLDQMSNGSVWFTDSSQNGKXALYCD 180
DB 121 VQTLTYLQGMALGNDTPAREVTYGFRLDQMSNGSVWFTDSSQNGKXALYCD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTYINVSQSGSGSQPMFTFNEALINLKSGLANDVPAQ 240
DB 181 GSIRPKQNDQCLTVGRDSVSTYINVSQSGSGSQPMFTFNEALINLKSGLANDVPAQ 240
QY 241 NPKLRRIIYPATKXNOMLPEVF 264
DB 241 NPKLRRIIYPATKXNOMLPEVF 264
RESULT 6
AAV25992 standard; Protein; 265 AA.
XX AAV25992;
XX 18-OCT-1999 (first entry)

XX Mistletoe lectin B1 variant protein fragment.
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.
XX Viscum album.
XX DEL9804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209118.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 14B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX (humoral response to bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B1 protein.
SQ Sequence 265 AA;
Query Match 97.5%; Score 1379; DB 20; Length 265;
Best Local Similarity 97.7%; Pred. No. 2.1e-131;
Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DDTYCSASPTVAIVSGKRVYEDDDPHDQNLQWFSKSNDDPQMTYKNDUTRS 60
DB 1 DDTYCSASPTVAIVSGKRVYEDDDPHDQNLQWFSKSNDDPQMTYKNDUTRS 60
QY 61 NSGCLTYGTAGVYVIMFPCNTAVRATIMQINDGTTIMPSSNLVLAASSGKGTIT 120
DB 61 NSGCLTYGTAGVYVIMFPCNTAVRATIMQINDGTTIMPSSNLVLAASSGKGTIT 120
QY 121 VQTLTYLQGMALGNDTPAREVTYGFRLDQMSNGSVWFTDSSQNGKXALYCD 180
DB 121 VQTLTYLQGMALGNDTPAREVTYGFRLDQMSNGSVWFTDSSQNGKXALYCD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTYINVSQSGSGSQPMFTFNEALINLKSGLANDVPAQ 240
DB 181 GSIRPKQNDQCLTVGRDSVSTYINVSQSGSGSQPMFTFNEALINLKSGLANDVPAQ 240
QY 241 NPKLRRIIYPATKXNOMLPEVF 264
DB 241 NPKLRRIIYPATKXNOMLPEVF 264
RESULT 7
AAV25989

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```
ID  AA125989 standard; Protein; 264 AA.
XX
XX  AA125989;
XX
XX  18-OCT-1999 (first entry)
XX
XX  Mistletoe lectin B4 protein fragment.
XX
XX  Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX  ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX  lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX  cancer; cytotoxicity; antigen; isoform; lectin B4.
XX
XX  Viscum album.
XX  DE19804210-A1.
XX  12-AUG-1999.
XX
XX  03-FEB-1998; 98DB-1004210.
XX
XX  03-FEB-1998; 98DB-1004210.
XX
XX  (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX  Morris P, Stiefel T, Voelter W, Welters P;
XX  WPI: 1999-44535/38.
XX  N-PSDB; NA209113.
XX
XX  Preparation of mistletoe lectins in heterologous systems.
XX  particularly for use as anticancer agents and immunostimulants
XX
XX  Claim 9; Fig 11B; 78pp; German.
XX
XX  This invention describes a novel mistletoe lectin (I) and its fragments
XX  which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX  of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX  ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX  lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX  fragments are used to treat uncontrolled cell growth (particularly of the
XX  cancer) and if they lack cytotoxicity, to increase the strength of the
XX  immune response, particularly to a co-administered antigen
XX  (tumour-associated, bacterial or viral). The method allows production of
XX  mistletoe lectin, and its individual chains, in many different isoforms
XX  and on a large scale, at any time of the year. Recombinant products are
XX  free from toxins present in natural mistletoe extracts. This sequence
XX  represents a fragment of a mistletoe lectin B4 protein.
XX
XX  Sequence 264 AA:
XX
XX  Query Match 97.0%; Score 1371; DB 20; Length 264;
XX  Best Local Similarity 97.3%; Pred. No. 1,36-13; Indels 0; Gaps 0;
XX  Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
XX
XX  1 DDTVTSASEPTVAVRVSQGVAVDDDDPHDQNGIQIOLPMSKSNDDPQMLTKEDNTIRS 60
XX  1 DDTVTSASEPTVAVRVSQGVAVDDDDPHDQNGIQIOLPMSKSNDDPQMLTKEDNTIRS 60
XX
XX  61 NSGCLITTYGTYAGVYVIMFDCTNAREATVQIMDNTIINPRSNVLAASGKGTIT 120
XX  61 NSGCLITTYGTYAGVYVIMFDCTNAREATVQIMDNTIINPRSNVLAASGKGTIT 120
XX
XX  121 VQIDLTGCGMLAGNDAPREAVITVQPDLCMSNSGQVWETCDSSQKQVMAIYCD 180
XX  121 VQIDLTGCGMLAGNDAPREAVITVQPDLCMSNSGQVWETCDSSQKQVMAIYCD 180
XX
XX  181 GSIRPKONODCLTVGRDVSIVINIVSCGASGSGQVWFTNEVALINLKGPMADVQA 240
XX  181 GSIRPKONODCLTVGRDVSIVINIVSCGASGSGQVWFTNEVALINLKGPMADVQA 240
XX
XX  241 NFKLRITITPATKGNQMLPVF 264
XX  |||||||||||||||||||||||||||
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```
DB  241 NFKLRITITPATKGNQMLPVF 264
XX
XX  RESULT 8
XX  AA125995
XX  AA125995 standard; Protein; 265 AA.
XX
XX  AA125995;
XX
XX  18-OCT-1999 (first entry)
XX
XX  Mistletoe lectin B4 variant protein fragment.
XX
XX  Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX  ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX  lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX  cancer; cytotoxicity; antigen; isoform; lectin B4.
XX
XX  Viscum album.
XX  DE19804210-A1.
XX  12-AUG-1999.
XX
XX  03-FEB-1998; 98DB-1004210.
XX
XX  03-FEB-1998; 98DB-1004210.
XX
XX  (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX  Morris P, Stiefel T, Voelter W, Welters P;
XX  WPI: 1999-44535/38.
XX  N-PSDB; NA209113.
XX
XX  Preparation of mistletoe lectins in heterologous systems.
XX  particularly for use as anticancer agents and immunostimulants
XX
XX  Disclosure; Fig 17B; 78pp; German.
XX
XX  This invention describes a novel mistletoe lectin (I) and its fragments
XX  which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX  of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX  ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX  lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX  fragments are used to treat uncontrolled cell growth (particularly of the
XX  cancer) and if they lack cytotoxicity, to increase the strength of the
XX  immune response, particularly to a co-administered antigen
XX  (tumour-associated, bacterial or viral). The method allows production of
XX  mistletoe lectin, and its individual chains, in many different isoforms
XX  and on a large scale, at any time of the year. Recombinant products are
XX  free from toxins present in natural mistletoe extracts. This sequence
XX  represents a fragment of a variant mistletoe lectin B4 protein.
XX
XX  Sequence 265 AA:
XX
XX  Query Match 97.0%; Score 1371; DB 20; Length 265;
XX  Best Local Similarity 97.3%; Pred. No. 1,46-130; Indels 0; Gaps 0;
XX  Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
XX
XX  1 DDTVTSASEPTVAVRVSQGVAVDDDDPHDQNGIQIOLPMSKSNDDPQMLTKEDNTIRS 60
XX  1 DDTVTSASEPTVAVRVSQGVAVDDDDPHDQNGIQIOLPMSKSNDDPQMLTKEDNTIRS 60
XX
XX  61 NSGCLITTYGTYAGVYVIMFDCTNAREATVQIMDNTIINPRSNVLAASGKGTIT 120
XX  61 NSGCLITTYGTYAGVYVIMFDCTNAREATVQIMDNTIINPRSNVLAASGKGTIT 120
XX
XX  121 VQIDLTGCGMLAGNDAPREAVITVQPDLCMSNSGQVWETCDSSQKQVMAIYCD 180
XX  121 VQIDLTGCGMLAGNDAPREAVITVQPDLCMSNSGQVWETCDSSQKQVMAIYCD 180
XX
XX  181 GSIRPKONODCLTVGRDVSIVINIVSCGASGSGQVWFTNEVALINLKGPMADVQA 240
XX  181 GSIRPKONODCLTVGRDVSIVINIVSCGASGSGQVWFTNEVALINLKGPMADVQA 240
XX
XX  241 NFKLRITITPATKGNQMLPVF 264
XX  |||||||||||||||||||||||||||
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Db 181 GSIRPKQNDQCLTSGRDSVTVIVIVSCGASGSGRWVFNMGALINLKSGPMVDYQA 240
Qy 241 NPKLRILITYPATGKQNMPLPVF 264
Db 241 NPKLRILITYPATGKQNMPLPVF 264

RESULT 9

AAV25990
ID AAV25990 standard; Protein: 264 AA.

AAV25990;

18-OCT-1999 (first entry)

Mistletoe lectin B5 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-44535/38.

XX N-PDB: Aa209114.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 12B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MIA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B5 protein.

XX Sequence 264 AA;

XX Query Match 96.5%; Score 1364; DB 20; Length 264;

XX Best Local Similarity 96.6%; Pred. No. 6; 9e-130; Indels 0; Gaps 0;

XX Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DVTGCSAEPFVIRVGRGKRVDDPDHNGQIQIOWPKSKNDPQWLTIKEDTIRIS 60

Db 1 DVTGCSAEPFVIRVGRGKRVDDPDHNGQIQIOWPKSKNDPQWLTIKEDTIRIS 60

Qy 61 NNSCLTGYGTAGVYVIMFDCKTVAEATITWIMNDGTTIFNRSNVLVAASGIGKTTT 120

Db 61 NNSCLTGYGTAGVYVIMFDCKTVAEATITWIMNDGTTIFNRSNVLVAASGIGKTTT 120

Qy 121 VQTLVYTLQCGWLAGNDTAREVITVGRFLDCHESQGSVWFETCSQDNQGNALYD 180
Db 121 VQTLVYTLQCGWLAGNDTAREVITVGRFLDCHESQGSVWFETCSQDNQGNALYD 180
Qy 181 GSIRPKQNDQCLTSGRDSVTVIVIVSCGASGSGRWVFNMGALINLKSGPMVDYQA 240
Db 181 GSIRPKQNDQCLTSGRDSVTVIVIVSCGASGSGRWVFNMGALINLKSGPMVDYQA 240
Qy 241 NPKLRILITYPATGKQNMPLPVF 264
Db 241 NPKLRILITYPATGKQNMPLPVF 264

RESULT 10

AAV25996
ID AAV25996 standard; Protein: 265 AA.

AAV25996;

18-OCT-1999 (first entry)

Mistletoe lectin B5 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-44535/38.

XX N-PDB: Aa209120.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 18B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MIA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.

XX Sequence 265 AA;

XX Query Match 96.5%; Score 1364; DB 20; Length 265;

XX Best Local Similarity 96.6%; Pred. No. 7e-130; Indels 0; Gaps 0;

XX Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DVTGCSAEPFVIRVGRGKRVDDPDHNGQIQIOWPKSKNDPQWLTIKEDTIRIS 60

Db 1 DVTGCSAEPFVIRVGRGKRVDDPDHNGQIQIOWPKSKNDPQWLTIKEDTIRIS 60

Qy 61 NSGCLITGYGVYVIMFDQCNVAREXTTQIMDNGTINPESNLYLAASSGIKGTTLT 120
 Db 61 NSGCLITGYGVYVIMFDQCNVAREXTTQIMDNGTINPESNLYLAASSGIKGTTLT 120
 Qy 121 VQTLDTYLGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCSQNGKALYGD 180
 Db 121 VQTLDTYLGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCSQNGKALYGD 180
 Qy 181 GSIRPKONODQCLTGRDSVSTVINIVSCGASGQRMVFTNEVAIINTKSLAMDVAQA 240
 Db 181 GSIRPKONODQCLTGRDSVSTVINIVSCGASGQRMVFTNEVAIINTKSLAMDVAQA 240
 Qy 241 NPKLRITITTPANGKRNQMLPY 264
 Db 241 NPKLRITITTPANGKRNQMLPY 264

RESULT 11

AAZ5985
 ID AAZ5985 standard; Protein; 263 AA.

AAZ5985;

18-OCT-1999 (first entry)

Mistletoe lectin B protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
 ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B.

Vascun album.

DEL9804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-44535/38.

N-PSDB; AAZ09109.

Preparation of mistletoe lectins in heterologous systems.

particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 7b; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MA) of
 the mistletoe lectin binds to, and inactivates, the 28S subunit of
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 lymphokine-producing macrophages, so stimulate immunity. (I) and its
 fragments are used to treat uncontrolled cell growth (particularly of the
 tumour-associated, bacterial or viral). The method allows production of the
 (tumour-associated, bacterial or viral) and its individual chains, in many
 different isoforms and on a large scale, at any time of the year. Recombinant products are
 free from toxins present in natural mistletoe extracts. This sequence
 represents a fragment of a mistletoe lectin B protein.

Sequence 263 AA;

Query Match 92.4%; Score 1306.5; DB 20; Length 263;
 Best Local Similarity 93.5%; Fred. No. 4,7e-124;

Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
 Qy 1 DDTVTSASEPTVIRIVGRSGKRDVYDDEDPHQNOIOLWPSKSNDDPQMLTQKQDNTIRS 60
 Db 1 DDTVTSASEPTVIRIVGRSGKRDVYDDEDPHQNOIOLWPSKSNDDPQMLTQKQDNTIRS 60
 Qy 61 NSGCLITGYGVYVIMFDQCNVAREXTTQIMDNGTINPESNLYLAASSGIKGTTLT 120
 Db 61 NSGCLITGYGVYVIMFDQCNVAREXTTQIMDNGTINPESNLYLAASSGIKGTTLT 120
 Qy 121 VQTLDTYLGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCSQNGKALYGD 180
 Db 121 VQTLDTYLGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCSQNGKALYGD 180
 Qy 181 GSIRPKONODQCLTGRDSVSTVINIVSCGASGQRMVFTNEVAIINTKSLAMDVAQA 240
 Db 181 GSIRPKONODQCLTGRDSVSTVINIVSCGASGQRMVFTNEVAIINTKSLAMDVAQA 240
 Qy 241 NPKLRITITTPANGKRNQMLPY 263
 Db 241 NPKLRITITTPANGKRNQMLPY 263

RESULT 12

AAZ5991
 ID AAZ5991 standard; Protein; 264 AA.

AAZ5991;

18-OCT-1999 (first entry)

Mistletoe lectin B variant protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
 ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B.

Vascun album.

DEL9804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-44535/38.

N-PSDB; AAZ09115.

Preparation of mistletoe lectins in heterologous systems.

particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 18b; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MA) of
 the mistletoe lectin binds to, and inactivates, the 28S subunit of
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 fragments are used to treat uncontrolled cell growth (particularly of the
 tumour-associated, bacterial or viral). The method allows production of the
 (tumour-associated, bacterial or viral) and its individual chains, in many
 different isoforms and on a large scale, at any time of the year. Recombinant products are
 free from toxins present in natural mistletoe extracts. This sequence
 represents a fragment of a variant mistletoe lectin B protein.

XX Sequence 264 AA;
 SQ Query Match 92.4%; Score 1306.5; DB 20; Length 264;
 Best Local Similarity 93.9%; Pred. No. 4,7e-124;
 Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTTCASAEPTVRIYGRSGKRVYRDDPHDGNQIQIMPESKNDPQWLTKKNTIRS 60
 DB 1 DVTTCASAEPTVRIYGRSGKRVYRDDPHDGNQIQIMPESKNDPQWLTKKNTIRS 60
 QY 61 NSGCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSRLVLAASGKKTILT 120
 DB 61 NSGCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSRLVLAASGKKTILT 120
 QY 121 VQTLDTYTLGGWMLAGNDYAFREVTIYGFRLCMESNGSGVWVETCDSSQNGKALYGD 180
 DB 121 VQTLDTYTLGGWMLAGNDYAFREVTIYGFRLCMESNGSGVWVETCDSSQNGKALYGD 180
 QY 121 VQTLDTYTLGGWMLAGNDYAFREVTIYGFRLCMESNGSGVWVETCDSSQNGKALYGD 180
 DB 181 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDVAQA 240
 DB 186 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDVAQA 239
 QY 241 NPKLRRIITYPATGKPNOMLPEV 263
 DB 240 NPKLRRIITYPATGKPNOMLPEV 262

RESULT 13
 AA25979
 ID AAY25979 standard; Protein; 531 AA.
 AC AAY25979;
 DT 18-OCT-1999 (first entry)
 DE Mistletoe lectin I protein fragment.
 XX Mistletoe lectin I protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin I.
 XX Viscum album.
 XX DEL9804210-AI.
 PD 12-AUG-1999.
 XX 03-FEB-1998; 98DB-1004210.
 PF 03-FEB-1998; 98DB-1004210.
 PR 03-FEB-1998; 98DB-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 PI MPI; 1999-445335/38.
 DR N-PSDB; AA209103.
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Claim 7, Fig 1B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 XX

XX Sequence 531 AA;
 SQ Query Match 92.4%; Score 1306.5; DB 20; Length 531;
 Best Local Similarity 93.9%; Pred. No. 1e-123;
 Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTTCASAEPTVRIYGRSGKRVYRDDPHDGNQIQIMPESKNDPQWLTKKNTIRS 60
 DB 269 DVTTCASAEPTVRIYGRSGKRVYRDDPHDGNQIQIMPESKNDPQWLTKKNTIRS 328
 QY 61 NSGCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSRLVLAASGKKTILT 120
 DB 329 NSGCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSRLVLAASGKKTILT 388
 QY 121 VQTLDTYTLGGWMLAGNDYAFREVTIYGFRLCMESNGSGVWVETCDSSQNGKALYGD 180
 DB 389 VQTLDTYTLGGWMLAGNDYAFREVTIYGFRLCMESNGSGVWVETCDSSQNGKALYGD 447
 QY 181 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDVAQA 240
 DB 448 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDVAQA 507
 QY 241 NPKLRRIITYPATGKPNOMLPEV 263
 DB 508 NPKLRRIITYPATGKPNOMLPEV 530

RESULT 14
 AA25982
 ID AAY25982 standard; Protein; 532 AA.
 AC AAY25982;
 DT 18-OCT-1999 (first entry)
 DE Mistletoe lectin I (variant) protein fragment.
 XX Mistletoe lectin I (variant) protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin I.
 XX Viscum album.
 XX DEL9804210-AI.
 PD 12-AUG-1999.
 XX 03-FEB-1998; 98DB-1004210.
 PF 03-FEB-1998; 98DB-1004210.
 PR 03-FEB-1998; 98DB-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 PI MPI; 1999-445335/38.
 DR N-PSDB; AA209106.
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 4B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response. (1) is a bacterial toxin that causes antigen production of
 CC (tumour-associated bacterial or viral). The secreted antigen isoforms
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 XX
 SQ Sequence 532 AA:
 Query March 92.4%; Score 1306.5; DB 20; Length 532;
 Best Local Similarity 93.9%; Pred. No. 1.9e-123;
 Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
 QY 1 DDVTCASBPVTVRIYGRNRCVVDVDDPFDGQIOLWPKSKNDPQWLTKIKDITRS 60
 DB 269 DDVTCASBPVTVRIYGRNRCVVDVDDPFDGQIOLWPKSKNDPQWLTKIKDITRS 328
 QY 61 NSCLITTYGTAGVYVWFDCNTAVREATVQINDGTTINPNSNVLVAASGKIGTIT 120
 DB 329 NSCLITTYGTAGVYVWFDCNTAVREATVQINDGTTINPNSNVLVAASGKIGTIT 388
 QY 121 VQILDYTLGGMLAGNDTAPREVTVIGFDLQWESNGSVWVETQDSQKQWALVGD 180
 DB 389 VQILDYTLGGMLAGNDTAPREVTVIGFDLQWESNGSVWVETQDSQKQWALVGD 447
 QY 181 GSIRPKQNDQCLTVGRSSTVINIVSCASGSGRWFTNBYALINLKSGLMDVQA 240
 DB 448 GSIRPKQNDQCLTVGRSSTVINIVSCASGSGRWFTNBYALINLKSGLMDVQA 507
 QY 241 NPKLRILITTPATGKPKQWMLPV 263
 DB 508 NPKLRILITTPATGKPKQWMLPV 530
 RESULT 15
 AA#64662
 ID AA#64662 standard; Protein; 263 AA.
 AC AA#64662;
 DT 23-OCT-1998 (first entry)
 XX
 DE Mistletoe RWLB variant protein.
 XX
 DE Lectin B-chain, mistletoe; RWLB; fusion protein; effector; cytotoxic;
 XX internalized; processing module; protease recognition; targeting module;
 XX autoimmune disease; allergy; tumour; ricin; translocation.
 XX
 OS Viscum album.
 XX
 FH Key
 FT Protein 1..263 Location/Qualifiers
 FT /note= "partial protein"
 XX
 XX MO9829540-A2.
 XX
 XX 09-JUL-1998.
 XX
 XX 02-JAN-1998; 98WD-EP00009.
 XX
 XX 02-JAN-1997; 97EP-010012.
 XX
 XX (BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION NZ.
 XX
 XX Eck J, Schmidt A, Zinke H;
 XX
 XX WPI; 1998-38812/33.
 XX
 XX N-PSDB; AA#51344.

XX Nucleic acid encoding fusion protein containing mistletoe lectin A
 FT chain - useful for treatment of proliferative and autoimmune
 FT diseases, allergies and tumours
 XX
 XX Disclosure; Fig 11b'; 115p; German.
 XX
 CC This sequence represents a variant mistletoe lectin B-chain, RWLB. This
 CC sequence can be used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC covalently bonded to the processing module, able to bind specifically to
 CC the surface of a cell so as to mediate internalisation of the fusion
 CC protein. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated activation of cells, especially
 CC autoimmune disease, allergy and tumours. The proteins can be administered
 CC e.g. by injection or topically but especially by intravenous injection,
 CC and/or by oral administration.
 CC Fusion proteins can develop toxic activity in a wide range of target
 CC cells. The processing module prevents extracellular dissociation and
 CC fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the ML A-chain from the
 CC endoplasmic reticulum to the cytoplasm.
 XX
 SQ Sequence 263 AA:
 Query March 92.0%; Score 1300.5; DB 19; Length 263;
 Best Local Similarity 93.5%; Pred. No. 1.9e-123;
 Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
 QY 1 DDVTCASBPVTVRIYGRNRCVVDVDDPFDGQIOLWPKSKNDPQWLTKIKDITRS 60
 DB 1 DDVTCASBPVTVRIYGRNRCVVDVDDPFDGQIOLWPKSKNDPQWLTKIKDITRS 60
 QY 61 NSCLITTYGTAGVYVWFDCNTAVREATVQINDGTTINPNSNVLVAASGKIGTIT 120
 DB 61 NSCLITTYGTAGVYVWFDCNTAVREATVQINDGTTINPNSNVLVAASGKIGTIT 120
 QY 121 VQILDYTLGGMLAGNDTAPREVTVIGFDLQWESNGSVWVETQDSQKQWALVGD 180
 DB 121 VQILDYTLGGMLAGNDTAPREVTVIGFDLQWESNGSVWVETQDSQKQWALVGD 179
 QY 181 GSIRPKQNDQCLTVGRSSTVINIVSCASGSGRWFTNBYALINLKSGLMDVQA 240
 DB 180 GSIRPKQNDQCLTVGRSSTVINIVSCASGSGRWFTNBYALINLKSGLMDVQA 239
 QY 241 NPKLRILITTPATGKPKQWMLPV 263
 DB 240 NPKLRILITTPATGKPKQWMLPV 262
 Search completed: December 11, 2003, 14:07:44
 Job time : 27.0864 secs

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rapb

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OK protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 17.0129 Seconds
2886.029 Million cell updates/sec

Title: US-09-601-667C-8
Perfect score: 1414
Sequence: 1 DVTGCSASEPTVIVGRSGM.....RRITIVPANGKPNQMLPVP 264

Scoring table: BLOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 684280 seqs, 18593659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA*
1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpa/US06_PUB.pep.*
3: /cgn2_6/prodata/1/pubpa/US06_PUB.pep.*
4: /cgn2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpa/US07_PUB.pep.*
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10: /cgn2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpa/US10_PUB.pep.*
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Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1300.5	92.0	263	9	US-09-347-064-10
2	1300.5	92.0	263	9	US-09-347-064-10
3	1300.5	92.0	263	9	US-09-347-064-10
4	1300.5	92.0	263	9	US-09-347-064-10
5	1300.5	92.0	263	9	US-09-347-064-10
6	1300.5	92.0	263	9	US-09-347-064-10
7	1300.5	92.0	263	9	US-09-347-064-10
8	1300.5	92.0	263	9	US-09-347-064-10
9	1300.5	92.0	263	9	US-09-347-064-10
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11	1300.5	92.0	263	9	US-09-347-064-10
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14	1300.5	92.0	263	9	US-09-347-064-10
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16	1300.5	92.0	263	9	US-09-347-064-10
17	1300.5	92.0	263	9	US-09-347-064-10
18	1300.5	92.0	263	9	US-09-347-064-10

16	116.5	8.2	492	9	US-09-770-621-7	Sequence 7, Appl
17	116.5	8.2	492	12	US-10-286-993-4	Sequence 4, Appl
18	106	7.5	41	15	US-10-137-077-20	Sequence 20, Appl
19	105	7.4	43	15	US-10-137-077-19	Sequence 19, Appl
20	93.5	6.6	340	15	US-10-128-714-8037	Sequence 8037, Ap
21	93	6.6	623	15	US-10-128-714-8037	Sequence 15008, Ap
22	90.5	6.4	464	15	US-10-156-761-15008	Sequence 9647, Ap
23	89.5	6.4	464	15	US-10-156-761-15008	Sequence 9647, Ap
24	89	6.2	295	9	US-09-841-132-356	Sequence 384, Appl
25	88	6.2	1723	9	US-09-841-132-356	Sequence 11833, A
26	87	6.2	278	15	US-09-845-242-11833	Sequence 3037, Ap
27	84	5.9	1781	10	US-09-895-749A-2	Sequence 2, Appl
28	83.5	5.9	579	14	US-10-001-851-29	Sequence 29, Appl
29	83	5.9	770	9	US-09-815-656-11	Sequence 31, Appl
30	82	5.8	833	9	US-09-815-656-11	Sequence 10551, A
31	81.5	5.8	2353	10	US-09-797-862-33	Sequence 33, Appl
32	81.5	5.8	423	10	US-09-813-398-32	Sequence 32, Appl
33	81.5	5.8	510	12	US-10-190-115-46	Sequence 48, Appl
34	81	5.7	612	10	US-09-828-457-41	Sequence 41, Appl
35	81	5.7	864	10	US-09-828-457-41	Sequence 41, Appl
36	81	5.7	1032	11	US-09-733-643-16	Sequence 16, Appl
37	81	5.7	1032	12	US-10-120-801-64	Sequence 64, Appl
38	81	5.7	2771	10	US-09-808-602-82	Sequence 82, Appl
39	81	5.7	2771	10	US-09-808-602-82	Sequence 70, Appl
40	81	5.7	2771	11	US-10-137-077-2	Sequence 2, Appl
41	80.5	5.7	293	15	US-09-770-621-6	Sequence 6, Appl
42	80	5.7	434	9	US-09-770-621-6	Sequence 126, App
43	79.5	5.6	165	12	US-10-252-896-126	Sequence 62, Appl
44	79.5	5.6	556	12	US-10-252-896-62	Sequence 23, Appl
45	79.5	5.6	559	14	US-10-001-851-23	

ALIGNMENTS

US-09-347-064-10	Application US/09347064A
Sequence 1	
1	US-09-347-064-10
2	Sequence 1
3	Sequence 1
4	Sequence 1
5	Sequence 1
6	Sequence 1
7	Sequence 1
8	Sequence 1
9	Sequence 1
10	Sequence 1
11	Sequence 1
12	Sequence 1
13	Sequence 1
14	Sequence 1
15	Sequence 1
16	Sequence 1
17	Sequence 1
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20	Sequence 1
21	Sequence 1
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32	Sequence 1
33	Sequence 1
34	Sequence 1
35	Sequence 1
36	Sequence 1
37	Sequence 1
38	Sequence 1
39	Sequence 1
40	Sequence 1
41	Sequence 1
42	Sequence 1
43	Sequence 1
44	Sequence 1
45	Sequence 1

QY 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 180
 DB 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 179
 QY 181 GSIRPKQK 240
 DB 180 GSIRPKQ 239
 QY 241 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 263
 DB 240 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 262

RESULT 2
 US-09-347-064-4
 / Sequence 4, Application US/09347064A
 / Patent No. US2002045209A1
 / GENERAL INFORMATION:
 / APPLICANT: ECK, Jürgen
 / APPLICANT: Schmalz, Alfred
 / APPLICANT: Zihlke, Hans-Joachim
 / TITLE OF INVENTION: Recombinant Fusion Proteins Based on
 / TITLE OF INVENTION: Ribosome-Inactivating Proteins of the miscelae viscum
 / TITLE OF INVENTION: album
 / FILE REFERENCE: 09282-5
 / CURRENT APPLICATION NUMBER: US/09/347,064A
 / EARLIER FILING DATE: 1999-07-02
 / EARLIER APPLICATION NUMBER: PCT/EP98/00009
 / EARLIER FILING DATE: 1998-01-02
 / EARLIER APPLICATION NUMBER: EP 97 10 0012.0
 / NUMBER OF SEQ ID NOS: 138
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 4
 / LENGTH: 267
 / TYPE: PRT
 / ORGANISM: Viscum album
 US-09-347-064-4

Query Match 92.0%; Score 1300.5; DB 9; Length 267;
 Best Local Similarity 93.5%; Pred. No. 2.1e-125;
 Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
 QY 1 DDTVCASAPTVIYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTIS 60
 DB 1 DDTVCASAPTVIYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTIS 60
 QY 61 NSGCLTYYGAGVYVIFPCYVAVETIYVQWNGTIIINRSNLYLAASGIGTITL 120
 DB 61 NSGCLTYYGAGVYVIFPCYVAVETIYVQWNGTIIINRSNLYLAASGIGTITL 120
 QY 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 180
 DB 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 179
 QY 181 GSIRPKQK 240
 DB 180 GSIRPKQ 239
 QY 241 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 263
 DB 240 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 262

RESULT 3
 US-10-083-336A-1
 / Sequence 1, Application US/10083336A
 / Publication No. US2003018165A1
 / GENERAL INFORMATION:
 / APPLICANT: Olson, Mark A
 / APPLICANT: Willard, Charles B
 / APPLICANT: Byrne, Michael P
 / APPLICANT: Mannheimacker, Robert W

QY 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 180
 DB 121 VGTLDYTLGGWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 179
 QY 181 GSIRPKQK 240
 DB 180 GSIRPKQ 239
 QY 241 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 263
 DB 240 NPKLRITIIYPATGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 262

Query Match 63.4%; Score 896.5; DB 12; Length 576;
 Best Local Similarity 63.5%; Pred. No. 2.2e-83;
 Matches 165; Conservative 33; Mismatches 61; Indels 1; Gaps 1;
 QY 5 CSASPTVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 64
 DB 318 CSASPTVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 377
 QY 65 LTTGTVAGVYVIFPCYVAVETIYVQWNGTIIINRSNLYLAASGIGTITL 124
 DB 65 LTTGTVAGVYVIFPCYVAVETIYVQWNGTIIINRSNLYLAASGIGTITL 124
 QY 125 DYTLDGQWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 184
 DB 125 DYTLDGQWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 184
 QY 148 IYVSGQWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 196
 DB 148 IYVSGQWMLAGNDIAPREVTIYGRDLCEESNGSVMETCDSSGQKQKMLYCD 196
 QY 185 PKQK 244
 DB 185 PKQ 244
 QY 245 RIIYVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 264
 DB 245 RIIYVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 264
 QY 557 KQIIYVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 576
 DB 557 KQIIYVIRVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 576

RESULT 4
 US-10-137-077-17
 / Sequence 17, Application US/10137077
 / Publication No. US20030092109A1
 / GENERAL INFORMATION:
 / APPLICANT: Gaudet, Ivan D.
 / APPLICANT: Knäuper, Robert P.
 / APPLICANT: Knäuper, Robert P.
 / TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lect
 / FILE REFERENCE: UN-07124
 / CURRENT APPLICATION NUMBER: US/10/137,077
 / EARLIER FILING DATE: 2002-05-02
 / EARLIER APPLICATION NUMBER: 60/288,596
 / EARLIER FILING DATE: 2001-05-03
 / EARLIER APPLICATION NUMBER: 60/354,322
 / NUMBER OF SEQ ID NOS: 2002-02-04
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 17
 / LENGTH: 44
 / TYPE: PRT
 / ORGANISM: Ricinus communis
 US-10-137-077-17

Query Match 12.8%; Score 181; DB 15; Length 44;
 Best Local Similarity 75.0%; Pred. No. 2.4e-11;
 Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 12 VYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 55
 DB 12 VYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 55
 QY 1 VYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 44
 DB 1 VYVIRSGKRVYRDDPHDGNQIQLPFSKSNDDPNQMTIRKNTISNSG 44

RESULT 5
 US-10-074-527-5
 / Sequence 5, Application US/10074527

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```
Publication No. US20020142456A1
GENERAL INFORMATION:
APPLICANT: Odera, Peter U.
APPLICANT: Odera, Rachel E.
APPLICANT: Odera, Robert A.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 33945. A human glycosyltransferase and
FILE REFERENCE: WP13001-018P10CPI (W)
CURRENT APPLICATION NUMBER: US/10/074,527
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/269202
INVENTOR: Odera, Peter U.
INVENTOR: Odera, Rachel E.
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 145
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-5

Query Match
Best Local Similarity 11.9%; Score 168; DB 14; Length 145;
Matches 45; Conservative 19; Mismatches 59; Indels 14; Gaps 4;

QY 11 TTVRYGSGVYVDDPHDQDQIOLPMSKSNPNQIWT--KEDNTIRNS--CYTNG 64
DB 7 TTVVNGSGRLDVTSSSSSDQDQVLMCHSNPGRQKMSLTYSDDGIRSVNNDIC 66
QY 65 LTTGYTAGVYVAIFDQNTVAREATIQIWDNGTITP-----RSNIVT--AASGIG 116
DB 67 LTVANSPSEVYLYQCDTSITDQKMLINDGLGKRLILNVTGLVLDVYSGDTONG 126
QY 117 TTVVQTLDTYTLGGQML 133
DB 127 TTVLTVTCGSGRQML 143
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```
RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHITA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
INVENTOR: Odera, Peter U.
INVENTOR: Odera, Rachel E.
INVENTOR: Odera, Robert A.
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14970
LENGTH: 420
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14970
```

```
Query Match
Best Local Similarity 10.7%; Score 182; DB 15; Length 420;
Matches 43; Conservative 20; Mismatches 68; Indels 10; Gaps 5;

QY 1 DD--VTCGAEPTVAVIGSGNRYVDDPHDQDQIOLPMSKSNPNQIWTIRKNDTI 58
DB 1 DD--VTCGAEPTVAVIGSGNRYVDDPHDQDQIOLPMSKSNPNQIWTIRKNDTI 58
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DB 284 DVYKTTGDSGAPITGLAKCQVAVGSSSANGAPVQLY--DQNGTTAKQNTVANSQTL 341
QY 59 RNSGSL--TTVGYTAGVYVAIFDQNTVAREATIQIWDNGTITPNS--LVLASGSI 114
DB 342 RALGKCLDVTENGTDGDSVQLDWDGGSANOK--VVTAAQDIVPNQKCLDVTGNNSA 399
QY 115 KQTTLVQTLDTYTLGGQMLAG 135
DB 400 NGTRLDQWSSGASQANQKWRG 420
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RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHITA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
INVENTOR: Odera, Peter U.
INVENTOR: Odera, Rachel E.
INVENTOR: Odera, Robert A.
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9724
LENGTH: 658
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-9724
```

```
Query Match
Best Local Similarity 9.8%; Score 140.5; DB 15; Length 658;
Matches 59; Conservative 17; Mismatches 56; Indels 9; Gaps 5;

QY 17 RSGVAVYVDDPHDQDQIOLPMSKSNPNQIWT--KEDNTIRNS--CYTNG 73
DB 539 QSGRCADIVYVTTNGTQALM--DQNGPNSWYTKRELVLQKRLDANVLTGTTNG 596
QY 74 VYVAFDQNTVAREATIQIWDNGTITPNSVLA--SSGIGKTTLVQTLDTYTLGG 131
DB 597 TKVYLVNCGANOK--WNINSGITVYVMAQLDVAATNATGSLVWMSCTQDNOK 654
QY 132 N 132
DB 655 N 655
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```
RESULT 8
US-10-156-761-8170
Sequence 8170, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHITA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
```

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;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 8170
;; LENGTH: 536
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
Best Local Similarity 30.1%; Pctd No. 0.000160
Matches 40; Conservative 17; Mismatches 60; Indels 16; Gaps 6;

QY 14 IVGSGMR-VVVEDDHPDGNQIOLWPSKSNNDPQWLTIKEDNITRANG--SCITTY-- 68
DB 409 IVGSSNRCLDAYDNGTAPGTKEIWDG--GGANQAVITTAGELRYGQTCLDAYN 465
QY 69 GTTAGVYVAIPDCNTAVR--EATITWQIMDNGTIIIPRSNLVLA--ASSGIGTITVQ 122
DB 466 GTTSGTRVQLTTCNGANOR--WELNPGVITGTSGCLDVTGSDQSNVNGTALRM 523
QY 123 TLDITTCQCTAG 135
DB 524 TONGANQWELD 536

RESULT 9
US-10-137-077-18
;; Sequence 18, Application US/10137077
;; Publication No. US2003092109A1
;; GENERAL INFORMATION:
;; APPLICANT: GlaxoSmith, Irwin J.
;; APPLICANT: GlaxoSmith, Irwin J.
;; APPLICANT: Krieger, Robert P.
;; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
;; FILE REFERENCE: US-07124
;; CURRENT APPLICATION NUMBER: US/10/137,077
;; CURRENT FILING DATE: 2002-05-02
;; PRIOR APPLICATION NUMBER: 60/288,596
;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 60/354,322
;; PRIOR FILING DATE: 2002-02-04
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Ricinus communis
US-10-137-077-18

Query Match
Best Local Similarity 59.0%; Pctd No. 3.9e-06;
Matches 23; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 226 IINXSGIAMPYQAMPTREITTYRANGKNDMLPVP 264
DB 3 IINXSGIAMPYQAMPTREITTYRANGKNDMLPVP 41

RESULT 10
US-09-973-457-5
;; Sequence 5, Application US/09973457
;; Publication No. US2002016746A1
;; GENERAL INFORMATION:
;; APPLICANT: Kapelle, Libermann, Resana
;; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
;; FILE REFERENCE: 10448-099001
;; CURRENT APPLICATION NUMBER: US/09/973,457
;; CURRENT FILING DATE: 2001-10-09
;; PRIOR APPLICATION NUMBER: 60/238,849
;; PRIOR FILING DATE: 2000-10-06
;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
Best Local Similarity 29.1%; Pctd No. 0.000190
Matches 41; Conservative 19; Mismatches 60; Indels 21; Gaps 8;

QY 14 IVGSGMRVYV--RDDPHDGNQIOLWPSKSNNDPQWLTI--KRDNITRANGS-CLTT 67
DB 7 IGGNTGCLDVGNSSESSESDNVPQWMDCHGGG--NQLMKLYNESDGLRINSDCLTV 64
QY 68 YGTAGVYVAIPDCNTAVR--EATITWQIMDNGTIIIPRSNLVLA--ASSGIGTITVQ 125
DB 65 NG-----TVLISCDGTGKMGNDQEVNNDGFTIRFR-NKRGVDSG-----LCDVWD 113
QY 126 YTLGGQMLAANDTPRETTY 146
DB 114 GNTQQLMTVCNSGDHPQKXID 134

RESULT 11
US-10-074-527-6
;; Sequence 6, Application US/10074527
;; Publication No. US20020142426A1
;; GENERAL INFORMATION:
;; APPLICANT: Olanib, Peter J.
;; APPLICANT: Meyers, Rachel E.
;; APPLICANT: Meyers, Rachel E.
;; APPLICANT: Millanum Pharmaceuticals Inc.
;; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
;; FILE REFERENCE: MP12001-018PRCP1(M)
;; CURRENT APPLICATION NUMBER: US/10/074,527
;; CURRENT FILING DATE: 2002-02-12
;; PRIOR APPLICATION NUMBER: 60/269202
;; PRIOR FILING DATE: 2001-02-15
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 4.0
;; SEQ ID NO 6
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
Best Local Similarity 29.1%; Pctd No. 0.000190
Matches 41; Conservative 19; Mismatches 60; Indels 21; Gaps 8;

QY 14 IVGSGMRVYV--RDDPHDGNQIOLWPSKSNNDPQWLTI--KRDNITRANGS-CLTT 67
DB 7 IGGNTGCLDVGNSSESSESDNVPQWMDCHGGG--NQLMKLYNESDGLRINSDCLTV 64
QY 68 YGTAGVYVAIPDCNTAVR--EATITWQIMDNGTIIIPRSNLVLA--ASSGIGTITVQ 125
DB 65 NG-----TVLISCDGTGKMGNDQEVNNDGFTIRFR-NKRGVDSG-----LCDVWD 113
QY 126 YTLGGQMLAANDTPRETTY 146
DB 114 GNTQQLMTVCNSGDHPQKXID 134

RESULT 12
US-09-770-621-8
;; Sequence 8, Application US/09770621
;; Patent No. US20010024815A1

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GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vemaamper, Jari
APPLICANT: Fagerst m, Richard
APPLICANT: Jantto, Ralja
APPLICANT: M nyl, Arja
APPLICANT: Vemaamper, Jari
APPLICANT: Suomalainen, Pekka
APPLICANT: Iahnenp, Taro
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STEVEN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER RETRIEABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770.621
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATOMIC/ISOTOPE INFORMATION:
NAME: Buggi, Ky Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
STRANDNESS: 3' to 5'
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551

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Query Match      8.5%; Score 119.5; DB 9; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.0014;
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6

QY      7  AASP-----TWIRVRSGRGVDRDDEPHDGNQIQILPKSRKNDPQVLTMTKED 55
      111  ::::
Db       354  SSSPXXXXXXXXXADGGIGKVG-SGKCLDVPDASTSGDTQLQDWDHSGST--NQGMATPA 410
      111  ::::
QY      56  NIIIRNSG-SCLTGTTGATGATVTFIDCNARBEATITQIMDNTINPNSNVLAA--SS 112
      111  ::::
Db       411  GEAIVYDQDADAASTGSSNRSKQVTLISGSGDNQC--WKLNSDSVYGVGSGCLDLNAGV 468
      111  ::::
QY      113  GIKGKTLVYQVLTDLVLTGGAG 132
      113  ::::
Db       469  TANGKTLIQLYTCSGNSGNQRP 488
      113  ::::

```

```

RESULT 13
US-10-156-761-10246
? Sequence 10246, Application US/10156761
? Publication No. US2003019018A1
? INFORMATION:
? APPLICANT: OHSU, HANOSH
? APPLICANT: "TIED", HANSHI
? APPLICANT: ISHIKAWA, JIN
? APPLICANT: HORIKAWA, HIROSHI
? APPLICANT: SHIRA, TADAYOSHI
? APPLICANT: SAKAKI, YOSHIYUKI
? APPLICANT: HATTORI, NASHATRA
? TITLE OF INVENTION: NOVEL POLYMERICETIDES
? FILB REFERENCE: 249-262
? CURRENT APPLICATION NUMBER: US/10/156,761
? PRIOR FILING DATE: 2002-05-29
? PRIOR APPLICATION NUMBER: JP 2001-204089
? PRIOR FILING DATE: 2001-05-30
? PRIOR APPLICATION NUMBER: 2001-272697
? NUMBER OF SEQ ID NOS: 15409
? SEQ ID NO 10246
? LENGTH: 647
? TYPE: PRT
? ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

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[illegible]

RESULT 14
US-09-770-621-5
Sequence 5, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
Applicant: Anya, Aira
Applicant: Velempati, Richard
Applicant: Pavesetti m, Richard
Applicant: Lactito, Rajia
Applicant: Pachaimo, Marija
Applicant: Stomchenko, Pirkko
Applicant: Iantchen, Tairja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCE: 39
COMPLETION DATE: 1999-01-01
ADDRESSES: STEVEN KESSLER, COLASSETTI & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: DOS compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLIED DATA NUMBER: 08/590,563
APPLIED DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/ABSENT INFORMATION:
NAME: BUGALSKY, LAWRENCE B.
REGISTRATION NUMBER: 5,046
REGISTRATION DATE: 05/05/03/0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SPO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDNESS: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50

```

Query Match	8.2%;	Score 116.5;	DB 9;	Length 480;
Best Local Similarity	31.4%;	Pred. No. 0.0028;		
Matches	32;	Conservative	16;	Mismatches 49;
			Indels	5;
			Gaps	3;

Dz 379 IDVPNGNTADGQVQLYDCHSGS--NQMTTSSGFRIENKCKIDAGSSNRAWVQIYS 436

Qy 22 VVVRRDDDEHFDHQIQLPSPKSNNDPNQLMTIKRDNIRSGS-CLTYGTAGAYVMIED 80
:: :: : :: :: : :: :: : :: :: :

```

QY      81 CNTAVREATIWMQIMWNGTILNERSNLVLAASSGIKGTLTVQ 122
      |      :      |::      |::      |::      |::      |
Db 437 CWGGANOK--WELRADGTTIVQSGLCIDAVGGGTGNGTRLQ 476

```

RESULT 15
US-09-770-621-4
; Sequence 4, Application US/09770621

APPLICANT: Mervyn J. Aris
APPLICANT: Vehmanner, Jari
APPLICANT: Federestr m, Richard
APPLICANT: Lantto, Ralfs
APPLICANT: Paloheimo, Vaira
APPLICANT: Suominen, Pitko
APPLICANT: Lantien, Ralfs
TITLE OF INVENTION: Production and Secretion of Proteins of
the type of insulin
CORRESPONDENCE ADDRESS:
ADDRESSEE: STENE, KESSLER, GOLDSTEIN & POX, P. L. C.
STREET: 110 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent In Release #1.0, Version #1.30
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/770,621
8  FILING DATE:
9

```

```

1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 FILING DATE:
4 FILING DATE NUMBER: 08/590,563
5
6 CLASSIFICATION:
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 08/335,412
9 FILING DATE: 31-OCT-1994
10
11 CLASSIFICATION:
12 PRIOR APPLICATION DATA: US 08/282,001
13 FILING DATE: 29-OUL-1994
14
15 CLASSIFICATION:
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Bugalsky, Lawrence B.
18 REGISTRATION NUMBER: 35,086
19 REFERENCE/DOCKET NUMBER: 1050_0340003
20
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 202-571-2800
23 FAX: 202-571-2800
24 E-MAIL: law.sbg@idn.net
25
26 INVENTOR CHARACTERISTICS:
27 SCIENTIST CHARACTERISTICS: 4:
28 LENGTH: 492 amino acids
29 TYPE: amino acid
30
31 TOPOLOGY: linear
32
33 MOLECULE TYPE: protein
34
35 US-09-770-621-4

```

Query Match	8.2%;	Score 116.5;	DB 9;	Length 492;
Best Local Similarity	31.4%;	Pred. No. 0.0029;		

22 VDVRDDDFHDGNOIQIMPSSKNNNDENQWTIKRONTRISNGS-CLTTYGYTAGVYIMFD 80

QY 61 CMTAVREPTIOWINDNGTINPRSNVLASSGIGITLTWQ 122
| : ||| : | | | | |
477 GCGCCTCCATTCCTGGCTGTACCTGCAGCACTG 476

Search completed: December 11, 2003, 14:48:45
 Job time: 00:17:0120 sec

Job time : 17.0129 secs

Thu Dec 11 16:10:05 2003

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Page 3

QY 5 CSASEPTVRIYVGRGKRVYRDDEPHGNOIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 64
DB 282 CMDEPTVRIYVGRGKRVYRDDEPHGNOIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 341
QY 65 LITVGYTAGVYVIMFDCTAVRENTIWIQNDGTLINPSNLYLAASGSKETLLVYOTL 124
DB 342 LITKSSPRQOVYVIMFDCTAVRENTIWIQNDGTLINPSNLYLAASGSKETLLVYOTL 401
QY 125 DYTIGQWLAGNDPAPEVITVYGFRLCMESNGSVWVETCSGSGQKQWALYQDSIR 184
DB 402 IYVSGQWLPYNTQPFVITVYGLYQWCLQANSQWLEDC-TSEKACQWALYQDSIR 460
QY 185 PRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSGLAMDVQANPEL 244
DB 461 PRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSGLAMDVQANPEL 520
QY 245 RRIITVPATGKPNQWMLPVF 264
DB 521 KQIIVPFPNGMLQWMLPVF 540

RESULT 5

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5646028 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIORITY INFORMATION DATA: US 08/378761
APPLICATION NUMBER: US 08/378761
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-485-286-77

Query Match 54.1%; Score 764.5; DB 1; Length 540;
Best Local Similarity 55.0%; Pred. No. 7,3e-69;
Matches 143; Conservative 43; Mismatches 73; Indels 1; Gaps 1;

QY 5 CSASEPTVRIYVGRGKRVYRDDEPHGNOIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 64
DB 282 CMDEPTVRIYVGRGKRVYRDDEPHGNOIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 341
QY 65 LITVGYTAGVYVIMFDCTAVRENTIWIQNDGTLINPSNLYLAASGSKETLLVYOTL 124
DB 342 LITKSSPRQOVYVIMFDCTAVRENTIWIQNDGTLINPSNLYLAASGSKETLLVYOTL 401
QY 125 DYTIGQWLAGNDPAPEVITVYGFRLCMESNGSVWVETCSGSGQKQWALYQDSIR 184
DB 402 IYVSGQWLPYNTQPFVITVYGLYQWCLQANSQWLEDC-TSEKACQWALYQDSIR 460
QY 185 PRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSGLAMDVQANPEL 244
DB 461 PRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSGLAMDVQANPEL 520
QY 245 RRIITVPATGKPNQWMLPVF 264
DB 521 KQIIVPFPNGMLQWMLPVF 540

RESULT 6

US-09-512-342-14
Sequence 14, Application US/09512342
Patent No. 6388068
GENERAL INFORMATION:
APPLICANT: SATOH, SHINROU
APPLICANT: MASUDA, SHUNROU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
FILE REFERENCE: 081356/0142
CURRENT APPLICATION NUMBER: US/09/512,342
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-512-342-14

Query Match 12.7%; Score 179; DB 4; Length 293;
Best Local Similarity 26.6%; Pred. No 4,7e-10;
Matches 65; Conservative 36; Mismatches 103; Indels 40; Gaps 11;

QY 14 IYVGRGKRVYRDDEPHGNOIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 59
DB 41 LIVERGICLSPSP-----VYKAGIYFPTLSPCDERKOTOLMTVIGQGIIRPM 89
QY 60 SNGSCLTT--YGYTAGVYVIMFDCTAVRENTIWIQNDGTLINPSNLYLAASGSK 116
DB 90 NDFPCLAAEYFQVIA--KAVSSEGVSDPKKRWQKNDGTLALVDSRVLTGDLDY-- 145
QY 117 LITVQGLYTGAGTANDTPAEVITVYGFRLCMESNGS--VVFETCSGQKQW 174
DB 146 --VTIGSNKRTPSGSEWETLSNRYANTEMANLCLQSTDSHVLGNCTNTNXXQ-R 202
QY 175 WLYVQDSIRPRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSG 233
DB 203 WLYVQDSIRPRONODCLTVGRDSVSTVITVYSCSASGQWVFTNEVAILNKSG 260
QY 234 AMDV 237
DB 261 VLDV 264

RESULT 7

US-09-159-106-15
Sequence 15, Application US/09159106
Patent No. 6284509
GENERAL INFORMATION:
APPLICANT: FERRER, PAU
APPLICANT: DIERS, IVAN

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Page 4

APPLICANT: Halkier, Torben
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
EARLIER FILING DATE: 1998-09-23
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 132
TYPE: FRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

Query Match 8.8%; Score 125; DB 3; Length 132;
Best Local Similarity 34.7%; Pred. No. 4.3e-05;
Matches 43; Conservative 12; Mismatches 53; Indels 16; Gaps 6;

QY 18 SQMVDVDDDFDNDQIQMPKSKNDPQNLTKNDTIRNSGCLTTY--GYTAGY 75
DB 14 NMCQVVPWADPFDNFPVQVTCGN--AQWTGSDQTFALGKCDVRGSGTSGAA 71
QY 76 VAFPCNTVRENTIWOIW--DNCT--IINRSNVLAAASGI--KSTTLVQTLDTL 128
DB 72 VQWVTCN-----GTGQKQVADNAGSKLNPQSLCDATGAPLRDGRQVTCNGTT 126
QY 129 GQGW 132
DB 127 AQGW 130

RESULT 8
US-09-159-106-11
Sequence 11, Application US/09159106
Patent No. 6284100
GENERAL INFORMATION:
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
EARLIER FILING DATE: 1998-09-23/796
EARLIER FILING DATE: 1998-12-04/796
EARLIER FILING DATE: 1996-08-23/796
EARLIER FILING DATE: 1997-04-14/796
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 435
TYPE: FRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match 8.8%; Score 125; DB 3; Length 435;
Best Local Similarity 34.7%; Pred. No. 0.00024;
Matches 43; Conservative 12; Mismatches 53; Indels 16; Gaps 6;
QY 18 SQMVDVDDDFDNDQIQMPKSKNDPQNLTKNDTIRNSGCLTTY--GYTAGY 75
DB 317 NMCQVVPWADPFDNFPVQVTCGN--AQWTGSDQTFALGKCDVRGSGTSGAA 374

QY 76 VAFPCNTVRENTIWOIW--DNCT--IINRSNVLAAASGI--KSTTLVQTLDTL 128
DB 375 VQWVTCN-----GTGQKQVADNAGSKLNPQSLCDATGAPLRDGRQVTCNGTT 429
QY 129 GQGW 132
DB 430 AQGW 433

RESULT 9
US-08-468-812-8
Sequence 8, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaanker, Jari
APPLICANT: M nyl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Ralfja
APPLICANT: Palchamov, Maria
APPLICANT: Leminen, Eirko
APPLICANT: Keskitalo, Eeva
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/322,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Buzalsky, Larry B.
REGISTRATION NUMBER: 35,086
REGISTRATION DATE: 1985.0340002
TRIAL INFORMATION:
TELEPHONE: 202-371-2540
FAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FUNCTION: 11,000
CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match 8.5%; Score 119.5; DB 2; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.001;
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;
QY 7 ASEP-----TVAIVGRSGNRVDVDDDFDNDQIQMPKSKNDPQNLTKND 55

Db 354 SSEPXXXXXXXXXADGQIKGVG-SGRCLDVPDASTSDGTOLQIMWCHSGT--NQOMATDA 410
QY 56 NTRISNG-SCLTGYGTAGVYVMIIPDCTAVREATVQIMDNGTIIINRSNVLAA--SS 112
Db 411 GELVYGDKCLDADATNSKQVLSCKGDNQK--WINSDSVGVGGLCLDAVANG 468
QY 113 GIKGTTLVQTLDTYTLGGQW 132
Db 469 TANGTLIQLYTCSNGSNQPM 488

RESULT 10
US-08-590-563-8
Sequence 8, Application US/08590563
Accession: 620114
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Pagarst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURR. APP. NO. NUMBER: US/08/590,563
FILING DATE: 06-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-771-2800
TELEFAX: 202-771-2800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
US-08-590-563-8

Query Match 8.5%; Score 119.5; DB 4; Length 491;

Best Local Similarity 28.6%; Pred. No. 0.001,
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;
QY 7 ASPE-----TVATYGRSGNRVYRDDDPDHDNQIQIMPSKSNNDPVQLATIKRD 55
Db 354 SSEPXXXXXXXXXADGQIKGVG-SGRCLDVPDASTSDGTOLQIMWCHSGT--NQOMATDA 410
QY 56 NTRISNG-SCLTGYGTAGVYVMIIPDCTAVREATVQIMDNGTIIINRSNVLAA--SS 112
Db 411 GELVYGDKCLDADATNSKQVLSCKGDNQK--WINSDSVGVGGLCLDAVANG 468
QY 113 GIKGTTLVQTLDTYTLGGQW 132
Db 469 TANGTLIQLYTCSNGSNQPM 488

RESULT 11
US-09-770-621-8
Sequence 8, Application US/09770621
Accession: 658323
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Pagarst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURR. APP. NO. NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-771-2800
TELEFAX: 202-771-2800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:

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Page 6

CHROMOSOME/SEGMENT: M64551

Query Match 8.5%; Score 119.5; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.001;

Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;

Qy 7 ASEP-----TVLVRSQKRVYRDDPHDGNQIQLPKSKNDPNQWTKED 55
Db 354 SSBPXXXXXXADGGQIRNGV-SGRCLDVPDASTSGTQLDMDCHST--NQOMATDRA 410

Qy 56 NTRISNG-SCLTVGYTPAGYVYVFPDNTAFREATIQIWDNGFIINPSNVLAA--SS 112
Db 411 GELAVYGDKCLDAAGTSNSKVOIYSCWGDNDK--WRINSDSVVGQGLCDVANGTAVNG 468

Qy 113 GIKGTVTVQITDLYTLQGM 132
Db 469 TANGTILQIYTCNSNSQNR 488

RESULT 12

US-08-392-828C-39

/ Sequence 39, Application US/08392828C

/ Patent No. 5795962

/ GENERAL INFORMATION:

/ APPLICANT: IMANAGA, SADAAKI

/ APPLICANT: MOTA, TATSUSHI

/ APPLICANT: SEKI, NORIAKI

/ APPLICANT: ODA, TOSHIO

/ TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING

/ NUMBER OF SEQUENCES: 39

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &

/ STREET: 53 STATE STREET

/ CITY: BOSTON

/ STATE: MA

/ COUNTRY: USA

/ ZIP: 02109

/ COMPUTER READABLE FORM:

/ MEDIA TYPE: floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/392,828C

/ FILING DATE: 28-FEB-1995

/ CLASSIFICATION: 530

/ ATTORNEY/AGENT INFORMATION:

/ NAME: CAMPBELL, PAULA A

/ REGISTRATION NUMBER: 32,503

/ REFERENCE/DOCKET NUMBER: F08-033

/ TELEPHONE: (617) 248-7100

/ TELEFAX: (617) 248-7100

/ INFORMATION FOR SEQ ID NO: 39:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 127 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ FEATURE:

/ NAME/KEY: Peptide

/ LOCATION: 1..127

/ OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

US-08-392-828C-39

Query Match 8.4%; Score 119; DB 1; Length 127;
Best Local Similarity 29.8%; Pred. No. 0.00016;

Matches 37; Conservative 18; Mismatches 61; Indels 8; Gaps 5;

Qy 12 VELVRSQKRVYRDDPHDGNQIQLPKSKNDPNQWTKEDNTRISNG-SCLTVGY 70
Db 6 INGV-SGRCLDVPDASTSGTQLDMDCHST--NQOMATDRAELRYGDKCLDAAGT 62
Qy 71 TACVYVIFPDCTVREATIQIWDNGFIINPSNVLAA--SSGIKGTTLVQITDLYTL 138
Db 63 SNOSKVOIYSCWGDNDK--WRINSDSVVGQGLCDVANGTAVNGTILQIYTCNS 120
Qy 139 GQGM 132
Db 121 NQM 124

RESULT 13

US-09-330-945-39

/ Sequence 39, Application US/09330945

/ Patent No. 6077946

/ GENERAL INFORMATION:

/ APPLICANT: IMANAGA, SADAAKI

/ APPLICANT: MOTA, TATSUSHI

/ APPLICANT: SEKI, NORIAKI

/ APPLICANT: ODA, TOSHIO

/ TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB

/ NUMBER OF SEQUENCES: 39

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &

/ STREET: 125 HIGH STREET

/ CITY: BOSTON

/ STATE: MA

/ COUNTRY: USA

/ ZIP: 02111

/ COMPUTER READABLE FORM:

/ MEDIA TYPE: floppy disk

/ OPERATING SYSTEM: IBM PC compatible

/ SOFTWARE: PC-DOS/MS-DOS

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/330,945

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 09/119,995

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: PITCHER, EDUND R

/ REGISTRATION NUMBER: 27,829

/ REFERENCE/DOCKET NUMBER: F08-032DV

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (617) 248-7000

/ TELEFAX: (617) 248-7100

/ INFORMATION FOR SEQ ID NO: 39:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 127 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ FEATURE:

/ NAME/KEY: Peptide

/ LOCATION: 1..127

/ OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

US-09-330-945-39

Query Match 8.4%; Score 119; DB 3; Length 127;
Best Local Similarity 29.8%; Pred. No. 0.00016;

Matches 37; Conservative 18; Mismatches 61; Indels 8; Gaps 5;

Qy 12 VELVRSQKRVYRDDPHDGNQIQLPKSKNDPNQWTKEDNTRISNG-SCLTVGY 70
Db 6 INGV-SGRCLDVPDASTSGTQLDMDCHST--NQOMATDRAELRYGDKCLDAAGT 62

Qy 71 TACVYVIFPDCTVREATIQIWDNGFIINPSNVLAA--SSGIKGTTLVQITDLYTL 138
Db 63 SNOSKVOIYSCWGDNDK--WRINSDSVVGQGLCDVANGTAVNGTILQIYTCNS 120

Qy 139 GQGM 132
Db 121 NQM 124

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Page 7

Qy	71	TAAVYVWIPFCTVAEATIMQIMDGGIIPRSVLAA--SSGKQITLLVQITLITL	128
		:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
Db	63	SNSKQIGTISCMGSDNQ--IRLNSDSVVGVSGLDANGNTAKGTLLQITTCNSGS	120
Qy	129	GGGW	132
Db	121	NSRW	124

```

1 RESULT 1 US-08-468-812-5
2 US-08-468-812-5
3 Sequence 5, Application US/08468812
4 Patent No. 5935836
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Wemaupesi, Urii
9 APPLICANT: Mupfisi, Mita
10 APPLICANT: Pasipati, Richard
11 APPLICANT: Lantio, Paila
12 APPLICANT: Palohimo, Marja
13 APPLICANT: Sumiham, Pirkko
14 APPLICANT: Lahtinen, Tarja
15 APPLICANT: Kristo, Paula
16
17 TITLE OF INVENTION: Actinomadura Xylanase
18
19 TITLE OF INVENTION: of use
20
21 NUMBER OF SEQUENCES: 25
22
23 CORRESPONDENCE ADDRESS:
24
25 STERN, KESSLER, GOLSTEIN & FOX
26 STREET 100 New York Ave., N.W.
27 CITY: Washington
28 COUNTRY: U.S.A.
29
30 ZIP: 20005
31
32 COMPUTER READABLE FORM:
33
34 MEDIUM TYPE: Floppy disk
35
36 COMPUTER: IBM PC compatible
37
38 OPERATING SYSTEM: PC DOS/MS-DOS
39
40 SOFTWARE: Patent Release #1.0, Version #1.30
41
42 CURRENT APPLICATION DATA:
43
44 FILING DATE: 08/SEP/1994
45 FILING DATE: 08/SEP/1995
46
47 CLASSIFICATION: 435
48
49 PRIOR APPLICATION DATA:
50
51 PRIOR APPLICATION NUMBER: US 08/332,412
52
53 FILING DATE: 31-OCT-1994
54
55 CLASSIFICATION: 435
56
57 PRIOR APPLICATION NUMBER: US 08/282,001
58
59 APPLICATION DATA:
60
61 CLASSIFICATION: 435
62
63 CLASSIFICATION: 435
64
65 ACTIONARY/AGENT INFORMATION:
66
67 NAME: Bugalsky, Larry B.
68
69 REGISTRATION NUMBER: 35,086
70
71 REFERENCE/DOCKET NUMBER: 1050,0340002
72
73 TELECOMMUNICATION INFORMATION:
74
75 TELEPHONE: 202-371-2600
76
77 TELEFAX: 202-371-2640
78
79 INFORMATION FOR SEQ ID NO: 5:
80
81 SEQUENCE CHARACTERISTICS:
82
83 TYPE: amino acids
84
85 STRANDNESS: not relevant
86
87 TOPOLOGY: linear
88
89 MOLECULE TYPE: peptide
90
91 POSITION IN GENOME:
92
93 CHROMOSOME/SEGMENT: AM50
94
95 US-08-468-812-5

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Query Match      8.2%; Score 116.5; DB 2; Length 480;
Rec. Local Similarity 3.1%; Pred. No. 0.002;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3

QY 22 DVVRDDFDHQQLQCLMPKSKNNDDPNCQVLTPIKRDNTIRNSGS-CLTGYGTAGVYVWID 80
      :::::|:::|:::|

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Db 379 IDVPKGTADTQYQJQJCHSSS--NQWTTSYSSGFFKPKCKLDAGSSNGNVQIYS 436

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US-08-590-563-5
RESULT 15
US-08-590-563-5
? Sequence 5, Application US/08590563
? Patent No. 630014
? GENUS/SP. INFORMATION:
? APPLICANT: Vahmamiyeh, Ajia
? APPLICANT: Vahmamiyeh, Tari
? APPLICANT: Pascret m, Richard
? APPLICANT: Lalico, Salia
? APPLICANT: Palohelmo, Marja
? APPLICANT: Suomien, Pirkko
? APPLICANT: Laitinen, Tarja
? TITLE OF INVENTION: Production and Secretion of Proteins of
? NUMBER OF SEQUENCES: 39
? CORRESPONDENCE ADDRESS:
? ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
? STREET: 1100 New York Ave., N.W. Suite 600
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/590.563
? FILING DATE: 26-JAN-1996
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 06/469,812
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/332,412
? FILING DATE: 31-OCT-1994
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/282,001
? FILING DATE: 29-JAN-1994
? CLASSIFICATION: 516
? ATTORNEY/AGENT INFORMATION:
? NAME: Biagisky, Lawrence B.
? REGISTRATION NUMBER: 35,086
? REFERENCE/DOCKET NUMBER: 1050,0340003
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 5:
? LENGTH: 480 amino acids
? STRAND: amino acid
? STRANDS: 1
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: AM50
US-08-590-563-5

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Query Match      8.2%  Score 116.5  DB  4;  Length 480;
Best Local Similarity 31.4%;  Pred No. 0.002149;
Matches 32;  Conservative 16;  Mismatches 19;  Indels 5;  Gaps 3
22 VVVDDDDPDDDDGICGLMSSKNNDDNLTWTKKDDNTTSSNGS-CLTGYVATGATGATMFD 80

```


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us-09-601-667c-8.ra1

Page 8

Db 379 IVPNGNTADTQVQVLDCHSGS--NQWYTSGBRIFGNKCLDAGSSNGATVQIYS 436
Qy 81 CNTAVRENTIWOIMNGTIIINPRSNLYLAAGGKGTTLTVO 122
Db 437 CWGANQX--WEIADGTIVGVOSGICLDVAGGTGNGTRIQ 476

Search completed: December 11, 2003, 14:11:34
CDS time : 10.1403 secs

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rpr

Page 1

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 ; Search time 8.20622 Seconds

(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667C-9

Perfect score: 1417

Sequence: 1 DDVTCASAPPTVIRVGNK.....RRIIYPANGKQWLPVF 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1412	99.6	264	2	PD0019	mistletoe lectin I
2	1401.5	98.9	265	2	JM0090	lectin-I B chain -
3	907.5	64.0	576	1	RICSD	ricin D precursor
4	907.5	64.0	576	1	RICSD	ricin B - castor b
5	772	51.3	563	2	SR6330	abrin-8 precursor
6	772	51.3	563	1	RICSD	abrin-8 precursor
7	772	51.3	563	1	RICSD	abrin-8 precursor
8	772	51.3	563	1	RICSD	abrin-8 precursor
9	772	51.3	563	1	RICSD	abrin-8 precursor
10	772	51.3	563	1	RICSD	abrin-8 precursor
11	772	51.3	563	1	RICSD	abrin-8 precursor
12	772	51.3	563	1	RICSD	abrin-8 precursor
13	772	51.3	563	1	RICSD	abrin-8 precursor
14	772	51.3	563	1	RICSD	abrin-8 precursor
15	772	51.3	563	1	RICSD	abrin-8 precursor
16	772	51.3	563	1	RICSD	abrin-8 precursor
17	772	51.3	563	1	RICSD	abrin-8 precursor
18	772	51.3	563	1	RICSD	abrin-8 precursor
19	772	51.3	563	1	RICSD	abrin-8 precursor
20	772	51.3	563	1	RICSD	abrin-8 precursor
21	772	51.3	563	1	RICSD	abrin-8 precursor
22	772	51.3	563	1	RICSD	abrin-8 precursor
23	772	51.3	563	1	RICSD	abrin-8 precursor
24	772	51.3	563	1	RICSD	abrin-8 precursor
25	772	51.3	563	1	RICSD	abrin-8 precursor
26	772	51.3	563	1	RICSD	abrin-8 precursor
27	772	51.3	563	1	RICSD	abrin-8 precursor
28	772	51.3	563	1	RICSD	abrin-8 precursor
29	772	51.3	563	1	RICSD	abrin-8 precursor

30	93	6.6	875	2	140862	lora toxin component
31	92	6.5	895	1	10XICP	Ep-cadherin precursor
32	90.5	6.4	1008	2	T32986	hypothetical prote
33	89.5	6.3	471	2	A41478	cytochrome vha pre
34	89.5	6.3	624	2	T42247	polypeptide N-acet
35	89.5	6.3	962	2	AG2444	hypothetical prote
36	89.5	6.3	1711	2	AB1283	peptidoglycan link
37	89.5	6.2	962	2	SS8107	hypothetical WD-40
38	89.5	6.2	962	2	SS8107	hypothetical prote
39	88	6.2	1228	2	T42247	probable polypept
40	88	6.2	908	2	AG2254	probable polypept
41	88	6.2	1032	2	T43257	beta-1,3 exoglucan
42	88	6.2	1032	2	AG2493	hypothetical prote
43	87.5	6.2	2229	2	T16199	hypothetical prote
44	86.5	6.1	1231	1	A48490	endo-1,4-beta-xyla
45	86.5	6.1	1577	2	A35140	hemolysin A precu

ALIGNMENTS

RESULT 1

PD0019 mistletoe lectin I B chain - Viscum album (fragment)

C:Species: Viscum album

C:Date: 03-Jul-1998 #sequence_rev: 10-Jul-1998 #text_change 07-May-1999

R:Accession: PD0019

R:Schubert, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Berzel, C.; Voelter, W.

A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum al

A:Reference number: PD0018; PMID:96308123; PMID:9642133

A:Residue number: 1-264

A:Superfamily: ricin, RNA N-glycosidase homology

Query Match 99.6%; Score 1412; DB 2; Length 264;

Best Local Similarity 99.6%; Fred. No. 4.2e-111;

Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	DDVTCASAPPTVIRVGNKRVVDDDFHDSQQLMPKSNDDPNQWLTIRKDDTSS 60	
DB	1	DDVTCASAPPTVIRVGNKRVVDDDFHDSQQLMPKSNDDPNQWLTIRKDDTSS 60	
QY	61	NSCCLITGVYAGVYVMPFCQTVREATVQWNGIINPRNATVLAASGIGKTTTL 120	
DB	61	NSCCLITGVYAGVYVMPFCQTVREATVQWNGIINPRNATVLAASGIGKTTTL 120	
QY	121	VETLDVTLQGMASNDPAREVITYVFFDDCMESNGSVWVETCSQKQKQWALYGD 180	
DB	121	VETLDVTLQGMASNDPAREVITYVFFDDCMESNGSVWVETCSQKQKQWALYGD 180	
QY	181	GSIRPQNDQCTTSGRDSVSTVNIIVSSAGSGSRVFTNEGAIINIKTGILANDVQA 240	
DB	181	GSIRPQNDQCTTSGRDSVSTVNIIVSSAGSGSRVFTNEGAIINIKTGILANDVQA 240	
QY	241	NPKLRRIIYPANGKQWLPVF 264	
DB	241	NPKLRRIIYPANGKQWLPVF 264	

RESULT 2

PD0019 mistletoe lectin I B chain - Eucalyptus mistletoe

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_rev: 10-Jul-1998 #text_change 19-May-2000

R:Accession: JM0090

R:Solier, M.H.; Stoeva, S.; Voelter, W.

A:Title: Complete amino acid sequence of the B chain of mistletoe lectin I.

A:Reference number: JM0090; PMID:98289575; PMID:9618256

A:Accession: JM0090

A/Molecule type: protein
A/Residues: 1-265 <SD>
C/Superfamily: ricin; RNA N-glycosylase homology
C/Keywords: glycoprotein
F/61,96,136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.9%; Score 1401.5; DB 2; Length 265;
Best Local Similarity 99.2%; Pred. No. 3-2e-110;
Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 DVTGCASEPTVRIYGNMGAVDVRDDPDHGNQIQLMESKSNNDPNQWLTWKEDGTRIS 60
DB 1 DVTGCASEPTVRIYGNMGAVDVRDDPDHGNQIQLMESKSNNDPNQWLTWKEDGTRIS 60
QY 61 NSGCLTYGYTAGVYVWFDCNVAEEXTWQIWDNGTINPSSNVLAASSGIRKPTLT 120
DB 61 NSGCLTYGYTAGVYVWFDCNVAEEXTWQIWDNGTINPSSNVLAASSGIRKPTLT 120
QY 121 VQIDVTLGGQMLAANDTPAEVTLVGRDLQMSNGSGVWETDSQDQGMALVSD 180
DB 121 VQIDVTLGGQMLAANDTPAEVTLVGRDLQMSNGSGVWETDSQDQGMALVSD 180
QY 181 GSIRPKONODQITSGRDSVSTVINVCSGSGSQGWFTNEGALINLCTGLAMVDAQ 240
DB 181 GSIRPKONODQITSGRDSVSTVINVCSGSGSQGWFTNEGALINLCTGLAMVDAQ 240
QY 241 NFKRRRIILIPATGKPNQW-LPPV 264
DB 241 NFKRRRIILIPATGKPNQW-LPPV 265

RESULT 3
R/CSD
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C/Accession: A24041, S20513, A24614, A03372, A24010, A03374, S10903
R/Hallings, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13: 6015-6033, 1985
A/Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A/Reference number: S20513; MUID:9216016; PMID:1371405
A/Accession: A24041, MUID:8606724; PMID:293712
A/Molecule type: DNA
A/Residues: 1-576 <AL>
A/Cross-references: GB:X03179; NID:921082; PIDN:CA26939.1; PID:921083
R/Tegart, J.W.; Roberts, L.M.
Plant Mol. Biol. 18: 515-525, 1992
A/Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A/Reference number: S20513; MUID:9216016; PMID:1371405
A/Accession: S20513
A/Molecule type: RNA
A/Residues: 1-576 <RP>
A/Cross-references: EMBL:X52908; NID:921084; PIDN:CA23705.1; PID:921085
R/Lamb, F.I.; Roberts, L.M.; Lord, J.W.
Eur. J. Biochem. 148: 265-270, 1985
A/Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A/Reference number: A24614; MUID:85179479; PMID:3838723
A/Accession: A24614
A/Molecule type: mRNA
A/Residues: 12-75, 'D', 77-550, 'R', 552-576 <LM>
A/Cross-references: GB:X02288; NID:921077; PIDN:CA26230.1; PID:921078
R/Cornfield, J.; Roberts, L.M.; Lord, J.W.
Agric. Biol. Chem. 42: 1267-1274, 1978
A/Title: Isolation and sequences of peptic peptides, and the complete sequence of the cDNA
A/Accession: A03372
A/Molecule type: protein
A/Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>
R/Hallings, K.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13: 6015-6033, 1985
A/Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A/Reference number: A24010
A/Accession: A24010
A/Molecule type: protein
A/Residues: 315-383, 'PS', 386-576 <AB>
R/Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43: 2221-2224, 1979
A/Title: Primary structure of Ala chain of ricin D.
A/Reference number: A03374
A/Accession: A03374
A/Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LT', 573-574, 'P' <FNU>
A/Note: This paper, one of a series, summarizes the experimental details for the deter
R/Ready, M.P.; Kim, Y.; Roberts, J.D.
Proteins 10: 270-278, 1991
A/Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism
A/Reference number: A48237; MUID:91352006; PMID:1881883
A/Contents: annotation; active site
R/Ready, M.P.; Roberts, J.D.
A/Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A/Reference number: A48238; MUID:91352005; PMID:1881882
A/Contents: annotation; X-ray crystallography, 2.5 angstroms
R/Katzin, B.J.; Collins, E.J.; Roberts, J.D.
Proteins 10: 251-259, 1991
A/Title: Structure of ricin A-chain at 2.5 angstroms.
A/Reference number: A48239; MUID:91352004; PMID:1881881
A/Contents: annotation; X-ray crystallography, 2.5 angstroms
C/Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C/Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal sub
C/Comment: This paper summarizes the experimental details for the determination of the
C/Superfamily: ricin; RNA N-glycosylase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; se
F/1-35/Domain: signal sequence #status predicted <SIG>
F/16-302/Product: ricin D chain A #status experimental <ACH>
F/16-302/Domain: rRNA N-glycosidase homology <RNG>
F/315-576/Product: ricin D chain B #status experimental <ACH>
F/315-576/Domain: rRNA N-glycosidase homology <RNG>
F/45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/215/Active site: 820 #status predicted
F/294-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
F/348,369/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status experimental
F/348,369/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status experimental

Query Match 64.0%; Score 907.5; DB 1; Length 576;
Best Local Similarity 63.8%; Pred. No. 2.4e-68;
Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 5 CSASPTVRIYGNMGKVDVRDDPDHGNQIQLMESKSNNDPNQWLTWKEDGTRIS 64
DB 318 CSASPTVRIYGNMGKVDVRDDPDHGNQIQLMESKSNNDPNQWLTWKEDGTRIS 64
QY 65 LTTGYTAGVYVWFDCNVAEEXTWQIWDNGTINPSSNVLAASSGIRKPTLT 124
DB 65 LTTGYTAGVYVWFDCNVAEEXTWQIWDNGTINPSSNVLAASSGIRKPTLT 124
QY 121 VQIDVTLGGQMLAANDTPAEVTLVGRDLQMSNGSGVWETDSQDQGMALVSD 180
DB 121 VQIDVTLGGQMLAANDTPAEVTLVGRDLQMSNGSGVWETDSQDQGMALVSD 180
QY 181 GSIRPKONODQITSGRDSVSTVINVCSGSGSQGWFTNEGALINLCTGLAMVDAQ 240
DB 181 GSIRPKONODQITSGRDSVSTVINVCSGSGSQGWFTNEGALINLCTGLAMVDAQ 240
QY 241 NFKRRRIILIPATGKPNQW-LPPV 264
DB 241 NFKRRRIILIPATGKPNQW-LPPV 265

RESULT 4

506330
Ricin B - castor bean (fragment)
N>Contactins: Chain B: rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C/Spectrum: Ricinus communis (castor bean)
C/Accession: 506330, J05381, GenBank 51-Mar-1990 #ext: change 20-Aug-1999
R/Author: B.F. Murray, B.E.; Halling, A.C.; Halling, K.C.; Tlakarova, N.; Long, G.L.; Plant Mol. Biol. 9, 287-295, 1987
A>Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis ag
A/Reference number: 506330
A/Accession: 506330
A/Molecule type: RNA
A/Residues: 1-263 (RNA)
A/Cross-references: EMBL:M17631; NID:g169714; PID:AA63506.1; PID:g169715
R/Author: T. Funatsu, G.
B/Title: The complete amino acid sequence of the B-chain of ricin E isolated from small-
A/Reference number: J05381; MIMD:87101186; PMID:380193
A/Accession: J05381
A/Molecule type: protein
A/Residues: 165, 167-72-209, 'A', 211-241, 243-250, 'V', 252-263 (cRNA)
A/Experimental source: seed
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
F/1-653/Product: ricin B chain B #status: experimental <DB>
F/17-59, 60-100, 103-141, 148-183, 187-228, 232-263/Region: 40-residue repeats
F/20-35, 63, 60, 151, 144, 190-207/Distilled bond: Helix predicted
F/53, 133/Binding site: carboxylate (Asn) (catalant) Helix experimental
Query Match 61.5% Score 871; DB 2; Length 263;
Best Local Similarity 61.3%; Pred. No. 1e-65;
Matches 160; Conservative 37; Mismatches 62; Indels 2; Gaps 2;
CY 5 CSASPPTVAVLGNAGVYRDDPDIDNOQIOWFSSNDPQWLTIKEDTTSNSQC 64
DB 4 GNDPPIVAVLGNAGVYRDDPDIDNOQIOWFSSNDPQWLTIKEDTTSNSQC 63
CY 65 LTTGGTAAVYVWIDPQWKEATVQIDMNGNITIPSSVLAASSGKSTTLVQTL 124
DB 64 LTTGGTAAVYVWIDPQWKEATVQIDMNGNITIPSSVLAASSGKSTTLVQTL 123
CY 125 DYTGGAGAGNDTAEVETVYRDLCKSSNGSWTETDSSQNGKALYGGTIR 184
DB 124 IYVSGGAGAGNDTAEVETVYRDLCKSSNGSWTETDSSQNGKALYGGTIR 183
CY 185 PQMDGCTGSDGVSSTVYVNSGQASGQWFWFNKAGLAKTGLANDVQWAMP- 243
DB 183 PQMDGCTGSDGVSSTVYVNSGQASGQWFWFNKAGLAKTGLANDVQWAMP- 242
CY 244 LKRIITVPAVSKENQWMLPVP 264
DB 243 LKRIITVPAVSKENQWMLPVP 263

RESULT 5
TIZSLA
Abn/a precursor - Indian licorice (fragment)
N>Contactins: rRNA N-glycosidase (EC 3.2.2.22)
C/Spectrum: Abn/a precursor (Indian licorice)
C/Accession: 532429, J070202; X33971, J01338, S14472; S24133; S74111
R/Author: C.H. Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A>Title: Primary structure of abn/a precursor, isolated by cDNA sequencing.
A/Reference number: 532429; MIMD:91332788; PMID:842133
A/Accession: 532429
A/Molecule type: cDNA
A/Residues: 'E', 2-528 (cRNA)
A/Cross-references: GI:898344; NID:g16994; PID:AA2624.1; PID:g16995
A/Note: the coding region for the sequence shown is preceded by an ATG codon
A/Note: residues 1-8 were derived from the synthesized primer

R/Author: G. Taguchi, Y.; Kametani, M.; Yanaka, M.
A/Reference number: 506330
A/Accession: 506330
A/Molecule type: protein
A/Residues: 1-201, 203-281 (cRNA)
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
R/Author: G. Taguchi, Y.; Kametani, M.; Yanaka, M.
A/Reference number: 506330
A/Accession: 506330
A/Molecule type: protein
A/Residues: 1-201, 203-281 (cRNA)
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Accession: 506330
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Accession: 506330
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A/Molecule type: protein
A/Residues: 1-201, 203-281 (cRNA)
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Reference number: 506330
A/Accession: 506330
A/Molecule type: protein
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Accession: 506330
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Reference number: 506330
A/Accession: 506330
A/Molecule type: protein
A/Residues: 1-201, 203-281 (cRNA)
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Reference number: 506330
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A/Molecule type: protein
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A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
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A/Reference number: 506330
A/Accession: 506330
A/Molecule type: protein
A/Residues: 1-201, 203-281 (cRNA)
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
R/Author: G. Taguchi, Y.; Kametani, M.; Yanaka, M.
A/Reference number: 506330
A/Accession: 506330

[illegible]

RESULT 6

agglutinin precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence: revision 31-Dec-1993 #ext: change 16-Jul-1999
CAccession: A24261; A24210
R:Roberts, L.W.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
U: Biol. Chem. 260, 15686-15686, 1995
A:Accession: the primary sequence of ricin was compared with the ricin communis agglutinin. Comparison with ricin.
A:Accession: A24261; A24261; PDB:6659449; PMID:9939230
A:Molecule type: mRNA
A:Residues: 1-564 ->ROB-
A:Cross-references: GB:M2089; NID:9169700; PID:AA33869.1; PID:9169701
R:Araki, T.; Yoshiohka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A:Title: The complete amino acid sequence of the B-chain of the Ricinus agglutinin
A:Reference number: A24210
A:Accession: A24210
A:Residues: 303-325 'P', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-564, 'D', 566-567, 'P'
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F:15-280/Domains: signal sequence #status predicted, <SIG>
F:15-280/Product: agglutinin chain A homology predicted <ACH>
F:15-281/Domains: rRNA N-glycosidase homology predicted <RNG>
F:153-554/Product: agglutinin chain B homology predicted <BOH>
F:153-554/Domain: agglutinin chain B homology predicted <BOH>
F:153-554/Repeat: 403-405, 430-435, 469-528, 551-564/Region: 40 to residue repeats
F:153-554/Repeat: 403-405, 430-435, 469-528, 551-564/Region: 40 to residue repeats
F:104-147/211-232/Binding sites: substrate (Gly, Tyr, Glu, Asn) #status predicted
F:200-303/Active sites: Glu, Arg #status predicted
F:283-306/327-331,365-382,453-465,492-509/Disulfide bond: Glu, Asn #status predicted
F:324-337/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F:337-357/Binding site: carbonylarginine (Asn) (covalent) #status experimental
F:356-357/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

	Best Local Match	Similarity	54.9%	Score	777.5	DB: 1	Length	564
				Pred. No.	1.9e-57			
	Matches	Conservative	41	Mismatches	73	Indels	1	Gaps
QY	5	CSASEPVTYIVKRNKGVVVDQDDPHDQGIQIMKSSKNDPNQITLTKRDQITINSKSG	64					
Db	306	QMPDEPTIVKRNKGVVVDQDDPHDQGIQIMKSSKNDPNQITLTKRDQITINSKSG	365					
QY	65	LTLYGVTGAGYVYVMDPDQAAVREKLTQVINDGNTIPNSKVLVAASGSKIGKLTFTQVL	124					
Db	366	LTLSKSRKQGVVYVNSSTAVGATQVMDKRTIIPSSGGLVAATSGNSGKLTFTQV	428					

QY 125 DYTLAGOAMLANDIARREAVITVYEFEDCMEHNSGGSVWEETDSSQIQOQKMLVGGDSGR 184
D 426 IYASVOOMPLTNNGPFTTIVELVYGMCIQANSKXMLEDC-TSEKAOQMLVADSESR 484
QY 185 PRONOCOLTSIRDSVSTYNIVYSGASSGSRVETEGALINLTGMLANDVQANPLU 244
D 435 FQONNECDILNANIGVYVILDSGASGSGRMHRDQILNINXGLTVYRSPBL 544
QY 245 RRIITVATGCGOAMMLEPVF 264
D 545 KQIIVHPFQNGNINMLEPLF 564

RESULT 7

A:biochem precursor - Indian jitorice (fragment)
 N:contamin: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian jitorice)
 C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 C:Accession: S32430; JCI199
 R:Hong, C.H.; Lee, W.C.; Lee, T.C.; Lin, D.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A:Title: Primary structure of three distinct isobornins determined by cDNA sequencing.
 A:Reference number: S32429; PMID:9313798; PMID:8421313
 A:Accession: S32430
 A:Molecule type: mRNA
 A:Residues: 1-527; rDNA
 R:cross-references: 68-M09345; NID:G162266; PIN:AA3625-1; FID:G166297
 R:Cross-references: 68-M09345; NID:G162266; PIN:AA3625-1; FID:G166297
 R:Biochem Biochem. Biophys. 57, 166-169, 1993
 A:Title: The complete amino acid sequences of the B-chain of Abirin-a and Abirin-b, toxins
 A:Reference number: TCI1398; PMID:93169023; PMID:7763442
 A:Accession: JCI1399
 A:Molecule type: protein
 A:Residues: 260-281; 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-440
 A:Experimental source: seed
 C:Keywords: disulfide bond, N-glycosidase homology
 C:Keywords: rDNA, N-glycosidase homology
 C:Keywords: rDNA, N-glycosidase homology
 F:1-250/Product: abirin-b chain A #status predicted <RCH>
 F:1-245/Domin: rRNA N-glycosidase homology #RCH
 F:162-277/Access: 68-106; 12148; 482-481; 449-427/Region: 40-residue repeat
 F:162-277/Access: 68-106; 12148; 482-481; 449-427/Region: 40-residue repeat
 P:1/Modified site: pyrroloisn carboxylic acid (Gln) #status predicted
 P:74,131,199,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 P:110,360,409/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:163,166/Active site: Glu, Arg #status predicted
 F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
 F:287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:199,550/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

[illegible]

RESULT 8
abrin-d precursor - Indian litorice
N:Contains: RNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian litorice)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C/Accession: S16022
R:Wood, K.A.; Lord, J.M.; Wawrzyniak, E.J.; Pataik, N.
Burr, J. Blochem. 198, 723-732, 1991
A:Title: Precursor: genomic cloning, characterization and the expression of the A-chain
A:Reference number: S16022; M01D:9126957; PMID:2050149
A:Accession: S16022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <MO>
A:Cross-references: EMBL:X5667; NID:916084; P1DN:GAA39202.1; P1D:916085
C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
the A and B chains are linked by a single disulfide bond, which is essential for toxic
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F:23-265/Product: abrin-d chain A #status predicted <RCH>
F:23-265/Product: abrin-d chain B #status predicted <RCH>
F:235-560/Product: abrin-d chain A #status predicted <RCH>
F:235-560/Product: abrin-d chain B #status predicted <RCH>
F:117-359-360-400-402-444-483-487-526-529-562/Region: 40-residue repeats
F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:108,201/active site: Glu, Arg #status predicted
F:234,287,395,435,436/Binding site: carboxylate (Asn) (covalent) #status predicted
F:281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
F:322,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 54.0%; Score 765; DB 2; Length 562;
Matches 143; Conservative 43; Mismatches 73; Indels 2; Gaps 2;
5 CSAS-EPYRIVGNKMKVYRDDPFDGNGQIOLMBSKSNNDPQWTTIKRDTIRSNKS 63
303 CSNRVEPTVAGSDKCKVDYDDGHNKRIILMKCKDLRNDWTLKSKTKIRSNK 362
64 CLTGYGAGVYVIMPPCPKVEENTVQWNGTINPNSNLYLAASGIGTTLVQT 123
363 CLTTEGAPGVYVIMYDCTSAVAVETWIDNGTILNPNSNLYLAASGIGTTLVQT 422
124 LDTLGGWGLAGNDPAEETVIGYERDLQESNGSGVWVETCSSQKQKMAIYDPSI 183
423 NEILKQGNATNNTSPFTSISGSDLCQAGQSNVWLADCNKKEQ-QVALYDPSI 481
184 RPKQNDQCLTSRDSVSTVINVSGSGASGSPWFNFGAIIINLKTGLADPAQANFK 243
482 RSYQVNNCLTSKDKQSGPIVLMACSNWGAQGMFLFDGSIYHLHDWVDYKSDPS 541
244 LRIIITPAGKPNQWMLPVP 264
542 LKEIITLPHYKXKNQWMLTF 562

RESULT 9
abrin-d precursor - Indian litorice (fragment)
N:Contains: RNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian litorice)
C>Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C/Accession: S32431; S34408
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
Burr, J. Bloem. 229, 263-267, 1993
A:Title: Primary structure of three distinct isobritins determined by cDNA sequencing. Cd
A:Reference number: S32431; M01D:9132798; PMID:8421313
A:Accession: S32431
A:Molecule type: mRNA
A:Residues: 1-528 <HN>

A:Cross-references: CB:M93346
R:Hung, C.; Lee, M.; Lee, T.; Lin, J.
Submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-169; C, 171-320, /L, 322-528 <H2>
A:Cross-references: CB:M93346
C:Comment: This is a fragment of an A chain, which inhibits protein synthesis by inactivating
the A and B chains are linked by a single disulfide bond, which is essential for toxic
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin;
F:1-251/Product: abrin-d chain A #status predicted <RCH>
F:7-246/Domain: RNA N-glycosidase homology <RNG>
F:261-528/Product: abrin-d chain B #status predicted <RCH>
F:261-528/Product: abrin-d chain B #status predicted <RCH>
F:1/Modified site: pyroglutamic acid (Glu) #status predicted
F:117-359-360-400-402-444-483-487-526-529-562/Region: 40-residue repeats
F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:108,201/active site: Glu, Arg #status predicted
F:234,287,395,435,436/Binding site: carboxylate (Asn) (covalent) #status predicted
F:281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
F:322,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 53.9%; Score 764; DB 2; Length 528;
Matches 143; Conservative 44; Mismatches 72; Indels 2; Gaps 2;
5 CSAS-EPYRIVGNKMKVYRDDPFDGNGQIOLMBSKSNNDPQWTTIKRDTIRSNKS 63
269 CSNRVEPTVAGSDKCKVDYDDGHNKRIILMKCKDLRNDWTLKSKTKIRSNK 328
64 CLTGYGAGVYVIMPPCPKVEENTVQWNGTINPNSNLYLAASGIGTTLVQT 123
329 CLTTEGAPGVYVIMYDCTSAVAVETWIDNGTILNPNSNLYLAASGIGTTLVQT 388
124 LDTLGGWGLAGNDPAEETVIGYERDLQESNGSGVWVETCSSQKQKMAIYDPSI 183
389 NEILKQGNATNNTSPFTSISGSDLCQAGQSNVWLADCNKKEQ-QVALYDPSI 447
184 RPKQNDQCLTSRDSVSTVINVSGSGASGSPWFNFGAIIINLKTGLADPAQANFK 243
448 RSYQVNNCLTSKDKQSGPIVLMACSNWGAQGMFLFDGSIYHLHDWVDYKSDPS 507
244 LRIIITPAGKPNQWMLPVP 264
508 LKQIITLPHYKXKNQWMLTF 528

RESULT 10
agglutinin I precursor - European elder
C:Species: Sambucus nigra (European elder)
C/Accession: S62627; S62619
R:van Damme, B.J.M.; Barre, A.; Ruge, P.; van Leeuwen, P.; Peumans, W.J.
Burr, J. Blochem. 235, 128-137, 1996
A:Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; M01D:9620926; PMID:8631319
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VN>
A:Cross-references: EMBL:U07122; NID:9141772; P1DN:AAC9458.1; P1D:9141773
A:Accession: S62619
A:Reference number: S62619
A:Accession: S62619
A:Molecule type: protein
A:Residues: 29-39,309-319 <VA>
C/Superfamily: ricin; RNA N-glycosidase homology
F:37-283/Domain: RNA N-glycosidase homology <RNG>

Query Match
Best Local Similarity 38.5%; Score 545; DB 2; Length 570;
Matches 143; Conservative 45.9%; Pred. No. 6, 2e-38;

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us-09-601-667c-9.rpr

Page 5

	Matches	115,	Conservative	33,	Mismatches	95,	Indels	12,	Gaps	6,
Qy	5	CSASEPTVAIVGNKNGKRDVADODDFPHQGNOLMFSSKSNNDNDLWTKDQITPNSGSC	64							
Db	316	GSVWETRIISGMDGLCADYRGVYIDGNPOLRP--CNECNDLWTRFDITPRLMGK	373							
Qy	65	LTFTGYAGVYVIMPDCAVYAEKTIWQINDGTIIPRSNIVLAASGIRGTYIVOTL	124							
Db	374	L-----TASSVMVLYDNCVPEEAKMTYSIDITINPESHGLVYLPQABKSLSTENN	428							
Qy	125	DYLGAGLAAINDTAPRSATYIIGVRDLCEMGSS--IHWETCSSGSGSKALVGGSS	182							
Db	429	IHAHQGTWG-DYELWYTIYGRKQKCLRENNETVYIELCVLRQO--EMALVDSGT	486							
Qy	183	IPKPNODCCGTSGRSYGVYVINTVSCSAGSCKRYFNEGALILWTLGADVAQAP	242							
Db	487	IKVSNNSLCVTSHEHRSDDLVLKCGE--SGNQKTFYNNGTISNPAAKLMDVAGQDV	545							
Qy	243	KLRRIIIVPATGKPNOML	261							
Db	546	SIRKIIIVPATGPNOMI	564							

RESULT 11.

JC7535

Chitinase [EC 3.2.1.14] 35 - Streptomyces thermoviolaceus
C.Species: Streptomyces thermoviolaceus
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #ext_change 30-Jun-2001
C.Accession: JC7535

R.Yajima, H., Okamoto, T., Hatano, N.; Miyawaki, K.; Watanabe, T.; Mitsutomi, M.; Inamori,
Biosci.: Biotechnol. Biochem. 64, 2445-2453, 2000

A>Title: Family 19 chitinases from Streptomyces thermoviolaceus OGC-520: Molecular cloning,
A.Reference number: JC7535; PMID:21036907; PMID:11934141

A.Accession: JC7535

A.Molecule type: DNA

A.Residues: 1..377 <TSU>

A.Cross-references: DDBJ|AB018442

A.Experimental source: strain OGC-520

C.Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation.
Lysochitinase-binding domain that is important in the efficient hydrolysis of insoluble c

GeneInfo:

A.Gene: CH15

K.Keywords: glycosidase; hydrolase

[illegible]

RESULT 12
J30589
endo-1,4-beta-xy/lanase (EC 3.2.1.8) A precursor - Streptomyces lividans
N/Alternate names: xy/lanase A

CSpecies: Streptomyces lividans
ClDate: 10-Mar-1994 #sequence_rev1usion 22-Nov-1996 #text_change 26-Feb-1999
CAccession: J05089; PS0238
RShaeek, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Klinefel, D.
Gene 107, 75-82, 1991
ATitle: Sequences of three genes specifying xylanases in Streptomyces lividans.
ACcession: J05089; M01D:J207439; EMBL:L74521
AMolecule type: DNA
AResidues: 1-477 <SHA>
ACross-references: GB:M64551
AAccession: PS0238
AMolecule type: Protein
AProtein length: 42-59 <SHZ>
CGenetics:
AGene: xlnA
CFunction:
ADescription: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xyans
APathway: xylan degradation
CSuperfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase B; extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F4e-417/Procdot: endo-1,4-beta-xylanase A Helms experimental <MRT>
F74-341/Domian: Streptomyces endo-1,4-beta-xylanase A homology <SKY>
F169-277/Active site: Gln #status predicted

```

Query Match      8.9% ; Score 125.5 ; DB 1 ; Length 477 ;
Best Local Similarity 29.9% ; Pred. No. 0.0079 ;
Matches          40 ; Conservative 20 ; Mismatches 61 ; Indels 13 ; Gaps 5

QY       7  AASP-----TVRYGNSGMGVDRVDDFDHNSQJOLMANSNNNDNQLTIRKRGTSISN 61
           :::::
Db        346 SSSPAGDGGKIVNG--SRLCLVDVPASTSDGLQIMCHSGT--NOQAATAGELRVY 402
QY       62  G-SCTIYGAVGKVVMT-GRSCNTAAREATINQINDGTINPSUWLA--SSGLKXTT 118
           ::::
Db        403 GPCKLDPAATSNASKVQYVSOCWDGNOK--WRLNSDGSVGVVGSLCLDAVGNVTANGL 460
QY       119 LTYQTLLDYTLTGQG 132
           ::
Db        461 IQLYTCSNSNQNR 474

```

```

RESULT 13
T34603
Xylanase A - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
C:Accession: T34603
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajadream, M.A.
submitted to the SCSB Data Library, January 1998
I:Reference number: Z21548
A:Stroma_preliminary
A:Stroma_preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-383 <DNR>
A:Cross-references: EMBL:AL021599; PIRN:CAA1468.1; GSPDB:GN00070; SCSOEB:SC10A5.36C
A:Experimental source: Strain A3(2)
C:Genetics:
A:Gene: xlnA; SCSOEB:SC10A5.36C
C:Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase A
I:-247;Domain: Streptomyces endo-1,4-beta-xylanase A homology <X>

```

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Query Match      8.6%; Score 122.5; DB z; Length 353;
Best Local Similarity 25.5%; P-idx. No. 0.011;
Matches         40; Conservative 19; Mismatches 62; Gaps 6;
Indels 13;
Qy ASP-----TATGAGNAGVAVZPDDEPNHGOJGLMCKNSKNDENCLWTKIORTSEEN 61
Db SSPSPADSCOLIKRG--SRCLDVPDPASTSDGGLOLDMCHSGC--NOOMAAVDGELARY 308
Qy          62 G-SCTTTGTAGTAYVMLEPCNTAFAEATIKQIMWDGITITNPESMLYLA--SSGIKWTT 118
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Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rpr

Db 309 GPKCLDAAGTNSKVVQYSCGQDNCK--RLNSDPSGVVQVQSLCLDVANGTANGL 366
QY 119 LTVQTLDTYLAQGM 132
Db 367 IQLVTCNSGNSNRM 380

RESULT 14

33697
arabinofuranosidase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
P/Murphy, J. 1999. D. Parkhill, J. Barrall, B.G. Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A/Reference number: Z21548
A/Accession: T33697
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-475 <MOR>
A/Cross-references: EMBL:AL021411; PDB:1AAL6189.1; GSPDB:GN00070; SCOPDB:SC7H1.02
A/Experimental source: strain A3(2)
C/Genetics:
A/Genes: adB; SCOPDB:SC7H1.02

Query Match 8.2% Score 115.5; DB 2; Length 475;
Best Local Similarity 24.1%; Read No. 0.064; Indels 25; Gaps 10;
Matches 52; Conservative 35; Mismatches 104;

QY 6 SASPTVTVRYGNGKRVNDVDDDFHDSNQIQLWPKSNNDPQQLATIKNDGTHANG-SC 64
Db 37 AAGSGALNRGAGNRC-LDVZSGSDDBALLQLDYCKGGT--NOQWSTDTGRLTVYGKX 93
QY 65 LTTTGYTA--GVTWMPDCTAVREATITWQIMNGIINPRSNLV--AASSG-IGKTLT 120
Db 94 LDVPEHATNPGTRVQWCSGAGNQ--WRNSDGVVGVSGCLERAGAGNGTAVQ 151
QY 121 VOITDYLQGLAGNTPAREVT-----TGRDLCKSNSSGQWYETCP--SSQKQK 174
Db 152 LWTGNGGNGQWGTGLTGPPTDGTCLPETHSSSTGTLAQPKSGWYALNDPTVTNRSR 211
QY 175 WALYGDG-----IREKONODCLTSGRDSYS 201
Db 212 HLYVGSSTSGSGYGMVFSPTNMDMAGQANAN 247

RESULT 15

33904
endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - Oerskovia xanthineolytica
C/Species: Oerskovia xanthineolytica
C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
C/Accession: A39094
R/Shen, S.H.; Christen, P.; Bastien, L.; Siliaty, S.N.
J. Biol. Chem. 266, 1058-1063, 1991
A/Title: Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Express
A/Reference number: A39094; PMID:91093212; PMID:1985933
A/Accession: A39094
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-488
A/Cross-references: GB:M60926; GB:M61734; NID:9150444; PDB:1AA25520.1; PTD:9150445
C/Keywords: glycosidase; hydrolase

Query Match 8.0% Score 114; DB 2; Length 548;
Best Local Similarity 31.3%; Read No. 0.087; Indels 20; Gaps 7;
Matches 41; Conservative 18; Mismatches 52;

QY 16 GSNQARV-----DYRDDPHGNGQIQLWPKSNNDPQQLATIKNDGTHANGSC--TT 67
Db 422 GSNALHSTLCIDFWADPDITNVOVL--ATCSGNAQQWTRGTGTVRALGKCLDVAR 479
QY 68 YGTAGVYVMTEDCK-TARENTITQINDGT--TTPSKNVLAASSGI--KQTLTV 121

Db 480 SGTAADGTAVITVTCNGTNGAQKVT---YDARTKALRNPOSKCLDAQSGAPLNDQKVO 535
QY 122 QTLDTYLAQGM 132
Db 536 WTCQTEAQRW 546

Search completed: December 11, 2003, 13:55:44
Job time: 8.20622 secs

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rfp

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 4.53677 Seconds
(without alignments)
2736.539 Million cell updates/sec

Title: US-09-601-667C-9

Sequence: 1 DDVTCASAEPTVRIVERNQM.....RLIIYPATGKQNMWLPVF 264

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Swissprot_41.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB ID	Description
1	1412	99.6	264	1	MUB VIRAL
2	907.5	64.0	576	1	RIC1 RICCO
3	779	55.0	528	1	ABRA ABRR
4	777.5	54.9	564	1	AGOL RICCO
5	769	54.3	527	1	ABRB ABRR
6	765	54.0	562	1	ABRC ABRR
7	528.5	37.3	563	1	NIOB SMWI
8	428.5	8.9	477	1	KYMA SMWI
9	428.5	8.9	477	1	ABRB STRIO
10	428.5	8.9	477	1	ABRB STRIO
11	428.5	8.9	477	1	ABRB STRIO
12	428.5	8.9	477	1	ABRB STRIO
13	428.5	8.9	477	1	ABRB STRIO
14	428.5	8.9	477	1	ABRB STRIO
15	428.5	8.9	477	1	ABRB STRIO
16	428.5	8.9	477	1	ABRB STRIO
17	428.5	8.9	477	1	ABRB STRIO
18	428.5	8.9	477	1	ABRB STRIO
19	428.5	8.9	477	1	ABRB STRIO
20	428.5	8.9	477	1	ABRB STRIO
21	428.5	8.9	477	1	ABRB STRIO
22	428.5	8.9	477	1	ABRB STRIO
23	428.5	8.9	477	1	ABRB STRIO
24	428.5	8.9	477	1	ABRB STRIO
25	428.5	8.9	477	1	ABRB STRIO
26	428.5	8.9	477	1	ABRB STRIO
27	428.5	8.9	477	1	ABRB STRIO
28	428.5	8.9	477	1	ABRB STRIO
29	428.5	8.9	477	1	ABRB STRIO
30	428.5	8.9	477	1	ABRB STRIO
31	428.5	8.9	477	1	ABRB STRIO
32	428.5	8.9	477	1	ABRB STRIO
33	428.5	8.9	477	1	ABRB STRIO

Result No	Score	Match	Length	DB ID	Description
34	82.5	5.8	1258	1	Y900 ANASP
35	82.5	5.8	1683	1	Y124 ANASP
36	82	5.8	499	1	Y204 ANASP
37	81.5	5.8	248	1	Y432 LISMO
38	81.5	5.8	501	1	Y452 LISIN
39	81.5	5.8	501	1	Y452 LISIN
40	81.5	5.8	552	1	Y452 LISIN
41	81.5	5.8	552	1	Y452 LISIN
42	81.5	5.8	552	1	Y452 LISIN
43	81.5	5.8	552	1	Y452 LISIN
44	81.5	5.8	552	1	Y452 LISIN
45	81	5.7	1207	1	RPOC STRR3

ALIGNMENTS

Result No	Score	Match	Length	DB ID	Description
34	82.5	5.8	1258	1	Y900 ANASP
35	82.5	5.8	1683	1	Y124 ANASP
36	82	5.8	499	1	Y204 ANASP
37	81.5	5.8	248	1	Y432 LISMO
38	81.5	5.8	501	1	Y452 LISIN
39	81.5	5.8	501	1	Y452 LISIN
40	81.5	5.8	552	1	Y452 LISIN
41	81.5	5.8	552	1	Y452 LISIN
42	81.5	5.8	552	1	Y452 LISIN
43	81.5	5.8	552	1	Y452 LISIN
44	81.5	5.8	552	1	Y452 LISIN
45	81	5.7	1207	1	RPOC STRR3

FT VARIANT 231 231 N -> S OR T.
FT VARIANT 231 233 NGL -> KGP.
FT VARIANT 232 235 GLAM -> SIMV.
SQ SEQUENCE 264 AA: 28981 WW: 7DDDC326C6CF6F5A4 CRC64:
Query Match 99.6%; Score 1412; DB 1; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.1e-112;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DQVTCASSEPTRIYVGNKGVVADDDPHGQIQDLPKESNDPNOQMTTTPGCTIS 60
DB 1 DQVTCASSEPTRIYVGNKGVVADDDPHGQIQDLPKESNDPNOQMTTTPGCTIS 60
QY 61 NSCCLTYGYTAGVYVNI-FPCNTPVREPTVQIQMDGFIINPRSNVYLAASGIGTTLT 120
DB 61 NSCCLTYGYTAGVYVNI-FPCNTPVREPTVQIQMDGFIINPRSNVYLAASGIGTTLT 120
QY 121 VQTDVYTLQGMLAGNDTAPREVITYGFEDLCWESNGSVWETCDSSQXQKQALYGD 180
DB 121 VQTDVYTLQGMLAGNDTAPREVITYGFEDLCWESNGSVWETCDSSQXQKQALYGD 180
QY 181 GSIRPKNDQCLTSGDSYGVYTNIVYCSGASGSGRWTFMEALINKTGLAMDVQA 240
DB 181 GSIRPKNDQCLTSGDSYGVYTNIVYCSGASGSGRWTFMEALINKTGLAMDVQA 240
QY 241 NPQLRRITTYFATGKFNQMLVPF 264
DB 241 NPQLRRITTYFATGKFNQMLVPF 264
RESULT 2
TITLE: RICIN
AUTHOR: RICIN
AC P02879; P02880; PRT; 576 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor [contains: Ricin A chain (RNA N-glycosidase)
(BC 3.2.2.22); Ricin B chain).
OS Ricinus communis (Castor bean).
OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eudicotyledons; eudicotyledons; core eudicotyledons; Rosidae;
OC Malvaceae; Malvaceae; Euphorbiaceae; Ricinus.
OC Ricinus communis (Castor bean).
RN [1] TextID:3987;
RP SEQUENCE FROM N.A.
RX MEDLINE=6067214; PubMed=2999712;
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
RT Weaver R.P.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
RT communis";
RT Nucleic Acids Res. 13:8019-8033 (1985).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=9216301; PubMed=1371405;
RA Tregear J.W., Roberts L.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
RT ricin gene and three lectin pseudogenes";
RL Plant Mol. Biol. 18:515-525 (1992).
RN [3]
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=383723;
RA Lamb A., Roberts L.M., Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin";
RN [4]
RN J. Biochem. 148:265-270 (1985).
RP SEQUENCE OF 36-302
RA Yoshitake S., Funatsu G., Funatsu M.;
RT "Isolation and sequences of peptide peptides, and the complete
RT sequence of the chain of ricin-D";
RL Agric. Biol. Chem. 42:1267-1274 (1978).
RN [5]
RP SEQUENCE OF 315-576.
RA Funatsu G., Kimura M., Funatsu M.;
RT "Primary structure of A1a chain of ricin D";
RN [6]
RN Agric. Biol. Chem. 43:2221-2224 (1979).
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=136817;
RA Kimura Y., Kusuku H., Tada M., Takagi S., Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant";
RN [7]
RN Agric. Biol. Chem. 54:157-162 (1990).
RP REVIEW.
RX MEDLINE=21480122; PubMed=1195634;
RA Ohtsuka S., Kozlov J.V.;
RN [8]
RN Toxicol. 39:1723-1728 (2001).
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=87165983; PubMed=158397;
RA Montfort W., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B.,
RT Rubenher E., Xiong N.H., Hamlin R., Robertus J.D.;
RN [9]
RN J. Biol. Chem. 262:5398-5403 (1987).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=9352005; PubMed=180881;
RA Katzin B., Collins E., Robertus J.D.;
RT "Structure of ricin A-chain at 2.5 A";
RN [10]
RN Proteins 10:251-259 (1997).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1881882;
RA Rubenher E., Robertus J.D.;
RT "Structure of ricin B-chain at 2.5-A resolution";
RN [11]
RN Proteins 10:260-269 (1997).
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=7990130;
RA Weston S.A., Tucker A.D., Thatcher D.R., Darbyshire D.J.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution";
RN [12]
RN J. Mol. Biol. 244:410-421 (1994).
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HTS-215.
RX MEDLINE=96374222; PubMed=870513;
RA Day F.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
RT "Structure of ricin A-chain at 2.2-A resolution";
RN [13]
RN J. Biol. Chem. 269:1043-1049 (1997).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9086280;
RA Yan X., Hollis T., Swinich M., Day P., Monzingo A.F., Milne G.W.,
RT "Structure-based identification of a ricin inhibitor";
RN [14]
RN J. Mol. Biol. 266:1043-1049 (1997).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=93165632; PubMed=1287657;
RA Kin Y., Robertus J.D.;
RT "Analysis of several key active site residues of ricin A chain by
RT mutagenesis and X-ray crystallography";
RN [15]
RN Protein Eng. 5:775-779 (1992).
RP FUNCTION: Ricin is highly toxic to animal cells and to a less
RP extent to plant cells. The A chain is responsible for inhibiting
RP protein synthesis through the catalytic inactivation of 60S
RP ribosomal subunits. It acts as a glycosidase that removes a
RP specific adenine residue from an exposed loop of 28S ribosomal
RP rRNA. The loop is involved in the binding of elongation
RP factor-1. The loop is unable to support protein
RP synthesis. The A chain does not have a catalytic site. The
RP per minute, thus inactivating them faster than the cell can
RP new ones. A single A-chain molecule can therefore kill an animal

CC call The B chain binds to cell receptors and facilitates the
CC entry into the cell of the A chain; B chains are also responsible
CC for cell agglutination (lectin activity). It binds to beta-D-
CC galactopyranoside moieties.
CC -I- Specific activity: Anhydrocatalyzes of the N-glycosidic bond at one
CC specific amino acid residue, Asn609.
CC SUBUNIT: Disulfide-linked dimer.
CC -I- DOMAIN: The B chain is composed of two domains, each domain
CC consists of 3 homologous subdomains (alpha beta gamma)
CC -I- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC -I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSE-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC CATALYTIC: CONTAINS 2 HIGH-BLYE LECTIN DOMAINS.
CC -I- CAUTION: THIS ENZYME'S SUBSTRATES HAVE A HIGH NUMBER OF CONFLICTS
CC WITH THE SEQUENCE TRANSFORMER RECODER DNA (REF.1, REF.2 AND REF.3).
CC -I- DAINAMIS: NAME-Protein Spotlight.
CC NOTE=entry 31 of February 2003;
CC WWW='http://www.expasy.org/spottlight/articles/sp1031.html'.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL consortium.
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CC or scientific purposes requires a license agreement (See <http://www.isb-sib.ch/commercial>
CC or send an email to license@sib-ch).
CC -----
CC EMBL_X031979; CAA26939.1; -
CC EMBL_X52980; CAA37095.1; -
CC EMBL_X02388; CAA26230.1; -
CC EMBL_A12892; CAA01058.1; -
CC PIR_A24041; RLCSO.
CC PDB_2A41; 3J-JUN-94.
CC PDB_2A41; 3J-JUN-94.
CC PDB_1P63; 3I-OCT-93.
CC PDB_1IF8; 14-JUN-98.
CC PDB_1IEF; 14-JUN-98.
CC PDB_1IEU; 14-JUN-98.
CC PDB_1R7C; 3I-OCT-93.
CC PDB_1OB8; 16-JUN-97.
CC PDB_1OGT; 16-JUN-97.
CC PDB_1BR5; 02-SEP-98.
CC PDB_1BR6; 02-SEP-98.
CC PDB_1LL3; 16-JAN-02.
CC PDB_1IL4; 16-JAN-02.
CC GlycoSiteDB: f02972.
CC DR InterPro: IPR000772; Ricin_B_lectin.
CC DR InterPro: IPR001574; RIP.
CC DR Pfam: PF00652; Ricin_B_lectin; 6.
CC DR Pfam: PF00161; RIP; 1.
CC DR PRINTS: PR00396; SHIGACIN.
CC SMART: SMO0458; RCIN; 2.
CC DR PROSITE: PS00231; RICIN_B_LLECTIN; 2.
CC DR PROSITE: PS00275; SHIGA_RICIN; 1.
CC KEGG: K05148; Hydroxylase, Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal; 3D-structure.
FT FT SIGNAL 1 315
FT CHAIN 36 302
FT PEPTIDE 303 314 LINKER PEPTIDE.
FT CHAIN 315 576 RICIN B CHAIN.
FT DOMAIN 321 448 RICIN B-TYPE LECTIN 1.
FT RESIDUE 331 373 RICIN B-TYPE LECTIN 2.
FT REPEAT 417 416 1-ALPHA.
FT REPEAT 417 416 1-BETA.
FT REPEAT 462 497 2-GAMMA.
FT REPEAT 501 540 2-BETA.
FT REPEAT 543 570 2-GAMMA.
FT ACT_SITE 212 312
FT DISULFD 294 358 INTERCHAIN.
FT DISULFD 334 353

Query Match	64.0% ; Score 907.5 ; DB 1 ; Length 576 ;
Best Local Similarity	64.8% ; Pred. No. 1, 66-69 ;
Matches 166 ;	Conservative 33 ; Mismatches 60 ; Indels 1 ; Gaps 1 ;
Db	NCBI
Query	5
Db	1
Query	124
Db	137
Query	147
Db	124
Query	184
Db	496
Query	244
Db	556
Query	264
Db	576
RESULT 3	
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ID	ABRA_ABRP
NC	528589 ;
DT	111110 ; 528589 ; 11 ; Created)
DT	01-JUN-1998 (Seq. 29 ; Last sequence update)
DT	28-FEB-2003 (Seq. 41 ; Last seq. update)
DE	Abra-1 precursor [comparative] ; Abra-1 A chain (tRNA N-glycosylase)
OS	(EC 3.2.2.22) ; Abra-1 A chain
OC	Abra-1 precursor (Indian loci) (Crab's eye)
OC	EmuMyoCyt, VitellinMyoCyt, Streptocyt, EmbryoMyoCyt, TracheoMyoCyt, Spermatocyte, MammaryMyoCyt, Endocyt, Core Endocyt, Rosidae
OC	eurosis 1 ; Fabalis ; Fabacae ; Papilionoideae ; Abrae ; Abrae
NCBI	taxid=3816 ;
NC	(11 ;
NC	SEQUENCE FROM N.A.
NC	NCBI:528589 ; Pubmed=642313 ;
NC	HmmC=5132789 ; C=1 ; In J -Y ;
RT	"Primary structure of three distinct isoenzymes determined by cDNA sequencing. Conservation and significance."
RT	J. Mol. Biol. 229:263-267 (1993) ;
RN	[2] ;
RN	SEQUENCE OF 1-251 ;
NC	TISUB=Seq ;
NC	Funatsi G. ; Taguchi Y. ; Kameosono M. ; Yanaka M. ;
NC	The complete amino acid sequence of the A-chain of abra-1, a toxic protein from the seeds of Abra precatorius."
NC	J. Biol. Chem. 268:1095-1097 (1993) ;
NC	SEQUENCE OF 1-251 FROM N.A.
NC	TISUB=Seq ;
NC	MEDLINE=91201329 ; Pubmed=2016300 ;
NC	Evenen G. ; Mathiesen A. ; Sundan A. ;
NC	"Direct molecular cloning and expression of two distinct abra

RT A-chains.";
RT J. Biol. Chem. 266:6848-6852(1991).
RN [4]
RX MEDLINE=92571656; PubMed=1505674;
RA "Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.,
RT "Crystal structure of abrin-a B chain";
RL FRS Lett. 309:115-116(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
RX MEDLINE=95333186; PubMed=7609980;
RA Tahirzy T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
RT "Crystal structure of abrin-a at 2.14 A.";
RL J. Mol. Biol. 250:354-367(1995).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- FUNCTION: THE B CHAIN IS RESPONSIBLE FOR FACILITATING THE
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: contains 2 ricin B-type lectin domains.
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CC -----
DR EMBL; M98344; AAA2624.1; ALT INIT.
DR GENBANK; J25862; NOT ANNOTATED CDS.
DR KJ574230; T828395.
DR PDB; 1A8R; 07-RESD95.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00295; SHIGA_RICIN; 1.
DR K01900; Ricin B-type lectin; Protein synthesis inhibitor; Toxin; Repeat;
KV Glycoprotein; Lectin; 3D-struc; aspartic carboxylic acid.
FT CHAIN 1 251
FT PEPTIDE 252 261
FT CHAIN 262 528
FT DOMAIN 273 400
FT DOMAIN 403 527
FT REPEAT 283 325
FT REPEAT 326 366
FT REPEAT 369 401
FT REPEAT 404 443
FT REPEAT 444 483
FT REPEAT 484 528
FT ACT SITE 164 164
FT ACT SITE 164 164
FT DISULFID 247 269
FT DISULFID 286 305
FT DISULFID 329 346
FT DISULFID 417 430
FT DISULFID 456 473
FT DISULFID 361 361
FT CARBOHYD 401 401
FT CARBOHYD 401 401
FT CONFLICT 202 202
MISSING (IN REF. 2).
FT CONFLICT 298 298
FT CONFLICT 427 427
FT CONFLICT 467 467
FT CONFLICT 483 483
FT TURN 5 8
FT TURN 10 11
FT HELIX 12 28
FT STRAND 12 32
FT STRAND 32 34
FT STRAND 34 36
FT STRAND 42 43
FT HELIX 47 49
FT STRAND 51 57
FT STRAND 63 69
FT TURN 70 72
FT TURN 75 79
FT STRAND 83 86
FT TURN 88 89
FT TURN 92 93
FT HELIX 94 101
FT STRAND 103 106
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FT STRAND 129 129
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FT STRAND 168 168
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FT TURN 319 320
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FT TURN 326 327
FT STRAND 328 332
FT TURN 337 338
FT TURN 340 344
FT TURN 346 348
FT TURN 351 353
FT HELIX 351 353
FT STRAND 353 355
FT STRAND 355 360
FT TURN 360 361
FT STRAND 364 366
FT TURN 367 370
FT STRAND 371 374
FT TURN 380 381
FT STRAND 383 383
FT STRAND 383 383
FT HELIX 385 387
FT HELIX 393 395
FT CONFLICT 398 399

Db	306	CHDEPPIVRIAYGNKLT	CVTVGSEFFPDGNT	QJWPKCKSNIDNWQ	WTLARSTIISNCK	366					
Qy	65	LITVYGVAGYVNI	PDCAINAREAT	ITWIDWGIIT	INPESVLVAASSGKIGTLVLT	122					
Db	366	LITKSPK	PRQGVVITINOS	STAVATK	WIMDRKTI	INPESVLVAASSGKIGTLVLT	422				
Qy	125	DYVIGWMLANP	PAEPIITV	YPRLOMSNG	HWTCJCSGR	QKSNK	YKGSRT	184			
Db	426	IAASGWL	LPNNIT	PFVITIVG	YKMLQANS	KWYLED	TSKKA	EQWALYNDSDH	482		
Qy	185	PKNQOQCLT	SGSDV	YVAIN	YSCGSSG	SRFWT	ITBGA	ILNITK	CLADYVAQANKK	244	
Db	485	PRQIRICG	CLITIDN	IKCTVY	ICSG	SPASSG	QRWFR	KNDG	ITILVNG	LAVDRSDSL	544
Qy	245	PRQIRICG	CLITIDN	IKCTVY	ICSG	SPASSG	QRWFR	KNDG	ITILVNG	LAVDRSDSL	264
Db	545	KQITV	IPRPHNLQ	IMLEP	564						

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CC RESULT 5
CC ABBR ABBR
CC ID ABBR ABBR STANDARD; PRT; 527 AA.
CC AC Q06077; E81374;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 18-DEC-1998 (Rel. 37, Last sequence update)
CC DT 18-FEB-2003 (Rel. 41, Last annotation update)
CC DE Abin-1 precursor [Contains: Abin-b A chain (tRNA N-glycosidase)
CC DS Abin-1 (2,227), Abin-b B chain]
CC OS Eukaryotes; Viridiplantae; Streptophyta; Charophyta;
CC EC Eukaryotes; Magnoliophyta; eudicotyledons; Rosidae;
CC eucotsids I; Fabales; Fabaceae; Papilionoideae; Abteeae; Abnne.
CC NCBI_TaxId=3816;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=93132798; PubMed=84213113;
CC RA Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
CC RT Primary structure of three distinct isoenzymes determined by cDNA
CC RT cloning and sequencing.
CC RL J Mol. Biol. 229:1263-267(1993).
CC [2]
CC RP SEQUENCE OF 260-527.
CC RX TISSUE=Seed.
CC CC MEDLINE=93169023; PubMed=7763422;
CC RA Kimura M., Sumitawa T., Funatsu G.;
CC RT "The complete amino acid sequences of the B-chains of abin-a and
CC RT abin-b, toxic proteins from the seeds of Abutilon theophrasti,"
CC RT Biochem. Biophys. Res. Commun. 57:161-169(1973).
CC CC FUNCTION THROUGH THE CATALYTIC ACTION OF 60S RIBOSOMAL
CC CC SYNTHESIS THROUGH THE CATALYTIC ACTION OF 60S RIBOSOMAL
CC CC SUBUNITS BY REMOVING ABININ FROM POSITION 4,924 OF 28S RNA.
CC CC ABININ-A IS MORE TOXIC THAN RICIN.
CC CC -1 FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC CC FACILITATES THE BINDING OF ABININ TO THE CELL MEMBRANE THAT
CC CC PRECEDES ENDOCYTOSIS.
CC CC -1 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC CC specific aspartine on the 28S rRNA.
CC CC -1 SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC CC -1 COMPOSITION: THE A CHAIN CONSISTS OF 216 AMINO ACIDS, THE B CHAIN
CC CC CONSISTS OF 3 HOMOLOGOUS SUBUNITS, A, B AND C (A, B, AND C).
CC CC -1 SIMILARITY: IN THE N-TERMINAL SECTION RESEMBLES THE RIBOSOME-
CC CC INACTIVATING PROTEIN FAMILY TYPE 2 RIP SUBFAMILY.
CC CC -1 SIMILARITY: Contains 2 ricin B-type lectin domains.
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Query Match	Best Local Similarity	55.3%;	Score 769,	DB 1;	Length 527;
Matches 144;	Conservative 42;	Mismatches 73;	Indels 2;	Gaps 2	
Dr	EMBL; M98345; A343625.1; -				
Dr	PIR; S32430; S32430.				
Dr	HSSP; P1140; 1ABR.				
Dr	Interpro; IPR000772; Ricin_B_lectin.				
Dr	Interpro; IPR001574; RFP.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				
Dr	SMART; SM00458; RICIN. 2.				
Dr	PROSITE; PS00231; RICIN_B_LECTIN; 2.				
Dr	PROSITE; PS00275; SHICACIN; 1.				
Dr	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;				
Dr	Glycoprotein; Lectin; Pyruvate carboxylic acid.				
Dr	EMBL; P00622; Ricin_B_lectin. 6.				
Dr	PIR; P00622; Ricin_B_lectin. 6.				
Dr	PRINTS; PR00346; SHICACIN.				

CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT FREEDOM
 CC ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC N-glycanic residue on the 28S RNA.
 CC -1- SIMILARITY: IN THE N-TERMINAL REGION OF THE RIBOSOME-
 CC -1- INACTIVATING PROTEIN FAMILY TYPE 2 RIB SUBUNIT.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC -----
 DR EMBL: U41299; AA839475.1;
 DR PIR: S37382; S37382;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RLP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR Plant: 14596; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 25
 FT CHAIN 26 297 NIGRIN B A CHAIN.
 FT CHAIN 298 563 NIGRIN B B CHAIN.
 FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 434 559 RICIN B-TYPE LECTIN 2.
 FT REPEAT 316 356 1-ALPHA.
 FT REPEAT 357 397 1-BETA.
 FT REPEAT 400 432 1-GAMMA.
 FT REPEAT 445 482 2-BETA.
 FT REPEAT 483 524 2-BETA.
 FT REPEAT 527 554 2-BETA.
 FT ACT SITE 186 186 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 274 302 BY SIMILARITY.
 FT DISULFID 319 338 BY SIMILARITY.
 FT DISULFID 360 377 BY SIMILARITY.
 FT DISULFID 448 463 BY SIMILARITY.
 FT DISULFID 489 506 BY SIMILARITY.
 FT CARBOHYD 221 221 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAc...) (POTENTIAL).
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 FT CONFLICT 39 39 K -> V (IN REF.2).
 SQ SEQUENCE 563 AA; 62300 MW; F250CB2461BFT1 CRG64;
 Query Match 37.3%; Score 528.5; DB 1; Length 563;
 Best Local Similarity 41.3%; Pred. No. 2.1e-37;
 Matches 109; Conservative 45; Mismatches 103; Indels 7; Gaps 5;
 QY 1 DVTGCSAEPVW-IVGNMCAVVDGDFDNGOIQWESKSNDDPQMTWKEDGTR 59
 DB 298 DEFTCTARTSTANTVNSGDLGVGNGYDTGTPQJWCCQGR--NQRPTSDDTLR 355
 QY 60 SNGSCLTGTYGAGVYVMDNDVAREKNTQINDGNTIPNSVYLAASGKKTTL 119
 DB 356 SNGKCMWANGNSNIVINISNSPAENAIWVEPIGSIWPSGLVWAPLARSITL 415
 QY 120 TVGTDPTLGGWAGNDPAPEVYTGPRDLCKSSNG--GSIVAVETDSGQNGKRAL 177
 DB 416 LLSNNTIYASQGWYTNVAVPVSIVGSKENCLDSKNNGNWMDCEATISIQ--CWAL 474

QY 178 VQDSRPRKQNDQCLSGRSDSYNTIVYSGSAGSGRWTFEGALINLTQANDV 237
 DB 475 VGRITRYNSTGCLVTGNSNSMLIKQGLP--SQRWTFNSGALVNRKSHRWDV 533
 QY 238 AQNPPLRRTIYTPATCKXNDWL 261
 DB 534 RASVSLREIILFPAIDNDCQWV 557
 RESULT 8
 XREF: SMR1
 ID XNN, STPL1 STANDARD; PRT; 477 AA.
 AC P26514; P96464;
 DT 01-NOV-1992 (Rel. 23, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 GN (1,4-beta-D-xylan xylanohydrolase A).
 OS Klebsiella pneumoniae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptococcaceae; Streptococcaceae; Streptococcus.
 RN [1] _taxid=1518;
 RP SEQUENCE FROM N.A.. AND SEQUENCE OF 42-92.
 RX STRAIN=66 / 1326;
 RX MEDLINE=92077439; PubMed=1743521;
 RA Shareck F., Roy C., Yasuchi M., Morosoli R., Kluepfel D.;
 RT "Sequences of three genes specifying xylanases in Streptococcus
 RT 'lividans'."
 RL Gene 107:75-92(1991).
 RN [2]
 RN REVIEWS TO 20 AND 140-141.
 RP STRAIN=66 / 1326;
 RX Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
 RX MEDLINE=9342232; PubMed=8063693;
 RA Derewenda U., Swenson L., Green R., Wei Y.Y., Morosoli R., Shareck F.,
 RA Kluepfel D., Derewenda Z.S.;
 RT "Crystal structure, at 2.6-A resolution, of the Streptococcus lividans
 RT xylanase A, a member of the F family of beta-1,4-D-glycanases."
 RL Biol. Chem. 269(20811-20814(1994).
 RL "The xylanase A of Streptococcus lividans is a member of the F
 RL -1- component of plant cell wall-degrading enzymes, the major
 RL as carbon sources.
 RL sequentially on the substrate to yield xylobiose and xylose
 RL as carbon sources.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC -----
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 CC -----
 DR EMBL: M64551; AAC28525.1;
 DR PIR: J58399; J58399;
 DR PDB: 1BQV; 25-MAY-02.
 DR PDB: 1E0W; 25-MAY-02.
 DR PDB: 1XUL; 19-JUN-02.
 DR PDB: 1KMW; 19-JUN-02.
 DR PDB: 1MC9; 11-SEP-02.
 DR InterPro: IPR001000; Glyco_hydro_10.

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DR BRIC, ALG3125; CNA1689.1; -
DR PR; t35697; t35697.
DR Interpro: IPR005193; Glyco_hydro_62.
DR Interpro: IPR001772; Ricin_b_lectin.
DR Pfam: PF03664; Glyco_hydro_65; 1.
DR Pfam: PF03652; Ricin_b_lectin; 1.
DR SMART: SM00428; Ricin_b_lectin; 1.
DR SMART: SM00428; Ricin_b_lectin; 1.
DR K12an degradation; Hydrolyase; Glycosidase; Signal; Lectin;
KW Complete proteome.
KW SIGNAL.
KW POTENTIAL.
KW ALPHA-L-ARABINOFURANOSIDAB.
KW CHAIN 38 475
KW DOMAIN 39 166
KW RICHIN B-TYPE LECTIN
SEQUENCE 475 AA; 50045 MW; 47E07FE54C660D CRO64;
CRO64

QY 6 SASSEYATVRYBNRGRVYVDDDDCHGCIQIOWPSKSNINPEVQMLTKKDTITRSNG-SC 64
 DB 37 AAGGAGRAKRSNR-EDVAGSODDIALQIDYDCGT--NQQNSIDTSLRLVLYGKC 93
 QY 65 LITVGTGA--GVYVPECNITVBEATIMQIMQNTIINPSENV-VAASG-IKSTTL 120
 DB 94 LNVGHAVTGVPTGVIVNSGGAGMQ--WRVNSDGVVGVSGICLFAASGANTQNVAVO 151
 Gaps: 25
 Mismatches: 57; Conservative: 35; Identical: 104; Indels: 25; Gaps: 10;

Db 152 LMTGNGGNGKWTGLTGTPPTDICALPSTYRWSTGLVLA
QY 175 WALYDGS-----TRKQNDQCLTGRDVS 201

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      RESULT 10
      E15H A19P8
      DT15-0UT-1998  STANDARD;          PRF: 5+8 AA.
      AC C691T6;
      DT 15-JUL-1998 (Rel. 36, Created)
      DT 15-OCT-1998 (Rel. 36, Last sequence update)
      DT 15-JUN-1998 (Rel. 36, Last sequence update)
      Db              212 HUYSTISGSGSYQSWAFSPFTNMDASACQNNMKN 247

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DE glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) (11-23) -beta
DE glucan endohydrolase (11-23) -beta-D-glucanase) .
GV GlcT.
GV Attribacter sp. (strain YCM3) .
OC Bacteroides, Actinobacteridae, Actinobacteriales; Actinomycetales;
OC Micrococci; Micrococcales; Actinobacter.
OX NCBI_TaxID=1667;
RN (1)
RP SEQUENCE FROM N.A.
RF Kacharava T., Aleksova H., Tanaka H., Doi K., Doi K.;
RA Kacharava T., Aleksova H., Tanaka H., Doi K., Doi K.;
CC FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC -1- IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
CC SIMILIARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity)
CC -1- in 1,3-beta-D-glucans.

CC -1- SIMILARITY: BELONGS TO FAMILY 94 OF GLYCOSYL HYDROLASES.
CC
CC
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC
CC
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CC   or send an email to license@isb.sib.ch/).  
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DR   EMBL; D23658; SNA04992.1; -.  
CC   NCBI; D23658; SNA04992.1; -.  
DR   InterPro; IPR000772; Ricin_B_lectin.  
DR   Pfam; PF00653; Ricin_B_lectin_3.  
DR   SMART; SM00451; RICIN.B_LECTIN.1.  
DR   PROSITE; PS50241; RICIN_B_LECTIN; 1  
KW   Hydroxylase; Glycosylase; Signal; Periplasmic; Cell wall; Lectin.  
FT   SIGNAL          1-56  
FT   DOMAIN          422-548  
FT   DOMAIN          548-548  
FT   REGION          422-548  
FT   REGION          548-548  
CC   SEQUENCE      548 AA; 58164 MW; BDE655A1431E75D596 CRC64;  
  
Query Match      8.0%; Score 114.1; DB 1; Length 548;  
Best Local Similarity 31.3%; Pred. No. 0.029;  
Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7  
  
OY    16 GENOMEV-----DYRDDDFHCNQTOLFKSSKNDPNQATIKDGTIRNSGSL--TT 67  
DB    422 GTAGAGIGSTGLCDIYPADPTFTRNQD--ACSGAGAQAQMTRETVIVASGLKLNVAR 479  
OY    68 YGYAPAYGWIPGPC--TANRATITGMWMDNG--HINRSNTVAASSGI--KDTLV 121  
DB    480 SCCTSDTYTWVLYTCNCTGCAQRT---YSATKALNPDSGSCLNDQGANLPIDQRYVL 535  
OY    122 QTDYTTLTGCGN 132  
DB    536 WYNQTFQEQNW 546  
  
RESULT 11  
E13B ORFXA  
ID    E13B ORFXA STANDARD; PRT; 548 AA.  
DC   P22222;1891 [Ref. 19, Created]  
DD   01-0UG-1891 [Ref. 19, Last sequence update]  
DT   01-0UG-1891 [Ref. 19, Last annotation update]  
DI   16-OCT-2001 [Ref. 40, Last annotation update]  
DE   Glucan endo-1,3-beta-glucosidase precursor (SC 3.2.1.39) ((1-3)-beta-  
DE   glucan endohydroxylase) ((1->3)-beta-glucanase).  
OS   Oerskovia xanthineolytica.  
OC   Bacetria; Actinobacteriales; Actinobacteria; Actinomycetales;  
OC   Micrococciaceae; Promotiromonoporaceae; Cellulosimicrobiun.  
RX   NCBI_TextMiner(170).  
RP   SEQUENCE FROM N.A. AND SEQUENCE OF 37-63.  
RX   MEDLINE=J1093212; PubMed=19585933;  
RA   Shen S.-H., Chretien P., Baeten L., Silaty S.N.;  
RA   "Primary sequence of the glucanase gene from Oerskovia  
RA   xanthineolytica: Expression and purification of the enzyme from  
RA   Escherichia coli." 158-163 (1991).  
RT   J. FUNCTIONAL LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.  
CC   -1. FUNCTIONAL LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.  
CC   -1. CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages  
CC   in 1,3-beta-D-glucans.  
CC   -1. STRUCTURAL LOCATIONS: Periplasmic.  
CC   -1. SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.  
CC   -1. SIMILARITY: Contains 1 rich-B-type lectin domain.  
CC   -1. SIMILARITY: Contains 1 rich-B-type lectin domain.  
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC   between the Swiss Institute of Bioinformatics and the EMBL databank.  
CC   The European Bioinformatics Institute. There are no restrictions on its  
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CC   entities requires a license agreement. See http://www.isb-sib.ch/announce  
CC   or send an email to license@isb-sib.ch/.  
DR   EMBL; M60826; AAA25520.1; -.  
DR   PIR; A30964; A30964.  
DR   HSPF; P02879; ZAA1.  
DR   InterPro; IPR000772; Ricin_B_lectin.
```

DR Pfam; PF00652; Ricin B lectin; 3
DR SMART; SMO0458; RICIN_B_LECTIN; 1
DR PROSITE; PS02031; RICIN-B_LECTIN; 1
DR HYDROLASE; Glycosidase; Signal
FT CHAIN 37 548 GLYCIN ENDO-1,3-BETA-GLUCOSIDASE.
FT DOMAIN 432 548 RICHIN B-TYPE LECTIN.
FT DOMAIN 37 430 POSSESSES BETA-GALACTANASE ACTIVITY, BUT IS
UNABLE TO LYSIS VIBRIO CELLS.
FT DOMAIN 472 548 ESSENTIAL FOR THE LYtic ACTIVITY, BUT NOT
FOR THE BETA-D-GALACTANASE ACTIVITY.
SO SEQUENCE 548 AA; 5908 MW; 4153XAAHAIICGARD Cnctel;

Query Match 8.0%; Score 114; DB 1; Length 548;
Best Local Similarity 31.3%; Pred. No. 0.029;
Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

OY 16 GENREV-----DVNDDPFDHGNOIQLPKRSNDPNQDLATRESDTSTNSGSL--TT 67
DB 422 GIGAHILSGSTCLADVMAWDELDTLNVQL--ATGSGAQAQQKRGTDGVIAKLKCDVAR 419
OY 68 YGTGAAGYVMPEDN-EVMEETATIMQMONT--IIPSENFVLAASGI---KEPTLV 121
DB 480 SGFADGGANVAVTYCOTNGTAQAKT---YBTKFKANRPGGXCLDAOGARLAPDSGYVOL 535
OY 122 QTLDTLYLGCGM 132
DB 536 WTCNQTRDQRW 546

RESULT 12
AAPA_STRL1 STANDARD; PRT; 475 AA.
AC AAPA_STRL1
AD P96163;
ID 15-DEC-1998 [Ref. 37, Created]
DT 23-PER-2008 [Ref. 47, last annotation update]
DE Alpha-L-arabinofuranosidase precursor (SC 3.2.1.55) (Arabinosidase).
DN ABRF.
OC Streptomyces lividans.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1916;
RN SOURCE FROM N.A.
RS STRAIN=66 / 1326;
RX MEDLINE=97220396; PubMed=9148759;
FA Vincent P., Shareck F., Dupont C., Morozzi R., Kluepfel D.;
RT "New alpha-L-arabinofuranosidases produced by Streptomyces lividans:
RT cloning and DNA sequence of the arbf gene and characterization of the
RT enzyme." J. 322:845-852 (1997).
FM 12)
CC CC
CC REVISIONS.
RC STRAIN=66 / 1326;
RA Shareck F.;
RB Submitted (JUL-1998) to the EMBL/Genbank/DDBJ databases.
CC -! FUNCTION: HAS A SPECIFIC ARABINOFRANOSE-DEGRADING ACTIVITY ON
CC XYLANS FROM GRAMINEAE. THIS STRAIN PRODUCES AN ARABINOXYLO-GLUCOSIDE
CC AND IT LIBERATES ARABINOSE AND AFTER PROLONGED INCUBATION, THE
CC PURIFIED ENZYME EXHIBITS SOME XYLANOLYTIC ACTIVITY AS WELL.
CC -! CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinofuranoside residues in alpha-L-arabinoxides.
CC -! PATHWAY: xylan degradation.
CC -! SUBCELLULAR LOCATION: Secreted;
CC -! SIMILARITY: BELONGS TO EMIL B-type Lectin domain.
CC -! SIMILARITY: CONCLUDES A HIGH B-type Lectin domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL consortium .
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PC STRAIN-BE1201 N2; PubMed:9525933;
 RA MEDLINE:9525933;
 RA Hagen P K, Nahrke K,
 RT "cDNA cloning and expression of a family of UDP-N-acetyl-D-
 RT galactosamine:polypeptide N-acetyl-galactosaminyltransferase sequence
 RT homologs from *Caenorhabditis elegans*,"
 RL J. Biol. Chem. 273:8268-8277(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE:9525933;
 RX MEDLINE:9525933;
 RA Wilson R, Almsrough R, Anderson K, Baynes C, Barks M,
 RA Bonfield J, Burton T, Connell M, Copey T, Cooper J, Coulson A,
 RA Craxton M, Dear S, Du Z, Durbin R, Favello A, Fraser A,
 RA Fulton L, Gardner A, Green P, Hawkin T, Hillier L, Jier M,
 RA Johnston L, Jones M, Karahaw J, Kirsten J, Laisner N,
 RA Latreille P, Lightning J, Lloyd C, Mortimore B, O'Callaghan M,
 RA Parsons J, Percy C, Rifkin L, Roopra A, Saunders D, Shownkeen R,
 RA Sims M, Smalton N, Smith A, Smith M, Smith M, Vaughan K,
 RA Stinson J, Thierley-Hag U, Thomas K, Smith K, Vaughan K,
 RA Wilson R, Wilson R, Wilson R, Wilson R, Wilson R,
 RA Mohlman P, Watson A, Watson A, Watson A, Watson A,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
 RT elegans*,"
 RL Nature 368:32-38(1994).
 RN [3]
 RP REVISIONS:
 RA Watson R,
 RA "FUNCTION: THIS PROTEIN CATALYZES THE INITIAL REACTION IN O-LINKED
 CC OLIGOSACCHARIDE BIOSYNTHESIS. THE TRANSFER OF AN N-ACETYL-D-
 CC GALACTOSAMINE RESIDUE TO A SERINE OR THREONINE RESIDUE ON THE
 CC PROTEIN RECEPTOR."
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide -
 CC UDP + N-acetyl-D-galactosaminyl-polypeptide.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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 CC -----
 DR EMBL: AF021033, AF021033.1;
 DR EMBL: AF021033, AF021033.1;
 DR PIR: T42243, T42243.4;
 DR MOPREP: ZK68.8, CE29649.
 DR Interpro: IPR001173; Glyco trans 2.
 DR Interpro: IPR000772; Ricin_B lectin.
 DR Pfam: PF00535; Glycoe_transf_2; 1.
 DR Pfam: PF00652; Ricin_B_lectin; 2.
 DR SMART: SM00458; Ricin; 1.
 DR PROSITE: PS00231; Ricin_B_lectin; 1.
 DR TRANSFERASE: glycosyltransferase; Transmembrane; Signal-anchor;
 DR PROSITE: PS00458; Ricin; 1.
 DR PROSITE: PS00231; Ricin_B_lectin; 1.
 DR PRINTS: PR00740; GHYDRBLSE27.
 DR PRODOM: P0002572; Glyco_hydro_GHD_1.
 DR SMART: SM00458; Ricin; 1.
 DR PROSITE: PS00512; ALPHA_GALACTOSIDASE; 1.
 DR PROSITE: PS00231; Ricin_B_lectin; 1.
 DR HYDROLASE: glycosidase; Signal; Glycoprotein; lectin.
 DR SIGNAL
 FT CHAIN 1 31 545 ALPHA-GALACTOSIDASE A.
 FT DOMAIN 35 612 (POTENTIAL).
 FT DOMAIN 478 612 (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 612 aa; 68911 MW; 50312259339958 CkC64;
 Query Match 7.64; Score 107; DB 1; Length 612;
 Best Local Similarity 27.34; Pred. no. 0.13;
 Matches 33; Conservative 23; Mismatches 49; Indels 16; Gaps 6;

GY 148 PROLCRESH-----GGSVWETEDSSKCKCKRRLVGGSGIRKXKNDQDCTNSR-DVST 202
 DB 492 FTEKVDVTHGKQQAPEIQACHAGKNGNA-WELCKGEIR---SDLTCSGHHVYQIS 547
 GY 203 VNIYVSGSAGSGQRWYF---NEGALINLTGTAMDVACAPKLRIRIIPATKRNQK 259
 DB 548 EKLKRSVSKINRVYVEDDQAGTLHKTRKCVTADQSVTLDEC---GLAKDQK 603
 GY 260 W 260
 DB 604 W 604
 RESULT 15
 AGAL ASPNG STANDARD; PRT; 545 AA.
 AC P28351;
 FT 01-DEC-1992 (rel. 24, Created)
 FT 01-DEC-1992 (rel. 24, Last sequence update)
 FT 01-DEC-1992 (rel. 24, Last sequence update)
 FT 01-DEC-1992 (rel. 24, Last sequence update)
 DE Alpha-galactosidase A precursor [EC 3.2.1.22] (Melibiose).
 CR ACIA
 OS Aspergillus niger.
 CC Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Basidiomycota; Trichocommataceae; Aspergillus.
 CC NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 32-59.
 RP MEDLINE:92118893; PubMed:120186;
 RA van der Hende I P., Rosell A.M.M., van Zuijlen C.M., Punt P.J.,
 RA "Cloning and expression of a member of the Aspergillus niger gene
 RT family encoding alpha-galactosidase."
 RL Mol. Genet. 233:404-410(1992).
 CC -1- FUNCTION: REPRESENTS A MINOR EXTRACELLULAR ALPHA-GALACTOSIDASE
 CC -1- ACTIVITY IN A NISER Melibiose, H1210 = galactose + glucose.
 CC -1- CATALYTIC ACTIVITY: Melibiose + H2O = galactose + glucose.
 CC -1- FOR O-GLYCOSYLATION
 CC -1- SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASES.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X63348; CAA44950.1;
 DR PIR: S23582; S23582.
 DR GlycoSiteDB: P28351;
 DR Interpro: IPR002241; Glyco_hydro_27.
 DR Interpro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF00535; Glycoe_transf_2; 1.
 DR Pfam: PF00652; Ricin_B_lectin; 2.
 DR PROSITE: PS00231; Ricin_B_lectin; 1.
 DR PRINTS: PR00740; GHYDRBLSE27.
 DR PRODOM: P0002572; Glyco_hydro_GHD_1.
 DR SMART: SM00458; Ricin; 1.
 DR PROSITE: PS00512; ALPHA_GALACTOSIDASE; 1.
 DR PROSITE: PS00231; Ricin_B_lectin; 1.
 DR HYDROLASE: glycosidase; Signal; Glycoprotein; lectin.
 DR SIGNAL
 FT CHAIN 1 31 545 ALPHA-GALACTOSIDASE A.
 FT DOMAIN 35 612 (POTENTIAL).
 FT DOMAIN 478 612 (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 612 aa; 68911 MW; 50312259339958 CkC64;
 Query Match 7.64; Score 107; DB 1; Length 612;
 Best Local Similarity 27.34; Pred. no. 0.13;
 Matches 33; Conservative 23; Mismatches 49; Indels 16; Gaps 6;

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FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL)
SO SEQUENCE 545 AA; 60148 MW; 2DC5A710CE95D59C CRC64;

Query Match

Best Local Similarity 7.1%; Score 100.5; DB 1; Length 545;
Matches 46; Conservative 43; Mismatches 97; Indels 45; Gaps 8;

QY 22 VDVHDDPFDGNOICLSPSKNDNDQWIKRQGTIRNSGSLTYGTA----- 72
DB 342 LDIILRSIANGDRLTLVANKNT-----IVRDLPVQW/SLTEIDCTVPAEDLMDGKIQ 395
QY 73 ---GVYWIPEGNTAVEATWQ---IWDGIIIPRSNLYLAASGKIGTLTVQTL 124
DB 396 KISDHKIEIASHTIVFRSLIPQGSVFTGLVNTASGNTLAS--NSVAFGSC 452
QY 125 DYLQGMALANDAPREVTYGRDLCHESNGSWTEGDSQKQKQKALYQGSIR 184
DB 453 NERTSQIMQVTSKTPVS--QTQLAADNLYLQKDSIDSDGKVTVPYTGSLK 509
QY 185 PKQFODQCTSGSDSVSTVINISGSGASGSGQWPTNEGAILNLTGLAM 235
DB 510 -NAKTDGCLTBES-----VQWKSQ-----IYERDQYFGIPSGVOL 544

Search completed: December 11, 2003, 14:09:06
Job time : 5.6201 secs

Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
QY 1 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 60
DB 269 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 328
QY 61 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 120
DB 329 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 388
QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 180
DB 389 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 447
QY 181 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 240
DB 448 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 507
QY 241 NPKLRRIIYPATGKPKQWMLPV 263
DB 508 NPKLRRIIYPATGKPKQWMLPV 530

RESULT 2

QBLK02 PRELIMINARY; PRT; 263 AA.
ID QBLK02
DT 01-OCT-2002 (Tremblrel, 22, Created)
DT 01-OCT-2002 (Tremblrel, 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DB Lectin chain B isoform 2 (fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Park C.-H., Song S.K.,
"CDNA cloning and sequence analysis of the lectin genes of the Korean
mistlecote (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.,
Submitted (MAY-2002) to the EMBL/GenBank/DBD databases.
DB Lectin chain B isoform 2 (fragment).
DR EMBL:AF569280; AY046936; F1; B; Lectin.
DR RefSeq: PF00652; R1CIN_B; Lectin; 5.
DR SMART: SMO0458; R1CIN_2.
DR PROSITE: PS00231; R1CIN_B; LECTIN; 2.
FT NON_TER 1
FT NON_TER 263
SQ SEQUENCE 263 AA; 29150 MW; B685EB7C49C8D1F CRC64;

Query Match 79.0%; Score 119.5; DB 10; Length 263;
Best Local Similarity 79.1%; Pred. No. 2, le-86;
Matches 208; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 60
DB 1 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 60
QY 61 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 120
DB 61 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 120
QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 180
DB 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 180

QY 181 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 240
DB 180 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 239
QY 241 NPKLRRIIYPATGKPKQWMLPV 263
DB 240 NPKLRRIIYPATGKPKQWMLPV 262

RESULT 3

QBLK23 PRELIMINARY; PRT; 565 AA.
ID QBLK23
DT 01-MAR-2002 (Tremblrel, 20, Created)
DT 01-MAR-2002 (Tremblrel, 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel, 22, Last annotation update)
DB VLA precursor (EC 3.2.2.22) (RNA N-glycosylase).
DE VLA precursor (EC 3.2.2.22) (RNA N-glycosylase).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA Park W.-B., Lyu S.,
Cloning of Viscum album subsp. coloratum (Korean mistlecote).";
RL Blochm. Biophys. Res. Commun. 0:0-01(2002).
CC -1- SIMILARITY: BEGINS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC -1- SIMILARITY: BEGINS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL: AF569661; AL40417.1; -1-
DR InterPro: IPR000772; R1CIN_B; Lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; R1CIN_B; Lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0458; R1CIN_2.
DR PROSITE: PS00231; R1CIN_B; LECTIN; 2.
RN HYDROLASE; Signal; Toxin.
FT NON_TER 1
FT NON_TER 22
FT CHAIN 23
FT CHAIN 565
SQ SEQUENCE 565 AA; 62401 MW; 991E399AD005F11 CRC64;

Query Match 78.1%; Score 1106.5; DB 10; Length 565;
Best Local Similarity 80.2%; Pred. No. 6, 7e-85;
Matches 211; Conservative 15; Mismatches 32; Indels 5; Gaps 2;

QY 1 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 60
DB 307 DDTGCSAEPYRIVGKMGKRVVADDDPHDQNOIQLPKSKNDPQWLTKRGGTIR 362
QY 61 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 120
DB 363 NSGCLTYGTAGYVYMFECNTATREATIQITNDGTTINPRSLVLAASSGIGTIT 422
QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 180
DB 422 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMSNGSGSVVETCSQKQKALYGD 481
QY 481 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 240
DB 482 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINKTGLAMDVAQA 541
QY 241 NPKLRRIIYPATGKPKQWMLPV 263
DB 542 NPKLRRIIYPATGKPKQWMLPV 564

RESULT 4
QBLK01 PRELIMINARY; PRT; 263 AA.
ID QBLK01

AC 091K01;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Lectin chain B (colortum).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 NCBI_TaxID=159976;
 RX SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 Do M.-S., Song S.K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF508919; AA046937.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR SMART: SM00458; Ricin_B_lectin; 6.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 FT NON TER 1
 FT NON TER 263
 SQ SEQUENCE 263 AA; 29071 MW; 3F9CADA860F61D CRC64;
 Query Match 76.6%; Score 1085.5; DB 10; Length 263;
 Best Local Similarity 77.2%; Pred. No. 1.5e-83;
 Matches 203; Conservative 22; Mismatches 37; Indels 1; Gaps 1;
 QY 1 DDVTGASAEPTVRIYGNKAKYVDVDDPHDQGLMPSKSNDDPMLTTRRGGTTS 60
 DB 1 DDVTGASAEPTVRIYGNKAKYVDVDDPHDQGLMPSKSNDDPMLTTRRGGTTS 60
 QY 61 NSCLTGYGTAGVYVMIPEOCITAVREATTIQTWINDGTTINPRSNLYL--AASGIGKT 120
 DB 61 NSCLTGYGTAGVYVMIPEOCITAVREATTIQTWINDGTTINPRSNLYL--AASGIGKT 120
 QY 121 VOTLDYTLGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 180
 DB 121 VOTLDYTLGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 180
 QY 181 GSIRKQNDQCTLSGRDSYSTVINIYSGASGSGRWFTNESAIIINLTGLANDVAQR 240
 DB 181 GSIRKQNDQCTLSGRDSYSTVINIYSGASGSGRWFTNESAIIINLTGLANDVAQR 240
 QY 241 NSKLRRIIIPATGKKNQMLPV 263
 DB 241 NSKLRRIIIPATGKKNQMLPV 263
 QY 240 NSKLRRIIIPATGKKNQMLPV 262
 DB 240 NSKLRRIIIPATGKKNQMLPV 262
 RESULT 5
 QY 091K03
 ID 091K03 PRELIMINARY; FRT; 266 AA.
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Lectin chain B isoform 1 (fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 NCBI_TaxID=159976;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=2156752; PubMed=1170524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 Do M.-S., Song S.K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF508917; AA046935.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR SMART: SM00458; Ricin_B_lectin; 5.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 FT NON TER 1
 FT NON TER 266
 SQ SEQUENCE 266 AA; 29537 MW; 4A51473C7B94C73 CRC64;
 Query Match 70.5%; Score 999; DB 10; Length 266;
 Best Local Similarity 69.5%; Pred. No. 3e-76;
 Matches 185; Conservative 21; Mismatches 46; Indels 4; Gaps 2;
 QY 1 DDVTGASAEPTVRIYGNKAKYVDVDDPHDQGLMPSKSNDDPMLTTRRGGTTS 60
 DB 1 DDVTGASAEPTVRIYGNKAKYVDVDDPHDQGLMPSKSNDDPMLTTRRGGTTS 60
 QY 61 NSCLTGYGTAGVYVMIPEOCITAVREATTIQTWINDGTTINPRSNLYL--AASGIGKT 117
 DB 61 NSCLTGYGTAGVYVMIPEOCITAVREATTIQTWINDGTTINPRSNLYL--AASGIGKT 120
 QY 118 TLTDTLTGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 177
 DB 118 TLTDTLTGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 179
 QY 121 TLTDTLTGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 179
 DB 121 TLTDTLTGQGLMAGNDTAPREVTIYGFEDLCMESNGSGVWETCGDSQKQKQKVAL 179
 QY 178 YGDSIRKQNDQCTLSGRDSYSTVINIYSGASGSGRWFTNESAIIINLTGLANDV 237
 DB 178 YGDSIRKQNDQCTLSGRDSYSTVINIYSGASGSGRWFTNESAIIINLTGLANDV 239
 QY 238 AANPRLRIIIPATGKKNQMLPV 263
 DB 238 AANPRLRIIIPATGKKNQMLPV 265
 QY 240 AANPRLRIIIPATGKKNQMLPV 265
 DB 240 AANPRLRIIIPATGKKNQMLPV 265
 RESULT 6
 QY 041174
 ID 041174 PRELIMINARY; FRT; 541 AA.
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)
 OS Homo sapiens (caenor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; core eudicots; Rosidae;
 OC eurosidae I; Malpighiales; Euphorbiaceae; Ricinus.
 NCBI_TaxID=3988;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=9338377; PubMed=163311;
 RA Roberts L.M., Tregear G.W., Lord J.M.;
 RL Molecular cloning of ricin".
 RL Targeted Disgn. Ther. 7:81-97(1992).
 CC -1- CATALYTIC ACTIVITY: KNOXHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 OF THE TWO N-GLYCOSIDIC SITES OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: S54056; JAB22582.1;
 DR HSPB: P02879; IIR6;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR SMART: SM00458; Ricin_B_lectin; 6.
 DR PROSITE: PS50231; Ricin_B_lectin; 6.

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DR PFam: PF00161; RNP_1
DR PRINTS; PF00366; SHIGARGCIN.
DR SMART; SMO0458; RIN_C1.
DR PROSITE; PS00241; SHIGAN_B; ACTIN_2.
DR PROSITE; PS00338; SGNACTHORMIN_2; 1.
KW Hydroxylase; Toxin;
FT NON TER 1
FT SEQUENCE 541 AA; 60281 MW; 28752CDBE12E3BD9 CRC64;

Query Match 64.2%; Score 909.5; DB 10; Length 541;
Best Local Similarity 63.8%; Pred. No. 2.5e-68;
Matches 166; Conservative 34; Mismatches 59; Indels 1; Gaps 1;

QY 5 CASASPVYIYVGRNGKRVYVDNDEPHQKQVGLMPEKSNNDPMQIMTAPQSTIRNSNC 64
Db CMDEPPIYVIVGRNGKICVADYRGRFHNGNAQLMPCAKNDTANQMLTKRNDTIRNSKXC 342
QY 65 LITTVGSAVYVYMFPCQTVARATITQIMDNGIINRNSVLAASSGIKGTLVOTL 124
Db 343 LITTVGSAVYVYMYCMTATADTATMDNGIINRNSVLAAASGISTLTVOTN 402
QY 125 DYTIGAGMLANDTAAREVITTVGPRDLCMESNGSVWETCSQKXQKGAIVDGSIR 184
QY 403 IYASQGMPLTNSQPTPTITVGLGICLQANSSQVMEED-SSEKRAQQMAYALDASSIR 461
Db 165 PQKQNDCTSGDSQPTPTITVGLGICLQANSSQVMEED-SSEKRAQQMAYALDASSIR 244
QY 462 PQKQNDCTGDSINIRFVTVKILSGPSSQSGRAMEKDSQGLINVSGLVYDHSBSL 521
QY 245 RRIIVYPAQXGNQMLVEF 264
Db 522 KQIILYDPLGSPNDIWELEF 541

	RESULT 7		
Q41143			
ID	PRELIMINARY;	PRT;	263 AA.
Q41143:			
DR	01-NOV-1996	(TrEMBLrel.) 01,	(Created)
DT	01-NOV-1996	(TrEMBLrel.) 01,	Last sequence update)
DZ	1-MAR-2003	(TrEMBLrel.) 23,	Last annotation update)
DE	Ricin A BETA CHAIN	(Fragment).	
GN	RICIN A BETA CHAIN		
OS	Bakerycots; Vasculariflorae; Streptophyta; Embryophyta; Tracheophytes;		
OC	Semiotropes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
CC	eucosids I; Malpighiales; Euphorbiaceae; Ricinus		
NCBI_TaxID=388;			
OX	[1]		
RS	SEQUENCE FROM N.A.		
KP	RICIN A BETA CHAIN		
RA	Long G.H., Hossain S.E.B., Halling A.C., Halling K.C., Tlalkatane N.,		
RT	Characterization of a cDNA encoding ricin A, a hybrid ricin-Rtms		
RT	characterization of a cDNA encoding ricin A, a hybrid ricin-Rtms		
RL	Plant Mol. Biol. 9:287-295(1987).		
EMBL:	M17631, AAA63506.1; -.		
HHSB:	P02879; ZNMI.		
InterPro:	IPR000772; Ricin_B lectin.		
SMART:	SM00450; RicinA_2		
SMART:	SM00456; RicinA_2		
PROSITE:	PS50231; RICIN_A_Lectin; 2.		
PROSITE:	PS00383; SOMATOCHROPIN_2; 1.		
NON_TER	1		
SEQUENCE	263 AA;		
FT	AB06FD1D1E144 CRC64;		

```

Query Match      63.3%      Score 871;  DB:10  Length 263;
Best Local Similarity 61.3%;  Pred. No. 1.8e-65;
Matches 160;  Conservative 37;  Mismatches 67;  Indels 2;  Gaps 2;

5  CAAEEPTVAVGNNCRVYDDEDDPHGNGQTGAPKSKNNIDNNQIAWIKEDGTSRNSNC 64

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[illegible]

RESULT 8	
Q94BM4	
ID Q94BM4	
CD Q94BM4	
PRELIMINARY:	
PRT: 560 PA.	

DT	01-DEC-2001	(TrEMBLrel. 19, Cereased)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)
DE	type 2 ribosome-inactivating protein cinmamomun II precursor	
DE	(R3.7.2.22) (rRNA N-glycosidase) .	
OS	Cinnamomum camphora (Camphor tree)	
OS	Skeletal muscle, tritrichloroacetate, streptophyta, Embryophyta, Tracheophyta,	
OC	Animalia, Eukaryota, Plantae, Eudicotyledons, Laurales, Gentianales, Cinnamomum.	
OC	NCBI TaxID:13429,	
LN	[1]	
LN	SEQUENCE FROM N.A.	
RA	Yang Q., Gong Z.Z., Liu M.Y.,	
RA	"Molecular cloning of the type 2 RIP (ribosome-inactivating protein)	
RT	genes encoding cinnamomun proteins and study of their expression	
RT	patterns."	
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	
RL	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RNA.	
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	EMBL: AY039802; AK892459.1; E.	
DR	InterPro: IPR007712; Ricin_B_lectin.	
DR	InterPro: IPR001574; RIP.	
DR	Pfam: PF00642; Ricin_B_lectin; 6.	
DR	Pfam: PF00161; Ricin_B_lectin; 6.	
DR	PRINTS: PR00386; SHIGANICIN.	
DR	SMART: SMO0458; RCIN: 2.	
DR	PROSITE: PS50231; RCIN_B_LECTIN; 2.	
KW	Hydrolase; Signal; Toxin.	
FT	SIGNAL	
FT	CHAIN	
FT	33 580	
FT	POTENTIAL.	
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN	
FT	CINNAMOMUN II.	
FT	SEQUENCE 580 AA: 64265 MW: 3754283ECCECCCF CEC64;	

Query Match	61.4%	Score 870	DB 10	Length 580
Best Local Similarity	62.9%	Pred. No. 5	Rec-65	
Matches 166	Conservative 32	Mismatches 64	Indels 2	Gaps 2
Dy	1	DDVTCASAPFETVAVGNGKRVDDVDHDDIOIOLPMSKSNDDPWLTKDKDGIYS	60	
Dy	317	NDDTDADPEFVPRVSRNGKCDVADKANNNGINDLWCKQNSVMDVLTARDPYIYS	376	
Dy	61	NKSLCTITVETAGVYVMIFFCQFVFAKVIQNDGTTINPSSNELYLAASSIGKLTLL	123	
Dy	377	KCKLCTINISGNDVYVLDCKETPLPSSVITPSPALGTTINPSSVLAHSSGNFRTLL	430	
Dy	121	YQTDVTLVAGGRTAGNDVAPREVTYGPDLCSNENSGVITVDDSCDQNMALYED	180	
Dy	437	YQANIVASRQMLAGNTEPEPTYSIVGNDLCQVQNGDMVIVVESSKRG-FKALYED	495	
Dy	181	GSIRKQNDQDCITS-GRDSVSTVIVINVSCGASGSGQWFTNEGATLLNRTKGADMDVQ	239	

Db 496 GSIRPHODRCLSTDMHSGSIIISCSFGSBOQWFWFNOGTLNLKGLVADYK 555
 Oy 240 ANPKLRRIIYPATGKQWMLPV 263
 Db 556 GNSPLHQLIIPATGKQWMLPV 579

RESULT 9

094BM3 PRELIMINARY; PRT; 580 AA.
 ID 094BM3
 AC 094BM3; (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel, 23, Last annotation update)
 DE Type II ribosome-inactivating protein cinamomol III precursor
 DE (EC 3.2.2.22) (RNA N-glycosylase)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinamomol proteins and study of their expression
 RT patterns." (2001) in the EMBL/GenBank/DBJ databases.
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SPECIFIC ACTIVITY: ENDORIBOSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; A039803; AK82460.1; -
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR PRINTS; PR00161; RIP, I.
 DR SMART; SM00396; SHIGARICIN.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 KM Hydrolyase; Signal; Toxin.
 FT SIGNAL 32
 FT CHAIN 33 580
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINAMOMOL III.
 SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7B558 CRC64;

Query Match 60.5%; Score 863; DB 10; Length 580;

Best Local Similarity 62.5%; Pred. No. 2,3e-64;

Matches 165; Conservative 33; Mismatches 64; Indels 2; Gaps 2;

Oy 1 DVTGASAPPTVIVGKNGKIVVDDDFDQNGIOLPESKNDPQGLMTIKDQTTIS 60
 Db 317 NDPTCADPEFTVIRSGNGLCVYDQKXNNGNITLQPFCKQSDVWQMLTARDQTTIS 376
 Oy 61 NSGCLTGYTAGYVYMI FDCQAVREATITQIWDNGIINPSSMVLAASSGIGKTTLT 120
 Db 377 NGKCLTNGSAGDYMIYDCRPVTLASIQWPAAGIINPQSLVLAESGAPETLT 436
 Oy 121 VQTLDTYLGQWLGNDTAPREVTIYGFQDLCHESGASVWETQDSQKQGNALYGD 180
 Db 437 VQADIVASRQWLGNDTAPREVTIYGFQDLCHESGASVWETQDSQKQGNALYGD 495
 Oy 181 GSIRPHODRCLSTDMHSGSIIISCSFGSBOQWFWFNOGTLNLKGLVADYK 239
 Db 496 GSIRPHODRCLSTDMHSGSIIISCSFGSBOQWFWFNOGTLNLKGLVADYK 555
 Oy 240 ANPKLRRIIYPATGKQWMLPV 263
 Db 556 GNSPLHQLIIPATGKQWMLPV 579

RESULT 10

094BM3 PRELIMINARY; PRT; 549 AA.

AC 094BM3
 DT 01-MAR-2001 (TREMblrel, 16, Created)
 DT 01-MAR-2001 (TREMblrel, 16, Last sequence update)
 DT 01-OCT-2002 (TREMblrel, 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinamomol (EC 3.2.2.22) (RNA
 DE N-glycosylase) (fragment)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RT "Molecular cloning of cinamomol A-, B-chain and the expression,
 RT purification, characterization and mutagenesis of the A-chain";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDORIBOSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ACTIVITY: ENDORIBOSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; A255548; AF68978.2;
 DR HSP; P02879; ZANI.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 5.
 DR PRINTS; PR00161; RIP, I.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 KM Hydrolyase; Toxin.
 FT SIGNAL 1
 FT CHAIN 33 549
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINAMOMOL II.
 SQ SEQUENCE 549 AA; 60648 MW; 02607F6507CM44B0 CRC64;

Query Match 58.2%; Score 824.5; DB 10; Length 549;

Best Local Similarity 59.6%; Pred. No. 3.7e-61;

Matches 188; Conservative 32; Mismatches 72; Indels 3; Gaps 2;

Oy 1 DVTGASAPPTVIVGKNGKIVVDDDFDQNGIOLPESKNDPQGLMTIKDQTTIS 60
 Db 285 NDPTCADPEFTVIRSGNGLCVYDQKXNNGNITLQPFCKQSDVWQMLTARDQTTIS 344
 Oy 61 NSGCLTGYTAGYVYMI FDCQAVREATITQIWDNGIINPSSMVLAASSGIGKTTLT 120
 Db 345 NGKCLTNGSAGDYMIYDCRPVTLASIQWPAAGIINPQSLVLAESGAPETLT 404
 Oy 121 VQTLDTYLGQWLGNDTAPREVTIYGFQDLCHESGASVWETQDSQKQGNALYGD 180
 Db 437 VQADIVASRQWLGNDTAPREVTIYGFQDLCHESGASVWETQDSQKQGNALYGD 495
 Oy 181 GSIRPHODRCLSTDMHSGSIIISCSFGSBOQWFWFNOGTLNLKGLVADYK 239
 Db 496 GSIRPHODRCLSTDMHSGSIIISCSFGSBOQWFWFNOGTLNLKGLVADYK 555
 Oy 240 ANPKLRRIIYPATGKQWMLPV 263
 Db 524 GNSPLHQLIIPATGKQWMLPV 579

RESULT 11

094BM3 PRELIMINARY; PRT; 581 AA.
 ID 094BM3
 AC 094BM3; (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel, 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinamomol I precursor
 DE (EC 3.2.2.22) (RNA N-glycosylase)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;

RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamon proteins and study of their expression patterns."

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOPHYTOXIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL: AF000772; RIPO00772; R1P.

DR InterPro; IPR000772; R1P.

DR Pfam; PF00652; R1P; 1. R1P.

DR PRINTS; PR00161; R1P; 1. R1P.

DR SMART; SM00458; R1CIN; 2.

DR PROSITE; PS0231; R1CIN_B; LECTIN; 2.

KW Hydrolase; Signal; Toxin.

FT CHAIN 1 32 POTENTIAL.

FT SIGNAL 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN

FT CHAIN 33 581 CINNAMOMIN 1.

SQ SEQUENCE 581 AA; 64215 MW; 58870 PIs; 66360 CRG64;

Query Match 58.2%; Score 824.5; DB 10; Length 581;

Best Local Similarity 59.6%; Pred. No. 4e-61;

Matches 158; Conservative 32; Mismatches 72; Indels 3; Gaps 2;

QY 1 DDTGSAEPFVRIYGRNKGKVDVDDPHQNOIQLPKSNMPPQMLTKIKDGTIRNS 60

DB 317 NDDTADPFPVRIYGRNKGKVDVDDPHQNOIQLPKSNMPPQMLTKIKDGTIRNS 376

QY 61 NSCLTYGTYAGVYMLPCTAVREATIQIWDNGTIIINRSNLYLAASGIGKTLTVOT 120

DB 377 MKCLITNGYNSDGYVMIYDCTPTMASIQVFNANGIITINQSAVLVASGSRITLVL 436

QY 121 VCTDLYTLGGMLAGNDAPRAVYTVYGFEDLCNHSNGSVYTCDSGQRQKVALYGD 180

DB 437 VQNTVYASQGMLAGNTEPEFTYSIVGFNDLCQANQDQAMWTEKCSYKAO-QNALYTD 495

QY 181 GSIRPQND--QCLTSGRDSYTVIVYSCGSGSGSWYTFEGALINTKGLANDVA 238

DB 496 GSIRPQNDPPAPACPLDINHPQCSITLISCSGSGSGSWYTFEGALINTKGLANDVA 555

QY 239 GANPGRATITVYATGKGNQMLTV 263

DB 556 GSNPLHQTIIIMPATKKNHMLPL 580

RESULT 12

Q06076 PRELIMINARY; PRT; 528 AA.

AC Q06076 (TREMBLrel. 01, Created)

DT 01-NOV-1998 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DB Abrin-d (EC 3.2.2.22) (IRNA N-91ycosidase)

OS Abrus precatorius (Indian licorice) (Crab's eye)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

NCBI_TaxID=3816;

RE SEQUENCE FROM N.A.

RA MEDLINE=3132798; PubMed=842133;

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RT Primary structure of the protein determined by cDNA

RT sequencing; conservation and stability.

RT J. Mol. Biol. 229:263-267(1993)

CC -1- CATALYTIC ACTIVITY: ENDOPHYTOXIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL: M96346; AAA2626.1; -

DR HSP6; P11140; IABK.

DR InterPro; IPR000772; R1CIN_B; LECTIN.

DR InterPro; IPR001574; R1P.

DR Pfam; PF00652; R1CIN_B; LECTIN; 6.

DR PRINTS; PR00161; R1P; 1. R1P.

DR SMART; SM00458; R1CIN; 2.

DR PROSITE; PS0231; R1CIN_B; LECTIN; 2.

DR PROSITE; PS0275; SHIGA_R1CIN; 1.

KW Hydrolase; Toxin.

FT NON TER 1 1

FT NON TER 528 528

SQ SEQUENCE 528 AA; 62624 PIs; 66360 CRG64;

Query Match 53.8%; Score 723; DB 10; Length 528;

Best Local Similarity 54.8%; Pred. No. 6.3e-50;

Matches 143; Conservative 44; Mismatches 72; Indels 2; Gaps 2;

QY 5 GSAS-EPTVRIYGRNKGKVDVDDPHQNOIQLPKSNMPPQMLTKIKDGTIRNS 63

DB 269 GSSEYEPVRIYGRNKGKVDVDDPHQNOIQLPKSNMPPQMLTKIKDGTIRNS 326

QY 64 CLTYGTYAGVYMLPCTAVREATIQIWDNGTIIINRSNLYLAASGIGKTLTVOT 123

DB 329 CLTYGTYAGVYMLPCTAVREATIQIWDNGTIIINRSNLYLAASGIGKTLTVOT 388

QY 124 LDVTLGGMLAGNDAPRAVYTVYGFEDLCNHSNGSVYTCDSGQRQKVALYGD 183

DB 389 NEYLMQGMETNNISFVTSIGSYEDLCQAGSNVLAQCNKXQ-QNALYTDGSI 447

QY 184 EFXQNDQCLTSGRDSYTVIVYSCGSGSGSWYTFEGALINTKGLANDVAQNP 243

DB 448 RSVQNTNCLTSGRDSYTVIVYSCGSGSGSWYTFEGALINTKGLANDVAQNP 507

QY 244 LERITVYATGKGNQMLTV 264

DB 508 LKQILMYTGNQMLTV 528

RESULT 13

Q8SA43 PRELIMINARY; PRT; 382 AA.

AC Q8SA43

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DB Abrin isoform G (EC 3.2.2.22) (IRNA N-91ycosidase)

OS Abrus precatorius (Indian licorice) (Crab's eye)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

NCBI_TaxID=3816;

RE SEQUENCE FROM N.A.

RA Cook J.P.; Roberts L.W.; Lord M.;

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RT Primary structure of the protein determined by cDNA

RT sequencing; conservation and stability.

RT J. Mol. Biol. 229:263-267(1993)

CC -1- CATALYTIC ACTIVITY: ENDOPHYTOXIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL: AF000772; RIPO00772; R1CIN_B; LECTIN.

DR InterPro; IPR000772; R1CIN_B; LECTIN.

DR Pfam; PF00652; R1CIN_B; LECTIN; 6.

DR SMART; SM00458; R1CIN; 2.

DR PROSITE; PS0231; R1CIN_B; LECTIN; 2.

DR PROSITE; PS0275; SHIGA_R1CIN; 1.

KW Hydrolase; Toxin.

FT NON TER 1 1

FT NON TER 382 382

SQ SEQUENCE 382 AA; 42743 MW; 60843 PIs; 66360 CRG64;

Query Match 52.8%; Score 748.5; DB 10; Length 382;
Best Local Similarity 54.3%; Pred. No. 5.9e-55;
Matches 139; Conservative 41; Mismatches 75; Indels 1; Gaps 1;

QY 9 EPTVAVGNNGEYVDVDDPDHGNQIQAMPKSNNDPNQWITTEKDTIRANSGLTTF 68
DB 128 EPTVAVGNNGEYVDVDDPDHGNQIQAMPKSNNDPNQWITTEKDTIRANSGLTTF 187
QY 69 GTVAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 128
DB 188 GTVAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 247
QY 129 GQCNLAGNDTAPREVITVGFEDLCESNGSGYVWETCSQXQKQKVALYDPSIRPK 188
DB 248 RQCKRTGNDTSPEVTSIAGISDCQWESNEMVLADQNKKEQ-QVALYDPSIRPK 306
QY 189 ODQCLTSGRDSYVTVINVSQSGASQWPTWEGATILNKTGLADPQANKEKRII 248
DB 307 TNNCLTSADHKQGSTVLMGCSNGASQWPTWEGATILNKTGLADPQANKEKRII 366
QY 249 IYPATGKNQWMLPEV 264
DB 367 IYPATGKNQWMLPEV 382

RESULT 14

ID Q9M69 PRELIMINARY; PRT; 547 AA.
AC Q9M69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preprogastrin (EC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Rattus preprogastrin (Indian litorice) (Crab's eye).
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC NCBI_Taxid=3816;

RP SEQUENCE FROM N.A.
RX MEDLINE-20102702; PubMed-10636890;
RA Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
RN Primary structure and function analysis of the abrus preprogastrin
RT Rattus preprogastrin (Indian litorice) (Crab's eye).
FT J. Biol. Chem. 275:1897-1901 (2000).
CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF190173; AF283093.1; .
DR HSSP; P11146; IABR.
DR INTERPRO; IPR000772; R1CIN_B_lectin.
DR Pfam; PF00652; R1CIN_B_lectin.6.
DR Pfam; PF00165; R1P_1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; R1CIN.2.
DR PROSITE; PS00231; R1CIN_B_lectin.2.
DR PROSITE; PS00275; SHIGA_R1CIN.1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 547 AA; 61248 MW; 3584325235A1BD CRC64;

Query Match 52.8%; Score 748.5; DB 10; Length 547;
Best Local Similarity 54.0%; Pred. No. 1e-54;
Matches 141; Conservative 40; Mismatches 78; Indels 2; Gaps 2;

QY 5 CSAS-EPTVAVGNNGEYVDVDDPDHGNQIQAMPKSNNDPNQWITTEKDTIRANSGLTTF 63
DB 288 CSAS-EPTVAVGNNGEYVDVDDPDHGNQIQAMPKSNNDPNQWITTEKDTIRANSGLTTF 347

QY 64 CLTGYAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 123
DB 348 CLTGYAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 407
QY 124 LDVTLQCGMLAGNDTAPREVITVGFEDLCESNGSGYVWETCSQXQKQKVALYDPSIR 183
DB 408 LDVTLQCGMLAGNDTAPREVITVGFEDLCESNGSGYVWETCSQXQKQKVALYDPSIR 466
QY 184 RPKQNDQCLTSGRDSYVTVINVSQSGASQWPTWEGATILNKTGLADPQANKEKRII 243
DB 467 RPKQNDQCLTSGRDSYVTVINVSQSGASQWPTWEGATILNKTGLADPQANKEKRII 526
QY 244 IRRITVATGKNQWMLPEV 264
DB 527 IRRITVATGKNQWMLPEV 547

RESULT 15

ID Q9M28 PRELIMINARY; PRT; 573 AA.
AC Q9M28;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA N-glycosidase)
GN LECRAX.
OS Rattus preprogastrin (Indian litorice) (Crab's eye).
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC Eukaryota; Chordata; Strepsorhiza; Eumetazoa; Tracheophyta;
OC NCBI_Taxid=3816;
RN [1]
RP SEQUENCE FROM N.A.
RX van Damme E.J.M., Peumans W.J.,
RA "this (this) hololactase var. professor Blaauw) plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue."
FT J. Biol. Chem. 275:1897-1901 (2000).
CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF256084; AF256093.1; .
DR INTERPRO; IPR001574; R1P.
DR Pfam; PF00652; R1CIN_B_lectin.6.
DR Pfam; PF00165; R1P_1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; R1CIN.2.
DR PROSITE; PS00231; R1CIN_B_lectin.2.
DR PROSITE; PS00275; SHIGA_R1CIN.1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 573 AA; 63759 MW; 1414A3BACD4F5C CRC64;

Query Match 48.0%; Score 679.5; DB 10; Length 573;
Best Local Similarity 48.2%; Pred. No. 1e-54;
Matches 133; Conservative 40; Mismatches 89; Indels 3; Gaps 3;

QY 1 DWTYVAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 60
DB 311 DWTYVAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLTQTLDTLT 370
QY 61 NSGCLTGYAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLT 120
DB 371 NSGCLTGYAGYVYVPCNTAVREAVTQWDEKTIINPBNLVLAASGIGTTLT 429
QY 121 VQTLDTLQCGMLAGNDTAPREVITVGFEDLCESNGSGYVWETCSQXQKQKVALYDPSIR 179
DB 430 VQTLDTLQCGMLAGNDTAPREVITVGFEDLCESNGSGYVWETCSQXQKQKVALYDPSIR 488
QY 180 DGSIRKQNDQCLTSGRDSYVTVINVSQSGASQWPTWEGATILNKTGLADPQANKEKRII 239
DB 489 DGSIRKQNDQCLTSGRDSYVTVINVSQSGASQWPTWEGATILNKTGLADPQANKEKRII 548

us-09-601-667c-9.rsp

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QY      240 ANPKRKRIITYPATGTGNOMLJFV 264
      : : : : : : : : : : : : : : : :
Db      549 SDPSLQDIITWSTGTGNQWTFTE 573
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Job time : 21.3487 secs